Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors

Inventors: Sridhar Ramaswamy, et al.

Dietinction	Distance	Perm 1% P	Perm 5% F	Perm (user) F	Feature C	Desc
	0.5000343	0 7140383	0.625628	0.46998745	19973_xpt at	ORF2: function unknown from Human Tigger1 transposable element, complete consensus sequence./ntype=DNA /annot=CDS
1 Bladder	0.5004972		0.580119	0,4378299 200010	00010_at	Germ line pseudogene for immunoglobulin rappa light of all peptide and variable region (subgroup V kappa I)
	0.4811056	0.6442664	0.558641	0.42185774 M31667_f		at CYTOCHROME P450 IA2
	0.4796712	0.6275353	0.545335	0.4101013 U49974	U49974_f_at	at Mariner2 transposable element, complete consensus sequence EST-ve04h07.r1 Homo sapiens cDNA clone 116797 5' similar to
5 Bladder	0.4633824	0.6154791	0.536003	0.40168163	T89571 f at L00389 f at	0.40168163 T89571 f at contains Alu repetitive element; (from Genbank)
6 Bladder	0.4475702	t t	0.021201	X X 0 3894528†	X52426_s_a	KRT13 Keratin 13
7 Bladder	0.437072	0.597.2022	0.020003	0.00		EST: EST17092 Aorta endothelial cells, TNF alpha-treated Homo
o Dobbot	0.4328913	0.5927864	0.51606	RC_AA30,3840424 44_f_at	RC_AA3043 44_f_at	RC_AA3043 sapiens cDNA 3' end similar to EST containing Alu repeat, mRNA 44 f_at sequence. (from Genbank)
o Diaunei	0.100	- i			Z19574_ma	
9 Bladder	0.4179855	0.5864499	0.511478	0.3795739 1_at	1_at	1 at Cytokeratin 1/
40 Bladder	0.4038961	0.5832233	0.506805		t	clone 783987 5', mRNA sequence. (from Genbank)
11 Bladder	0.4004278		1		0.37135372 Y07755_at	S100A2 gene, exon 1, 2 and 3
12 Bladder	0.3904162				₹i	DGS-F partial mKNA
13 Bladder	0.3821097	7 0.5749506			M74093 at	G1/S-SPECIFIC OYOLIN E
14 Bladder	0.380486	0.3804864 0.5716851	_			BACE Billelationia attugon
15 Bladder	0.3804649	9 0.5670317	0.489875	0.35994408 079301	3 U/9301 at	Olioped Annual School
18 Bladder	0.3804649	9 0.5661115	0.486512		7 U79301_at-2	0.35749477 U79301_at-2 Human clone 23842 mRNA sequence
17 Bladder	0.3795788				2 S79854 at	Type 3 iodothyronine delodinase
48 Bladder	0.3795788	8 0.5618347	0.482676		3 S79854 at-2	0.35260853 S79854_at-2 Deiodinase, iodothyronine, type III
19 Bladder	0.3735957				0.35047776 M65199_at	EDN2 Endothelin 2
20 Bladder	0.371968	0.3719681 0.5599971	1 0.479021	1	5 M19045 f e	0.34866765 M19045_f_at LYZ Lysozyme

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						HG3236-	
46	46 Bladder	0.2944566	0.5259358	0.448763	0.3161997	HT3413_f_at	0.3161997 HT3413 f at Neurofibromatosis 2 Tumor Suppressor (Gb:L27065)
į	:	1		(RC_AA4492	RC_AA4492 EST: xx03h11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
47	47 Bladder	0.2940576	0.5249827	0.447903	0.31523636 15	15_at	clone 785445 3', mRNA sequence. (from Genbank)
48	48 Bladder	0.2896088	0.5235943	0.447287	0.31431654 302871	J02871 s at	s at CYP4B1 Cytochrome P450 IVB1
49	49 Bladder	0.2892569	0.5219361	0.44638	0.31362706 M27826 at	M27826_at	Endogenous retroviral protease mRNA
50	50 Bladder	0.2879725	0.5209997	0.44545	RC_A 0.3127739 47_at	RC_AA1916 47_at	Ceruloplasmin (ferroxidase)
51	Bladder	0.2878275	0.5197005	0.444737	RC_A 0.3121669 64 at	RC_AA4469 64_at	RC_AA4469 Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete 64 at cds
52	52 Bladder	0.2859805	0.519376	0.443783	0.31148654	M86757_s_a t	S100A7 S100 calcium-binding protein A7 (psoriasin 1)
53	53 Bladder	0.2849908	0.5183376	0.443014	0.3106054 M14091 at	M14091 at	THYROXINE-BINDING GLOBULIN PRECURSOR
54	54 Bladder	0.2819153	0.5181242	0.442297	RC_A 0.3099225 51_at	RC_AA4534 51 at	EST: zx45a09.s1 Soares testis NHT Homo sapiens cDNA clone
55	55 Bladder	0.28164		0 441948	RC_A 0.30888793 59_at	A0013	EST: zh83d11.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
						41-	
56	56 Bladder	0.2761128	0.5164211	0.441108	0.30826807	H12969_s_a t	Albumin, Alt. Splice 3. Missplicing In Alloalbumin Venezia
57	Bladder	0.2755032	0.5156131	0.440289	0.30754557 U39487	at	XDH Xanthine dehydrogenase
58	58 Bladder	0.2752715	0.5147324	0.439671	A 0 30675669 +	AA252752_a	AA252752_a EST: zs26b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
59	59 Bladder	0.275238		0.438724	0.3059757 U51587	U51587 at	Goldi complex autoantigen coloin-07 mRNA
90	60 Bladder	0.2750438	0.2750438 0.5137218	0.438434	0.3053376 M60828		FGF7 Fibroblast growth factor 7 (keratinocyte growth factor)
61	61 Bladder	0.2740574		0.437479	0.30452663 X83618	at	Clone HSH1 HMG CoA synthase mRNA, partial cds
62	62 Bladder	0.272605	0.5126445	0.436951	0.3038781 U05861	्य	DDH1 Dihydrodiol dehydrogenase
63	Bladder	0.2710716	0.5120996	0.435736	0.3033949	RC_D59354 i at	EST: Human fetal brain cDNA 3'-end GEN-020E05, mRNA sequence. (from Genbank)
64	64 Bladder	0.2691142	0.5112219	0.434842	0.30258542	Z78285 f at	0.30258542 Z78285 f at mRNA sequence
65	65 Bladder	0.2685153	0.5103946	0.433993	0.30199873 J00124	J00124_at	KERATIN, TYPE I CYTOSKELETAL 14
99	66 Bladder	0.267924	0.5097284	0.433258	0 30147517 1	00137_cds	GHRF gene (growth hormone releasing factor) extracted from Human growth hormone-releasing factor (GRF) gene goon 1.
67	67 Bladder	0.2666138	0.5094423	0.432798	0,3009288 D87024	87024_at	Immunoglobulin lambda gene locus DNA, clone:92H4

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68 Bladder	0.266528	0.5088778	0.432136	RC 0.300221557	RC_AA1942 57_r_at	Contains ESTs, STSs and GSSs
69 Bladder	0.2664737	0.5080214	0.431398	0.29978427 T92512_at	F92512 at	Ye24g11.r1 Homo sapiens cDNA clone 118724 5'. (from Genbank)
70 Bladder	0.263522	0.5079261	0.430434	0.29906005 36	RC_AA0191 36_s_at	EST: ze58h09.s1 Soares retina N2b4HR Homo sapiens cDNA clone 363233 3', mRNA sequence, (from Genbank)
71 Bladder	0.2633922	0.5076373	0.430079	0.29859278	J02973_rna1 at	THBD gene extracted from Human thrombomodulin gene
72 Bladder	0.2592166	0.5074905	0.429281	0.2978743 H16876	416876 at	Ym34f05.r1 Homo sapiens cDNA clone 50123 5', (from Genbank)
73 Bladder	0.2590196	0.5071446	0.428868	0.29738238 J04093	1	
74 Bladder	0.2589375	0.5064912	0.4281	0.2967745	M31776_s_a t	BRAIN NATRIURETIC PEPTIDE PRECURSOR
75 Bladder	0.2584704	0.2584704 0.5051627	0.427958	0.2963655 Z48199 at	Z48199 at	SDC1 Syndecan 1
76 Bladder	0.2584312	0.5051627	0.427493	0.29592586	AA406087_s at	TAL1 (SCL) interrupting locus
77 Bladder	0.2580246	0.5046264	0.427095	0.2954576 M17236	M17236 at	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(2) ALPHA CHAIN PRECURSOR
					33	Rho7 gene extracted from Human BRCA1, Rho7 and vatl genes, and
/8 Bladder	0.2548651	0.5038334	0.42671	0.2950282 2_at	2_at	ipf35 gene, partial cds
70 Diados	0.0540600		77 (22 (7			
/ 9 bladder	0.2540633	0.5033087	0.425944	0.29452837	1_at	Gene encoding prepro form of corticotropin releasing factor
80 Bladder	0.2521889	0.2521889 0.5032067	0.425558	0.2939812 M92449	M92449_at	LTR mRNA, 3' end of coding region and 3' flank
81 Bladder	0.2482/04	0.5021519	0.424709	0.29351172 L40904	-40904_at	LGALS1 Ubiquinol-cytochrome c reductase core protein II
82 Bladder	0.2482704	0.5016	0.423835	0.29309762 L40904 at-2	.40904_at-2	Peroxisome proliferative activated receptor, gamma
83 Bladder	0.2470583	0.5045603	0.423187	RC_A	RC_AA1810	EST: zp67b07.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 625237 3' similar to contains element MIR repetitive
				000000000000000000000000000000000000000	X14008_rna	definent,, unava sequence. (non Gendank)
84 Bladder	0.2435404		0.422982	0.29208043	1_f_at	Lysozyme gene (EC 3.2.1.17)
85 Bladder	0.2431545	0.5006249	0.422559	0.29175875 L34355	.34355 at	(clone p4) 50 kD dystrophin-associated glycoprotein mRNA
86 Bladder	0.2431177	0.4993878	0.422214	0.29134393 X78678	(78678 at	KHK Ketohexokinase (fructokinase)
87 Bladder	0.2423082	0.4987399	0.421638	0.29083067 U04313	J04313_at	PI5 Protease inhibitor 5 (maspin)
88 Bladder	0.241649	0.498558	0.421146	0.29030737 D38024 at		Facioscapulohumeral muscular dystrophy (FSHD) gene region, D4Z4 randem repeat unit
89 Bladder	0.237779	0.498558	0.420855	0.28989312	AA365031_s at	EST: EST75974 Pineal gland II Homo sapiens cDNA 5' end, mRNA sequence (from Genbank)
On Bladder	0 9375737	40707040	O TOOL O			

Amerika den bemerkan dem men men mengan pengan peng

04 Bladder	0 2348844	0.4973496	0.42026	RC_AA4 0.2891052 06 s at	200	Sulfotransferase, estrogen-preferring
או חוממפני	200				16_a	
92 Bladder	0.2347219	0.497176	0.419864	0.28859422 t		Transcription factor 9 (binds GC-rich sequences)
93 Bladder	0.2344337	0.4966071	0.419805	AV 0.2883126a	8_8	clone 810754 5', mRNA sequence. (from Genbank)
				H		
94 Bladder	0.2338483	0.2338483 0.4950363	0.419115	0.28790048 HT4204_at		G1 Phase-Specific Gene
95 Bladder	0.2333825	0.2333825 0.4947473	0.418585	0.28760573 J05459_at		GSTM3 Glutathione S-transferase IVI3 (Drain)
96 Bladder	0.2310942	0.4947179	0.418104	RC_A 0.28733584 28_at	A0195	EST: ze55b02.s1 Soares retina Nzb4nK notito saptetis czrvz dorte 362859 3', mRNA sequence. (from Genbank)
97 Bladder	0.2304104	0.4945694	0.417913	0.28686494 S85963_at		Insulin receptor substrate-1 [human, skeletal muscle, mRNA, 5828 nt]
98 Bladder	0,2269905	0.4937859	0.417057	0.28648204 D14539 at		Human mRNA for LTG19. (from Genbank)
				<u> </u>	HG4099- HT4369_s_a	
99 Bladder	0.2261536	0.4934233	0.416613	0.28594053 t		Adrenergic Receptor, Alpha 1b
100 Bladder	0.2240019	0.493311	0.416367	0.28555343 5_st	AFFX-BioDn- 5_st.	AFFX-BioDn-5_st (endogenous control)
404 Diodor		0.4994493	0.416122	AFFX-1	AFFX-BioDn-5 st-2	AFFX-BioDn-5 st (miscellaneous control - 11k chips)
IOI DIACUEI	1	- 1		1	HG880-	
102 Bladder	0.2225575	5 0.4920135	0.41574	0.2848314 HT880_	1T880_at	Mucin 6, Gastric (Gb:L07517)
	T	(RC_D60246	EST; Human fetal brain cDNA 3'-end GEN-093H03, mRNA sequence.
103 Bladder	0.2222761	0.491765	0.415431	0.28452864	्यं	(from Genbank)
104 Bladder	0.2219926	3 0.4916041	0.414911	0.28418133 U78313_at	J78313_at	Myogenic repressor I-mf (MDFI) mRNA
				1	HG415-	olding Colibbia
105 Bladder	0.2218411	1 0.4908/51	0.414432	0.20392010 11413	11410 at	EST. vioRen2 11 Homo saniens CDNA clone 147098 5'. (from
106 Bladder	0.220422	2 0.4906752	0.414305	0.2835213 R80351	380351 at	Genbank)
		(Yj03b09.r1 Homo sapiens cDNA clone 147641 5' similar to
107 Bladder	0.2185662	2 0.489544	0.414071	0.28320196 R81217	381217 at	(HUMAN);contains Alu repetitive element;. (from Genbank)
408 Bladder	1			0 28279746	RC_AA4602 21 at	EST: zx67a02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796490 3', mRNA sequence. (from Genbank)
					RC_AA2931	EST: zt55e05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
109 Bladder	0.2163227	7 0.489161	0.412978	0.28249595	63 at	clone 7262723, mKNA sequence. (Iforn Genoalik)
110 Bladder	0.213694	4 0.4890391	0.412707	0.2821371	U48436_s_a t	FMR2 Fragile X mental retardation 2

				Mr. Bull Badt Hr. Hull Griff		alone president and account to the second se
111 Bladder	0.2136638	8 0.4886639	0.412328	RC 0.28179055 76	RC_AA3982 76_at	EST: zt60c07.s1 Soares testis NHT Homo sapiens cDNA clone 726732 3, mRNA sequence (from General)
112 Bladder	0.2124692	2 0.4883141	0.411691	0.28133968 W25945	W25945_at	EST: 17c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence (from Genhank)
113 Bladder	0.2095443	3 0.4861237	0.411485	0.28107503 \$82472	te 677688	Beta -pol=DNA polymerase beta (exon alpha to exon VII region)
114 Bladder	0.2085519	1 1				Indinan, Genomic, 124 nt, segment 1 of 2]
115 Bladder	0.2051885	5 0.485773	0.410788		0.28023028 X92475 at 2 ITBA4 2000	TRAY ASSOCIATION OF PUTATIVE KINGS finger protein, partial
116 Bladder	0.2051885	0.4856327	0.410303	L.	X92475 at	ITBA1 protein
117 Bladder	0.2042837	0.4854372	0.410004		L10377 s at	0.27974427 L10377 s at (clone CTG B37) mBMA
118 Bladder	0.203303	0.4847722	0 409887	0.27043682	AA167824_a	Section 1 many sequence
119 Bladder	0.2025079		0.409387	0.27905178 U60521	U60521 at	Cell division cycle 27
120 Bladder	0.2005113	0.4836244	0.409351	0 27870348 11360 at	11360 24	Systems professe ICE-LAP6 MKNA
121 Bladder	0.1985588	0.4834217	0.408793	HG742.	HG742-	Protocadnerin 42 mRNA, 3' end of cds for alternative splicing PC42-8
122 Bladder	0.1977808	1	0.000000	140100177.0	HG3432-	Latent Membrane Protein Lmp1
		1	0.400200	U.Z/808493 HT3621 HG3897	HT3621 at HG3897	Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 4, K-Sam Iv
123 Bladder 124 Bladder	0.193588	0.193588 0.4832549	0.408	0.27770907 HT4167	174167_at	Sodium Channel. Tyne III Alpha Subumit Brain
125 Bladder	0.1917242	0.4823633	0.407447	0.27743426 L20859 at	20859 at	Leukemia virus receptor 1 (GLVR1) mRNA
			0.00	0.211 10912 MT7484	477484 at	SPRR1B Small proline-rich protein 1B (cornifin)
126 Bladder	0.1886425	0.4816808	0.40615	0.27682626 1 f at	1_f_at	Antigen (MAGE-1) gene
127 Bladder	0.1874011	0.481662	0.406085	0.27646986 t	U08854_s_a t	IDP officerroad designations of the second s
128 Bladder	0.1869247	0.4815364	0.405623	0.27613884 t	AA444115_a	EST: zv51b08.r1 Soares testis NHT Homo sapiens cDNA clone
129 bladder	0.1868608	0.4811476	0.405244	0.27586403 M68840 at		MAOA Monoamine oxidate A
130 Bladder	0.1853088	0.4805843	0.404335	0.27548274	-	EST: Human fetal brain cDNA 3'-end GEN-102809, mRNA sequence.
131 Bladder	,	0.4805036	0.404256		A4213	EST: zugzdd4.st Soares ovary tumor NbHOT Homo sapiens cDNA
132 Bladder	0.1849799	0.4804439	0.403551	0.2748993 R11267	37 at	Cidne 739207 3', mRNA sequence, (from Genbank) Homo sapiens chromosome 19, cosmid 523330
133 Bladder	0,1838469	0.4800442	0.403114	HG3543- 0.2745337 HT3739_at	HG3543- HT3739_at	Insulin-Like Growth Factor 2
134 Bladder	0.1838098 0.4797981	0.4797981	0.403079	0.27426526 t	A099726_a	AA099726_a EST: zk86e10.r1 Soares pregnant uterus NbHPU Homo sapiens
						The sequence (from Genbank)

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135 Bladder	r 0.1827677	0.4797327	0.402715	0.27386442 X63755_at	t High-sulphur keratin
136 Bladder	0.1826186	0.4783266	0.402638	X56411_rna 0.27360818 1_at	ADH4 gene for class II alcohol dehydrogenase (pi subunit), exon 1
137 Bladder	r 0.1820319	0.478011	0.402448	RC_AA6001 0.27323318 50 at	01 EST: ae50d12.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950327 3', mRNA sequence. (from Genbank)
138 Bladder	r 0.181527	0.4777031	0.402212	0.2729088 L11708_a	at HSD17B2 17 beta hydroxysteroid dehydrogenase, type 2
139 Bladder	r 0.1814934	0.4775387	0.402193	0.2725679 R11710	at Transcobalamin I (vitamin B12 binding protein, R binder family)
	-			_	S
140 Bladder		0.180324 0.4774376	0.402158	0.27234975_at	clone 724313 5', mRNA sequence. (from Genbank)
141 Bladder	r 0.1786799	0.4773319	0.401829	0.27209738 X86163_a	at BDKRB2 Bradykinin receptor B2
142 Bladder	r 0.178492	0.476809	0.401671	0.27175963 U82303_at	
143 Bladder	r 0.1781216	0.4767463	0.401172	0.27164498 M94856	at FATTY ACID-BINDING PROTEIN, EPIDERMAL
144 Bladder	r 0.1779615	0.4756579	0.400715	0.27139875 U21931_at	it FBP1 Fructose-bisphosphatase 1
145 Bladder	0 1772622	0 4752239	0.400527	AC002450_0 2710882 t	Tal BAC clone GS244B22 from 7d21-d22 complete sequence
146 Bladder	1	-1	0.400298	M94167	at HGL Heregulin alpha
147 Bladder	r 0.1763088	0.4748522	0.400075	0.27047795 U61741 <i>«</i>	at Clone 18 (HL-18), dynein heavy chain (Dnahc14) mRNA, partial cds
148 Bladder	r 0.1757367	0.4746358	0.399853	HG4036- 0.27018142 HT4306 at	†
0 0 0		770774	000000		J04152_rna1 M1S1 gene extracted from Human gastrointestinal tumor-associated
150 Bladder	r 0.1732341		0.339288	0.20992038 s at	anigen GA/33-1 protein gene, cione usono
ייי בייי	1		0.033170	0.2031 0400 733203	
151 Bladder	r 0.1731842	0.473917	0.3989	0.2694124 U13680_at	at LDHC Lactate dehydrogenase C
152 Bladder	r 0.1731842	0.4738257	0.398534	0.26923758 U13680	at-2 Lactate dehydrogenase C
153 Bladder	r 0.1726749	0.4736018	0.39833	0.26886386 L13286_at	Mitochondrial 1,25-dihydroxyvitamin D3 24-hydroxylase mRNA
154 Bladder	r 0.1724232	0.4727036	0.397941	0.26854777 M64347	FGFR3 Fibroblast growth factor receptor 3 (achondroplasia, at thanatophoric dwarfism)
155 Bladder		0.17125 0.4724708	0.39794	0.26832888 W52431	EST: zc45b12.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325247 5' similar to SW:WDNM_RAT P14730 WDNM1 at PROTEIN. [2] PIR:S07807;, mRNA sequence. (from Genbank)
156 Bladder	r 0.1711476	0.4723066	0.397812	0.2681159 X60483	at H4/d gene for H4 histone
157 Bladder	r 0.1697957	0.4722235	0.397312	0.26771313 \$76965	Protein kinase inhibitor [human, neuroblastoma cell line SH-SY-5Y, at mRNA, 2147 nt]
158 Bladder	r 0.1695036	0.4717567	0.396946	0.2675112 L76465_a	at 15-HYDROXYPROSTAGLANDIN DEHYDROGENASE
159 Bladder	r 0.1670327	0.4715059	0.396541	RC_AA2358 0.26719064 03 i at	58 EST: zs42g06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687898 3', mRNA sequence. (from Genbank)
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CONCLAC				
0.1523489	1	0.389374	0.260719931	Derts Disease candidate gene
0.1514157	0.4636369	0.389343	0.26059705 U17566 at	SLC19A1 Solute carrier family 19 (folate transporter), member 1
				EST: zv26h12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
			~	754823 5' similar to contains Alu repetitive element;, mKNA
0.1510678	0.4633779	0.389199	0.26036578 at	sequence. (from Genbank)
0.1493747	0.1493747 0.4630102	0.388338	0.26025838 U90437_at	RP homolog mRNA, 3'UTR region
0.1486966	0.4628564	0.387982	0.25989565 L13436 at	Guanylate cyclase mRNA, complete mature peptide
0 7 7 7		0.77740	0.05064708 1108443 -+	Cockayne syndrome complementation group A CSA protein (CSA)
0.1483010	- 1	0.301118	0.23304100 U20413 at	
0.1458209	0.4623764	0.387711	RC_AA0045 0.25943288 21_at	Prostate cancer overexpressed gene 1
0.1430561	0.4621076	0.387191	0.25922918 J03915_s_at	at CHGA Chromogranin A
				CO: 2A1 Collagen, type II, alpha 1 (primary osteoarthritis,
0.1426495		0.387139		spondyloepiphyseal dysplasia, congenital)
		-	AA156215 a	EST: zo48h03.r1 Stratagene endothelial cell 93/223 Homo sapiens AA156215 a cDNA clone 590165 5' similar to contains element LTR8 repetitive
0.1402592		0.386983	0.25883964 t	element;, mRNA sequence. (from Genbank)
			D87002 cds	POM121-like 1 gene extracted from Human (lambda) DNA for
0.1400141	0.4610898	0.386866	0.25847828 2_at	immunoglobin light chain
0.1371618	0.4607078	0.386488	0.2581948 M27878_at	ZNF84 Zinc finger protein 84 (HPF2)
0.1359859	0.4605887	0.386441	0.2580553 D17793_at	DDH1 Dihydrodiol dehydrogenase
				ZNF42 Zinc finger protein 42 (myeloid-specific retinoic acid-
0.1359222	0.4602003	0.386036	0.2577661 M58297_at	responsive)
				EST: zk97d12.r1 Soares pregnant uterus NbHPU Homo sapiens
				cDNA clone 490775 5' similar to gb:L32179 Human arylacetamide
0 4358307		0 205885		AA122302_a deacetylase mKNA, complete cds. (HUMAN);, mKNA sequence.
0.100000	L	0.000000		(ioii) Odibain)
0.1357712		0.385622		Claudin 4
0.1357086		0.385516	0.25719333 L17330 at	Pre-T/NK cell associated protein (6H9A) mRNA
0.1356579		0.385479	0.25691405 S58733 at	Pp. 5.2
0 1332773	i	0.385202		(genomic clones lambda-[SK2-T2, HS578T]; cDNA clones RS-[3,4, 6]) cHa-ras1 proto-operate complete coding sequence
0.1323236		0.385044	н	ESK Estrogen receptor
0.1323236	1	0.384958	a) (
0.1321859	ł .	0.384709	X90579_s_a	-
	0.1486966 0.1485016 0.1430561 0.1426495 0.1371618 0.1371618 0.1359859 0.1359877 0.135772 0.135773 0.135773 0.1357336 0.132773 0.1323236	0.1486966 0.4628564 0.1485016 0.4625492 0.1458209 0.4623764 0.1430561 0.4621076 0.1426495 0.4618579 0.1371618 0.4607078 0.1359859 0.4605887 0.1359859 0.4605887 0.1358307 0.4598061 0.1357712 0.4596236 0.135773 0.4598063 0.135773 0.4599572 0.1323236 0.458384121 0.1323236 0.4583841		0.387982 0.25989565 0.387719 0.25964788 0.387711 0.25923288 0.387711 0.25922918 0.386983 0.25883964 0.386488 0.25847828 0.386441 0.2580553 0.386441 0.2580553 0.385625 0.2577661 0.385516 0.25738043 0.385516 0.25779333 0.385502 0.25738043 0.385502 0.25738043 0.385502 0.25738043 0.385502 0.25738043 0.385506 0.25691405 0.385504 0.25691405

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Docket	No.: 2825.2020-002
Title:	Genetic Markers for Tumors
Invento	rs: Sridhar Ramaswamy, et al.

207 Bladder	0 1321776	0.4583044	0.384104	RC_A	AA1506	RC_AA1506 EST: zl46a03.s1 Soares pregnant uterus NbHPU Homo sapiens
208 Bladder	0.1318411			0.255430341128055	8055 at	Month Macrophage attention of American (from Genbank)
209 Bladder	0.131518	0		0.25529942 U09850	11	ZNF143 Zinc finger profein 143 (clone nHZ-1)
210 Bladder	0.131518	0.4575949		0.25509372 U0	9850 at-2	0.25509372 U09850 at-2 Zinc finger protein 143 (clone pHZ-1)
211 Bladder	0.1312656	0.4575049	0.383516	X87 0.2548345 t	K87871_s_a	HEPATOCYTE NUCLEAR FACTOR 4
212 Bladder	0.1305731	0.4574514	0.382963	M6: 0.25465825 t	M62628_s_a t	Alpha-1 lg germline C-region membrane-coding region 3' and
213 Bladder	0.1301464	0.4573334	0.382934	0.25448054 N40774	0774_at	EST: yw81e10.r1 Homo sapiens cDNA clone 258666 5'. (from Genbank)
214 Bladder	0.1291867	0.457138	0.382732	0.2542403 N29076	9076 at	EST: yx41e01.r1 Homo sapiens cDNA clone 264312 5'. (from Genbank)
215 Bladder	0.1286372	0.4568807	0.382551	0.25397208 D45370		ApM2 mRNA for GS2374 (unknown product specific to adipose fissue)
216 Bladder	0.1267606	0.4563995	0.382377	0.25373286 W27720	at	Protocadherin 9
217 Bladder	0.1251471		0.382213	0.25353587 UGG		MAGE-9 antigen (MAGE9) gene
218 Bladder	0.1228662		0.382141	0.2532871 U03090		Ca2+-dependent phospholipase A2 mRNA
219 Bladder	0.1227494		0.381948	0.25299013 L14812	1812_at	RBL1 Retinoblastoma-like 1 (p107)
220 Bladder	0.1226272		0.381754	0.25286514 Z49826	3826 at	Hepatocyte nuclear factor 4, gamma
221 Bladder	0.1218462	0.4555458	0.381525	0.2527358 U76369	æ.	Cationic amino acid transporter-2B (ATRC2) mRNA. partial cds
				ŰΞ.		
222 Bladder	0.1214202	0.4548251	0.381504	HT3 0.25235754 t	HT3519_s_a t	ld1
223 Bladder	0.1210718	0.4545756	0.381286	0.2521806 t	U23430_s_a	CCKAR Cholecystokinin A receptor
224 Bladder	0.1201641	0.4545501	0.38099	0.2520379 N88827	#	EST: K5685F Fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K5685 5' similar to EST(Y103A03.R1), mRNA sequence. (from Genhank)
225 Bladder	0.1198097	0.4543718	0.380809	0.2518914 M13955	7	Mosothalial Loratin V7 (time II) - DNIA 21 - 1
226 Bladder	0.1197636	0.4541487	0.380737	0.251751 U17033	at .	180 kDa transmembrane PLA2 receptor mRNA
227 Bladder	0.1197636	0.4541327	0.380312	0.251514 U17	.033 at-2	0.251514 U17033 at-2 Human 180 kDa transmembrane PI A2 recentor mPNA
228 Bladder	0.1195144	0.4540066	0.380061	0.2513118 98	RC_AA4782 98_s_at	Human apM2 mRNA for GS2374 (unknown product specific to adipose tissue), complete cds
229 Bladder	0.1191743	0.4539329	0.379897	0.25112566 J032	242 s_at	0.25112566 J03242_s_at IGF2 Insulin-like growth factor 2 (somatomedin A)
230 Bladder	0.1185377	0.4537219	0.379699	0.25089055 34_a		Golgi SNAP receptor complex member 2

Docket No.	: 2825.2020-002
Title: Gen	etic Markers for Tumors
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231 Bladder	0.1166809	0.4536924	0.379043	0.25061813 M20030 f		at Small proline rich protein (sprtl) mRNA, clone 930
232 Bladder	0.1165407	0.4532436	0.378869	0,25044206 L36644	36644 at	Receptor protein-tyrosine kinase (HEK7) mRNA, 3' end
233 Bladder	0.1160006	0.4531906	0.378785	0.2503087 S66896_at	66896_at	SCCA1 Squamous cell carcinoma antigen 1
234 Bladder	0.115523	0.4529906	0.37865	0.25006074 U12139	112139_at	Alpha1(XI) collagen (COL11A1) gene, 5' region and exon 1
235 Bladder	0.1153378	0.4528299	0.37847	0.24985552 D79995	79995_at	KIAA0173 gene
236 Bladder	0.1153347	0.4525504	0.378374	A 0.24971482t	AA191072_a t	EST; zq43c11.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632468 5', mRNA sequence. (from Genbank)
237 Bladder	0.1151569	0.4521225	0.378062	0 2494406 97	RC_AA2533	Homo canians clone 24659 mBNA ceditance
238 Bladder	0.1150993		0.37796	0.24923792 M64936	164936_at	Retinoic acid-inducible endogenous retroviral DNA
239 Bladder	0.1140868	0.4514787	0.377625	RC_A 0.249107 10 at	RC_AA5984 10 at	EST: ae48b06.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950099 3', mRNA sequence. (from Genbank)
240 Bladder	0.1137273	0.451315	0.377383	0.24896084 D50582	50582 at	Inward rectifier K channel
241 Bladder	0.1128431	0.4512457	0.37728	0.24870318 S69369	69369 at	PAX3 Paired box homeotic gene 3 (Waardenburg syndrome 1){alternative products}
242 Bladder	0.1125664	0.4510102	0.37719	0.24852617 U11872 at	11872 at	Interleukin-8 receptor type B (IL8RB) mRNA, splice variant IL8RB1, partial cds
243 Bladder	0.1114162	0.4509441	0.3777167	0.2483537 M69225_at	169225_at	Bullous pemphigoid antigen (BPAG1) mRNA
244 Bladder	0.1107282	0.4506999	0.376905	RC 0.24801525 61		EST: zx97c05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 811688 3' similar to SW:RB25_RABIT P46629 RAS-RELATED PROTEIN RAB-25.;, mRNA sequence. (from Genbank)
245 Bladder	0.1092077	0.4502715	0.376715	U.24789566 t	U06641_s_a t	UDP glycosyltransferase 2 family, polypeptide B15
246 Bladder	0.1089967	0.4502694	0.376627	RC 0.24755578 77	RC_AA4432 77_at	Peroxisomal biogenesis factor 11A
247 Bladder	0.1085787	0.4499911	0.376484	M 0.24 7 3274 t	M12963_s_a t	ADH1 Alcohol dehydrogenase 1 (class I) alpha polymontido
248 Bladder	0.1081563	0.4499092	0.376362	0.24715394 X78549	78549 at	Brk mRNA for tvrosine kinase
249 Bladder	0.1074152	0.4498538	0.376034	0.24706167 X07730	11	APS Prostate specific antigen
250 Bladder	0.1071856	0.4497513	0.375816	0.24685101 L37199 at		(clone cD24-1) Huntington's disease candidate region mRNA fragment
251 Bladder	0.107177	0.4496127	0.375695	A 0.24649942 t	A027760_a	AA027760_a EST: HPLA_CCLEE_40f6ar HPLA CCLee Homo sapiens cDNA, t mRNA sequence. (from Genbank)
252 Bladder	0.1066559	0.4495788	0.375688	0.24634053 Y10275	at	L-3-phosphoserine phosphatase
253 Bladder	0.1051963	0.4494627	0.375335	0.24608266 ₂	87023_cds at	J1 gene extracted from Human (lambda) DNA for immunoglobin light chain
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254 Bladder	0.103103	0.4409240	0.01	AA282944 a	FST: 21508 11 NCI CGAP GCB1 Homo sapiens cDNA clone
255 Bladder	0 1045492	0.4488328	0.374925	0.24571495 t	
חחחחח		1		The state of the s	EST: zu41a09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
				RC_AA4775	
256 Bladder	0.1037243	0.4487698	0.374847	0.24553433 41_at	mRNA sequence. (from Genbank)
257 Bladder	0.1036713	0.4487619	0.374716	0.24533431 L32164 at	Zinc finger protein mRNA, 3' end
258 Bladder	0.1033749	0.4485939	0.374597	0.24522878 D88422 at	CYSTATIN A
259 Bladder	0.1033559	0.4483732	0.374326		Calcyclin
260 Bladder	0.103298	0.4478444	0.37427	0.2448629 M17316 at	Gamma-A-crystallin gene (gamma-G5), exon 3
261 Bladder	0.1032866	0.4477599	0.374207	0.24467142 D82636 at	EST: similar to none, mKINA sequence. (Irom Genuanik)
262 Bladder	0.1021394	0.4476731	0.374118	0.24449421 M31166 at	PTX3 Pentaxin-related gene, rapidly induced by IL-1 Deta
263 Bladder	0.1017572	0.4475309	0.373963	0.24418119 L48211 at	Angiotensin II receptor gene
			0000000	X82279_s_a	Eas Ano-1 cana (promoter and exon I)
264 Bladder	0.1002536	0.44/2213	0.373803	1,400,6047.0	7 1060 J Chalenge Sources the NTODAMI 037934 Homo
				AA130614 e	Zo10f0Z,r1 Stratagene neuroepitrieituri in zirzywii 357 zo4 riorio sapiens cDNA clone 567291 5' similar to TR:G1125026 G1125026 3-AA130614 a HYDROXYACYL COA DEHYDROGENASE:;; mRNA sequence.
265 Bladder	0.0978928	0.447211	0.37355	0.24383032 t	(from Genbank)
266 Bladder	0.0971292	0.4470733	0.373509	0.24365549 M26665_at	HISTATIN 3 PRECURSOR
267 Bladder	0.0970921	0.4467145	0.373438	0.24346629 Z15005_at	CENPE Centromere protein E (312kD)
268 Bladder	0.0969751	0.4466168	0.373278	0.24331836 M92357 at	B94 PROTEIN
				20011	OR17-228 gene extracted from Human olfactory receptor gene cluster
; ;			0.070004	0.0000/0.500 0.0000/0.500	OD17 25 periodogones
269 Bladder	0.090790	0.446361	0.37.3224	0.243 13343 1 at	
270 Bladder	0.0965342	0.4462171	0.372896	0.24308938 83_at	clone 784146 3', mRNA sequence. (from Genbank)
271 Bladder	0.09642	0.4459868	0.372862	0.24286085 H08988 at	EST: v/96d07.r1 Homo sapiens cDNA clone 46139 5'. (from Genbank)
272 Bladder	0.0961804			0.24270768 L14565 at	PERIPHERIN
273 Bladder	0.0961784		0.3	0.24264991 X90908 at	Ileal lipid binding protein mRNA
	0 0050074		0.979480		
275 Bladder	0.0956522	- !	0.371914		Placenta copper monamine oxidase mRNA
276 Rladder	0.095388	0 0953885 0 4455582	0.371872		Involucrin gene, exon 2
277 Bladder	0.0942626	0.0942626 0.4455047	0.37163		Protein phosphatase 2A beta subunit mRNA
278 Bladder	0.0933272	0.0933272 0.4454729	0.371611	0.2419099 M21494_at	CKM Creatine kinase, muscle
10000	1100000	7 0 1170010		1- 070001 10011100	Alacha C tains and tail the tail of

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors

Inventors: Sridhar Ramaswamy, et al.

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AA464368_s EST: zx81c11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	CIONE 810164 5, MKNA sequence. (from Genbank)	GRP Gastrin-releasing neptide	HPD-1 (hPD-1) mRNA	GCAP-Il/uroquanylin precursor	ZI80f04.r1 Soares testis NHT Homo sapiens cDNA clone 728671 5'	repetitive element;; mRNA sequence. (from Genbank)	EST: zs53c11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701204 5' similar to TR:G849227 G849227 SIMII AR TO		VAC1P: ,, mRNA sequence. (from Genbank)	PMS8 mRNA (yeast mismatch repair gene PMS1 homologue), partial cds (C-terminal region)	HLA-DQB1 Major histocompatibility complex, class II, DQ beta 1		Uncoupling Protein Ucp	RYR2 Ryanodine receptor 2 (cardiac)		RC_AA2333 EST: zr48f03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	666653 3', mRNA sequence. (from Genbank)	Deleted in split hand/split foot 1 (DSS1) mRNA	MAC30 mRNA, 3' end	Hepatic nuclear factor 1-alpha (TCF-1-alpha) gene, promoter region and partial cds	Beta subunit of epithelial amiloride-sensitive sodium channel	Alpha-cardiac actin gene, 5' flank and	Metallothionein I-B gene	HISTONE H1'	RC_AA2564 EST: zr81e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	08Z1Zb 3, mKNA sequence. (from Genbank)	Gamma-B-crystallin gene (gamma 1-2)	Choline Acetyltransferase	Variant urokinase plasminogen activator receptor (uPAR2) mRNA, partial cds	INPP1 Inositol polyphosphate-1-phosphatase
	at D40023	0.24123172 K02054 at	0.24100913 U64863 at	0.24080348 Z70295 at	, 5	AAJ3000J_ t		AA286726_a	7 t	9 D38503 at		HG3492-	at	at	0.23959109 X98330 at-2	RC_AA2333	3 71_at		0.23893073 L19183_at	ŧ	at	0.23819833 J00073 at		0.23792812 X03473_at	RC_AA2564	-	at	HG4051- 45807 HT4321_at	37565 X74039 at	20981 L08488 at
0 044 4000	0.24149861	0.2412317	0.2410091	0.2408034	THE PROPERTY OF THE PROPERTY O	0.24059094			0.24038087 t	0.24018839 D38503	0.23999457 M24364		0.2398406	0.23969305 X98330	0.2395910		0.23943353 71 at	0.239118	0.2389307	0.23849869 U73499	0.2384067 X87159	0.2381983;	0.2380985	0.2379281	0.0077706	0.2311123.0	0.23765811	0.2374580	0.2373756	0.2372098
0077700	0.371286	0.371218	0.37095	0.370718		0.370633			0.370261	0.370106	0.369734		0.369659	0.369659	0.369498		0.369191	0.369039	0.368855	0.368644	0.368509	0.368486	0.368362	0.368288	0 369105	0.000.0	0.36778	0.367632	0.367386	0.367176
0 4464696		0.4450832	0.4450159	0.4443892		0.4443661			0.4441937	0.4438813	0.4438038		0.4433568	0.442713	0.4426481		0.442355	0.4422826	0.4420766	0.4417574	0.4416733	0.4416101	0.4412853	0.4412217	0.4440428	041	0.4407405	0.4406396	0.4405462	0.4405345
0.0047383	0.0911961	0.091681	0.0914684	0.0912739		0.0912671			0.0898263	0.0896721	0.0895167			0.0892752	0.0892752				0.0886999	0.0866702	0.0860137			0.0845381	0.0840654		0.0838388	0.0835978	0.0830292	0.0825923
280 Bladder	281 Bladder	282 Bladder	283 Bladder	284 Bladder		285 Bladder			286 Bladder	287 Bladder	288 Bladder		289 Bladder	290 Bladder	291 Bladder		292 Bladder	293 Bladder	294 Bladder	295 Bladder	296 Bladder	297 Bladder	298 Bladder	299 Bladder	300 Bladder		301 Bladder	302 Bladder	303 Bladder	304 Bladder

litle: Genetic Markers for Tumors nventors: Sridhar Ramaswamy, et al. WT1 {antisense promoter, intron 1} [human, kidney, Genomic, 780 nt] AA018852_a EST: ze55a07.r1 Soares retina N2b4HR Homo sapiens cDNA clone DNL1L gene extracted from Homo sapiens chromosome X region gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 EST; af61a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone DCC=deleted in colorectal cancer {alternatively spliced, exon 1A} from filamin (FLN) gene to glucose-6-phosphate dehydrogenase NMDA receptor subtype 2B subunit (GRIN2B) mRNA, partial cds EST: yi33h04.r1 Homo sapiens cDNA clone 141079 5' similar to KNG gene (kininogen) extracted from Human kininogen gene CGM7 Carcinoembryonic antigen gene family member 7 [human, brain tumor, tumor no. 245, mRNA Partial, 216 nt] SH3-binding domain glutamic acid-rich protein 1046480 3', mRNA sequence. (from Genbank) 362868 5', mRNA sequence. (from Genbank) Indian hedgehog protein (IHH) mRNA, 5' end Basic Transcription Factor 2, 34 Kda Subunit 0.23570235 S72493_s_at KERATIN, TYPE I CYTOSKELETAL 17 HGMP071 gene for olfactory receptor aminin S B3 chain (LAMB3) gene TNNI1 Troponin I, skeletal, slow GC-Box binding protein BTEB2 0.23511922 J00209 f at IFNA10 Interferon, alpha 10 (HUMAN);. (from Genbank) HOXB1 Homeo box B1 , alpha-2 (VI) collagen Hair keratin, hHb6 G6PD) gene's Homeo box B1 YRRM1 X16666 s a AA249611_a 44140_cds U17760_rna M11437 cds RC_AA6211 0.23597614 31_at 0.23448847 X99142 at 0.23484787 X76059 at 0.23461165 M20777 at æ X16666 s 0.23549393 D14520 at 0.23546825 X64994 at 0.23615982 HT4010_at 0.23583408 S79781 at 0.23675118 D90276 at 0.23381096 J04760_at 0.23665693 R66772 at 0.23649456 L38517 at 0.23405662 | S81294 HG3740-0.2336519 4 s at 0.2343265|1 at 0.23684542 at 0.23349553|t-20.23343538 0.23528568 0.23408811 0,237051 0.364284 0.364161 0.364826 0.364502 0.366402 0.365998 0,365939 0.365573 0.365528 0.365182 0.36508 0.3649990.364758 0.365871 0.366712 0.367116 0.367049 0.366917 0.366792 0.366081 0.0811965 0.4400393 0.366988 0.367128 0.367067 0.0711982 0.4372383 0.0762364 0.4387546 0.4374299 0.0751428 0.4386492 0.0719037 0.4381318 0.07168 0.4380594 0.071674 0.4379069 0.4377245 0.0748573 0.4384134 0.4393560.0791087 0.4392524 0.0788124 0.4390661 0.0784234 0.4389373 0.0781659 0.4389108 0.0743545 0.4383839 0.0743271 0.4382954 0.0730864 0.4382481 0.4403704 0.0816293 0.4402723 0.0813425 0.4400959 0.0798617 0.4395228 0.0825844 0.4404194 0.0711982 0.0712361 0.0817482 0.079809

313 Bladder

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FIG. 1N

327 Bladder

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328 Bladder	lder	0.0710842	0.4370078	0.363812	HG4749 0.23330604 HT5197	HG4749- HT5197_at	Calmitine Calcium-Binding Protein, Mitochondrial
329 Bladder	lder	0.0707451	0.4368897	0.363323	0.23317932	Z80345_rna 1_s_at	SCAD gene, exon 1 and joining features
330 Bladder	lder	0.0706855	0.4368044	0.363309	0.23304388 W28091	W28091 at	EST: 41h4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
334 Bladdor	į	0.0704994	0.4284468	0.00000	000000000000000000000000000000000000000	RC_AA6088	EST: af04e03.s1 Soares testis NHT Homo sapiens cDNA clone
332 Bladder	Je Je	0.070108		0.36375	0.23300986 02_at	12_at	1030684 3', mRNA sequence. (from Genbank)
333 Bladder	lder	0.0700822	0.4362766	0.36308	0.23284133 Y00503		KRT19 Keratin 19
334 Bladder	der	0.069082	0.4360632	0.363032	0.23266093 W02342 at	W02342 at	Homo sapiens putative transmembrane protein (CLN5) mRNA,
335 Bladder	der	0.0688592	1	0.362743	H 0 23247996 t	AA043601_a	Uhimillin-coninatina anama ESH (hamalagain to your 11000)
336 Bladder	der	0.0679561	J	0,362692	RC_A 0.23228332 97 at	RC_AA4355 97_at	EST: zt85g06.s1 Soares testis NHT Homo sapiens cDNA clone
337 Bladder	der	0.0677295	0.0677295 0.4355727	718698 0	0 23244087 073042		EST: yi55f09.r1 Homo sapiens cDNA clone 143177 5' similar to
338 Bladder	der	0.0674489	0.0674489 0.4352745	0.362198	0.23191448 X54925	X54925 at	MMP1 Matrix metalloproteinase 1 (interstitial collamenase)
339 Bladder	der	0.0666082	0.4349769	0.362187	RC_A 0.23172474 46 at	RC_AA4180 46 at	EST: zv97f10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
340 Bladder	der	0.0662417	0.4349625	0.362012	0.2315955 t	VAZ80228_a	AA280228_a EST: zt04c11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
341 Bladder	der	0.0659497	0.4347339	0.361957	0.23149377 31	RC_AA4820 31 at	Ribosomal profein 1.37
342 Bladder	der	0.0655879	0.4346328	0.361864	HG3987- 0.23130578 HT4257 at	HG3987- HT4257 at	Cpa-Enriched Dna. Clone F06
343 Bladder	der	0.0654644	0.4345666	0.361771	0.23115334 47 at	10	EST: zv04a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 752624 31 mRNA sequence (from Genhank)
344 Bladder	der	0.0654236	0.4344904	0.361669	0.23103184 M20218	at	F11 Coagulation factor XI (plasma thromboplastin antecedent)
345 Bladder	der	0.0652238	0.4344266	0.36154	0.23094052 D83838	at	EST: similar to protein Nterminal asparagine amidohydrolase, mRNA sequence. (from Genhank)
346 Bladder	der	0.0649321	0.434416	0.36138	0.23082498 Z21156 at	221156 at	Homo sapiens mRNA for KIAA0826 protein, partial cds
347 Bladder	der	0.0649257	0.4343781	0.361287	RC_A 0.23061363 06 at	A1923	EST: zp97c12.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 628150.31 mRNA sequence (from Gorbank)
348 Bladder	der	0.0648475	0.4341822	0.36085	0.23055518 D50495	ਲ	Transcription elongation factor S-II, hS-II-T1
349 Bladder	der	0.0633066	0.0633066 0.4340169	0.360776	X87344 0.23026773 10 r at	sp.	DMA gene extracted from H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
350 Bladder	der	0.0627882	0.4334844	0.360689	0.23016667 X86400_at		Gamma subunit of sodium potassium ATPase
							Parties and the second

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351 Bladder	dder	0.0627882	0.433473	0.360542	0.23000255	x86400_at-2	0.23000255 X86400_at-2 ATPase, Na+/K+ transporting, gamma 1 polypeptide
352 Bladder	dder	0.062768	0.4334359	0.360326	0.22990637 M60047_at	M60047_at	Heparin binding protein (HBp17) mRNA
353 Bladder	dder	0.0627096	0.4333471	0.359872	RC_A 0.22973487 15_at	A4538	EST: aa19h06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 813755 3', mRNA sequence. (from Genbank)
354 Bladder	dder	0.0626819	0.433216	0.359675	0.229571 t	M19878_s_a t	Calbindin 27 gene, exons 1 and 2, and Alu repeat
355 Bladder	dder	0.0626531	0.433179	0.359586	0.22943208 L16464_at	_16464_at	ETS-RELATED PROTEIN PE-1
356 Bladder	dder	0.0625535	0.433179	0.359519	0.2292636 t	X57348_s_a t	SFN Stratifin
357 Bladder	dder	0.0622724	. 0.4331583	0.359442	0.22917165 W31287 at	N31287 at	EST: zb92a04.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320238 5', mRNA sequence. (from Genbank)
358 Blac	Bladder	0.0621258	0.4330452	0.359231	0.22900306 M at	AFFX-DapX- M_at	AFFX-DapX-M at (endogenous control)
359 Blac	Bladder	0.0621258	0.4330081	0.359152	0.22889638 M at-2	AFFX-DapX- M at-2	AFFX-DapX-M at (miscellaneous control - 11k chips)
360 Blac	Bladder	0.0620866	0.4329309	0.359047	RC 0.22872312 18	_AA3720 at	EST: EST83940 Parathyroid gland tumor I Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)
361 Blac	Bladder	0.0620314	0.4327582	0.358913	0.2285443 R81003	381003 at	EST: yi94e03.r1 Homo sapiens cDNA clone 146908 5'. (from Genbank)
362 Bladder	dder	0.0620106	0.4326507	0.358874	HG4058 0 22842196 HT4328	HG4058- HT4328 at	Oncodens Amil Evil 4 Euclos Activated
363 Bladder	dder	0.0619291	1	0.35877	0.22827314 M55153		PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE
364 Bladder	dder	0.0616514	0.4324747	0.35868	• RC_A 0.22817238 63 at	RC_AA4890 63_at	EST: aa54f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824777 3. mRNA sequence. (from Genbank)
365 Bladder	dder	0.061247	0.432313	0.358624	0.2279737 Y07867 at	707867 at	Pirin, isolate 1
366 Bladder	dder	0.0608551	0.4322478	0.358535	0.22778153 U31875_at	J31875_at	Hep27 protein mRNA
367 Bladder	dder	0.0608551	0.4321103	0.358316	0.2276842	J31875 at-2	0.2276842 U31875_at-2 Human Hep27 protein mRNA, complete cds
368 Blac	Bladder	0.060164	0.4320281	0.358063	0.22754622 56	२C_AA2363 56_at	RC_AA2363 Zr54a11.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone 56 at IMAGE:667196 3', mRNA sequence
369 Bladder	dder	0.0596682	0.4320262	0.357926	0.22742647 t	X99374_s_a t	Fertilin beta mRNA
	dder	0.0593514		0.357907	0,22728266 D84361	384361 at	P52 and p64 isoforms of N-Shc
371 Blac	Bladder	0.0589966	0.4318941	0.357811	0.22717111 D87953	087953_at	RTP
372 Blac	Bladder	0.0584637	0.4318597	0.357322	0.22707637 t	U14577_s_a t	MAP1A Microtubule-associated protein 1A
373 Bladder	dder	0.0577985	0.0577985 0.4317132	0.357159	0.2270034 Z49825	S	at HEPATOCYTE NUCLEAR FACTOR 4

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374 Bladder	0.0566229	0.4315885	0.357155	RC 0.22677158 23	RC_AA2437 23_at	RC_AA2437 EST: zr68g10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 23_at 668610 3', mRNA sequence. (from Genbank)
375 Bladder	0.0563572	0.4315208	0.356886	0.2265718 U67611	1	at-2 Mouse transaldolase gene mRNA, complete cds. (from Genbank)
376 Bladder	0.0563572	0.4314631	0.356767	0.22645459 U67611	J67611_at	Mouse transaldolase gene mRNA
377 Bladder	0.0563226	0 4310626	0.356688	0 22624591 S77812 at		FLT1 Fms-related tyrosine kinase 1 (vascular endotheilal growth
		t t			~ -	EST: z45b12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
378 Bladder	0.0561582	0.4307508	0.35657	0.22610949 26_at		666335 3', mRNA sequence. (from Genbank)
	200		7. 10	10000		
380 Bladder	0.0556085	0.430546	0.356406	0.22573191 L00205	113532 at 00205 at	Peroxisome Proliferator Activated Receptor (Gb:Z30972) KERATIN, TYPE II CYTOSKELETAL 6D
381 Bladder	0.0554827	0.4302088	0.35631	0.22558264	HG2566- HT4792 r at	HG2566- 0.22558264 HT4792 r at Microtubule-Associated Protein Tau, Alt. Splice 3, Exon 8
382 Bladder	0.0540595	0.4301117	0.356216	0.2254838 L33477	_33477 at	(clone 8B1) Br-cadherin mRNA
383 Bladder	0.0538207	0.4300621	0.356088	0.22544941 M36205	Ħ	SYNAPTOBREVIN 2
384 Bladder	0.0535315	0.4298687	0.356032	HG25930	, 7	Externally 17 hats data released
385 Bladder	0.0532402	1	0.355755	0.2254141 11120300 o	 	Citti Cirtamete ammeria licese (di tamine synthose)
:		1		1	35	OFFICE CINCALLING IN 19650 (BLACKHING SYTHINGS)
386 Bladder	0.0531437	0.429312	0.35564	0.22495985 2	748519_s_at	0.22495985 Z48519_s_at XG gene (clone RACE5)
387 Bladder	0.0526468	0.0526468 0.4292454	0.355554	RC 0.22488101 68	_AA2566 at	EST: zr82h02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682227 3', mRNA sequence. (from Genbank)
388 Bladder	0.05246	0.05246 0.4291433	0.355403	0.22477199 Y10209	710209 at	CD30L protein
389 Bladder	0.0524419	0.4289939	0.35516	0.2246155 S73840_at	373840_at	Type Ilx myosin heavy chain {3' region} [human, skeletal muscle, mRNA Partial, 827 nt]
300 Bladder	0.0514074	0.4288784	0.0564.07	2000	_AA2522	EST: zr29d01.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664801 3' similar to TR:G1060907 G1060907
הומתתם	0.0014044		0.333127	0.22453/85 89	39_at	UPRTASE;, mKNA sequence. (from Genbank)
391 Bladder	0.051141	0.4288498	0.354771	HG3513 0.2244242 HT3707	HG3513- HT3707 at	Myosin, Heavy Polypeptide. Light Meromyosin
392 Bladder	0.0510215	0.4287831	0.354764	0.2241888.U46499_at	J46499_at	GLUTATHIONE S-TRANSFERASE, MICROSOMAL
393 Bladder	0.0509701	0.4286442	0.354737	0.22409752 L12060	တ	at RARG Retinoic acid receptor, gamma 1
- C	00000		1000		١. ١	
395 Bladder	0.0309363	0.4281341	0.354/30	0.2239799 H13689	ਰ _਼ ਰ	Collagen, Type Ix, Alpha 1
הומתתבו	0.00000.0		0.334009	0.223913331	NUSUZI at	PLAT Plasminogen activator, tissue type (t-PA)
396 Bladder	0.0507932	0.4274685	0.354669	0.22378549)17716_at-2	0.22378549 D17716_at-2 glucosaminyltransferase
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Fitle: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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397 Bladder	0.0507932	0.0507932 0.4273799	0.35412	0.22371484 D17716_at		N-acetylglucosaminyltransferase V
398 Bladder	0.0506349		0.354048	0.22363096 S81419	381419 at	Dystrophin, dystrophin {Purkinje promoter, alternatively spliced} [human, cortical brain and adult heart, mRNA Partial, 377 nt]
399 Bladder	0.0498577	0.4271195		0.22351193 U55258_at	J55258_at	HBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene
400 Bladder	0.0494496	0.4269797	0.353738	RC 0.2232295151	_AA0589	EST: zl96f07.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 512485.3; mRNA sequence. (from Genbank)
401 Bladder	0.0487522		0.353573	0.22307876 12 at	AA2341	EST: zr74a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669104 3', mRNA sequence. (from Genbank)
				V	AA040628_a	
402 Bladder	0.0486552	0.4267403	0.353232	0.22288205t		SYNAPTOTAGMIN I
403 Bladder	0.0485486	0.4267225	0.353182	RC_A 0.2227764 65 at	RC_AA0106 65 at	EST: ze19f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 359459 3', mRNA sequence. (from Genbank)
404 Bladder	0.0479636	0.4267026	0.352935	D 2226968 1	D86096_cds	EP3-IV gene extracted from Human DNA for prostaglandin E receptor
405 Bladder	0.0479196	_t	0.352858	0.22252354 C06279	at	EST: similar to none, mRNA sequence, (from Genbank)
406 Bladder	0.0462434		0.352725	0.22240618 X02874	at	OIAS (2'-5') oligoadenylate synthetase
407 Bladder	0.0455019	0	0.352663	0.22217166 W27721		Homo sapiens KIAA0424 mRNA, partial cds
408 Bladder	0.0445774	0.4264267	0.352595	0.2220572 X06825	(06825_at	Skeletal beta-tropomyosin
409 Bladder	0.0443611	0 4263696	0.352314	M21:	M21551_rna	Nairomadin R mRNA
410 Bladder	0.044351	1	0.352142	0.22175573 D78725	at	Homo sapiens mRNA for KIAA0914 protein, complete cds
411 Bladder	0.0443297	0.4263149	0.352042	0.22169042 U33267	at	Glycine receptor beta subunit (GLRB) mRNA
		1			RC_AA6096	EST: af16a06.s1 Soares testis NHT Homo sapiens cDNA clone
412 Bladder	0.0434613	0.4261689	0.352001	0.2215224 42_at		1031794 3', mRNA sequence. (from Genbank)
44.9 Dloddor	0.0499594	405000	0.00		AA071223_a	EST: zf79f10.r1 Soares pineal gland N3HPG Homo sapiens cDNA
415 Diaduel	0.0432334	_ <	0.351828	0.221308/41	- 1	clone 383179 5, mKINA sequence. (from Genbank)
414 Bladder	0.042804	1	0.351756	0.22121264 1.08424		Achaete scute homologous protein (ASH1) mRNA
415 Bladder	0.0426014	0.4257000	0.331/34	0.22114015 015590	_	Heat shock protein 27 (HSP27) mKNA
410 Diaddel	0.0420211		0.351079	0.22105172 MZ8825 at		CUTA CUTa antigen (thymocyte antigen)
			200.0	1.2203030	HG3517-	racosylical stellage Z (sectleto) status ilicitudeu)
418 Bladder	0.0418525	0.4256518	0.351361	0.22082242 HT3711	H3711_at	Alpha-1-Antitrypsin, 5' End
419 Bladder	0.0414693	0.4252038	0.351217	0.22076039 H24127 at		EST: ym50f03.r1 Homo sapiens cDNA clone 51827 5'. (from Genbank)
420 Bladder	0.0414624	0.4250849	0.351122	0.2206557 X58377	ਜ਼	Adipogenesis inhibitory factor
421 Bladder	0.0398846	0.4250751	0.350929	0.22058696	//31606_at	PHKG2 Phosphorylase kinase, gamma 2 (testis)
422 Bladder	0.0398162	0.4249809	0.35077	0.22044958	AF000545_a t	Putative purinergic receptor P2Y10 gene
423 Bladder	0.0398053	0.4248788	0.350633	0.2202493 D90042 at	-	AAC2 Arylamine N-acetyltransferase, liver

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

424	Bladder	0.0394708	0.42473	0.350497	0.22018345 U24266_at	J24266_at	Pyrroline-5-carboxylate dehydrogenase (P5CDh) mRNA, long form
125	425 Bladder	0.0391943	0.4246208	0.350339	0.2201674 M25322_at	M25322_at	SELP Selectin P (granule membrane protein 140kD, antigen CD62)
126	426 Bladder	0.0391932	0.0391932 0.424458	0.350104	0.22012138 U73191	J73191 at	Inward rectifier potassium channel (Kir1.3)
127	427 Bladder	0.0389838	0.0389838 0.4243701	0.350092	0.22000156 L16782_at	_16782_at	Putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds
128	428 Bladder	0.0387155	0.0387155 0.4243444	0.349963	0.2198501 D78367	J78367_at	K12 keratin
129	429 Bladder	0.0384115	0.4241763	0.349917	0.21969792 Y10514 s		at CD152 protein
130	430 Bladder	0.0383238	0.4240741	0.349902	0.2195899 L02648		TCN2 Transcobalamin II
31	431 Bladder	0.038302	0.4238106	0.349862	HG1078- 0.21946108 HT1078 at	HG1078- HT1078_at	Lamin-Like Protein (Gb:M24732)
132	432 Bladder	0.0382422	0.4237583	0.349545	RC_A 0.21935992 52_at	RC_AA4589 52_at	EST: zx88e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810844 3', mRNA sequence. (from Genbank)
433	Bladder	0.0381575	0.4235728	0.349446	0.2192598 Y08417	တ	at CHRNB3 Cholinergic receptor, nicotinic, beta polypeptide 3
434	Bladder	0.0380313	0.4234776	0.349381	0.21914773	26	Synuclein, gamma (breast cancer-specific protein 1)
135	435 Bladder	0.0376956	0.4234432	0.349274	HG273- 0.21897194 HT273_at	HG273- HT273_at	Lymphocyte Antigen Hla-G3
361	436 Bladder	0.0376204	0.4229651	0.349165	0.21874294 W56102 at	W56102 at	EST: zc58g07.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 326556 5', mRNA sequence, (from Genbank)
37	437 Bladder	0.0368371	0.4228829	0.348811	0.21873634 Y00970	Y00970 at	ACR Acrosin
38	438 Bladder	0.0365929	0.4228408	0.348751	0.21868433 U42408	J42408 at	Ladinin (LAD) mRNA
39	439 Bladder	0.0360328	0.4228343	0.348625	0.21848868 U52969	J52969 at	BRAIN SPECIFIC POLYPEPTIDE PEP-19
40	440 Bladder	0.0360288	0.4228253	0.348459	0.2184533 R46311	746311_at	EST: yj53f04.r1 Homo sapiens cDNA clone 152479 5'. (from Genbank)
41	441 Bladder	0.0359417	0.422769	0.348259	HG2271- 0.21822183 HT2367 at	HG2271- HT2367 at	Profilacerin
42	442 Bladder	0.0358078	0.4227186	0.348095	0.2181951 D49493 at	749493 at	Bone morphogenetic protein-3b
431	443 Bladder	0.0355552	0.4227005	0.347944	0.2180428	AA017283_a t	EST: ze52b01.r1 Soares retina N2b4HR Homo sapiens cDNA clone 362569 5', mRNA sequence. (from Genbank)
44	444 Bladder	0.03536	0.422646	0.347856	0.21785907 t	D17408_s_a t	Calponin
45	445 Bladder	0.0352848	0.422445	0.347728	RC 0.21783951 98	RC_AA3499 98_at	EST: EST57271 Infant brain Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)
461	446 Bladder	0.034385	0.034385 0.4224347	0.347671	0.21768893.861053.34	2640E3 of	ERBB3 V-erb-b2 avian erythroblastic leukernia viral oncogene

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	2020.2020 002
Title:	Genetic Markers for Tumors
Invent	ors: Sridhar Ramaswamy, et al.

447 Bladder	ladder	0.0341425	0.4223525	0.347457	AA3 0.21748373 t	62598_a	AA362598_a EST; EST72534 Ovary II Homo sapiens cDNA 5' end, mRNA to secuence. (from Genhank)
							EST: zx74e07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809508 3' similar to TR:G973313 G973313 MYO-INOSITOL 1-
448 Bladder	ladder	0.034139	0.4223475	0.347401	0.21735802 54 at	A4545	PHOSPHAI E SYNTHASE ISOZYME-2: ;, mRNA sequence. (from Genbank)
449 Bladder	adder	0.0336015	0.422094	0.347346	AA4	AA426361_a	0.04-iii.s. 4
450 Bladder	adder	0.0333633	0	0.347217	0.2170272 A28102 at	102 at	GARAa recentor alpha-3 enhimit
			1		AA1	AA182909 a	EST: zp51d08.r1 Stratagene HeLa cell s3 937216 Homo sapiens
451 Bladder	adder	0.033234	0.4219986	0.347208	0.2168871 t	1	cDNA clone 612975 5', mRNA sequence, (from Genbank)
452 Bladder	adder	0.0325329	0.4218038	0.346788	0.21674153 U13220 at	220_at	Forkhead protein FREAC-2 mRNA, partial cds
							EST: zs57g01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
453 Bladder	adder	0.032036	0.4214408	0.346752	0.21664743 t	92609_a	AA292609_a IMAGE:701616 5' similar to contains L1.t1 L1 repetitive element ;, t
							EST: zw75d12.s1 Soares testis NHT Homo sapiens cDNA clone
454 Bladder	adder	0.0318354	0.4212161	0.346631	RC 0.21647991 71 g	RC_AA4295 71 at	782039 3' similar to contains element PTR7 repetitive element ;, mRNA sequence, (from Genbank)
455 BI	adder	0.0316793	0.4211663	0.346331	0.21644567 M64	936 f at	0.21644567 M64936 f at Homo saniens refinoic acid-inducible endogenous retroviral DNA
456 Bladder	adder	0.0316428	1	0.346211	0.21631482 02321	32.1 at	GSTM5 Clutathione Stransferase M5
					RC	1357	EST: zt77c11.s1 Soares festis NHT Homo saniens cDNA clone
457 Bladder	adder	0.0315946	0.4208423	0.346184	0.21626718 80_at		728372 3', mRNA sequence. (from Genbank)
-					HG3	HG3412-	
0	:	1			HT3	HT3593_s_a	
458 Bladder	adder	0.0315475		0.345941	0.216196251		Blue Cone Photoreceptor Pigment
459 Bladder	adder	0.0313778	0.4204664	0.345855	0.21611501 M21305_at		Alpha satellite and satellite 3 junction DNA sequence
460 Bladder	adder	0.0310702	0.4204147	0.345835	M10 0.21597345 t	M10051_s_a	INSR Insulin recentor
461 Bladder	adder	0.030811	0.4202842	0.345747	0.21593729 M93143 at		PLGL Plasminogen-like protein
462 Bladder	adder	0.0306993	0.420248	0.345654	0.21579945 D50863	at	TESK1
463 Bladder	adder	0.0306608	0.4202175	0.345593	0.2157324 X735	501 at-2	0.2157324 X73501_at-2 KERATIN, TYPE CYTOSKELETAL 20
464 Bladder	adder	0.0306608	0.4200984	0.345498	0.21555227 X73501	at	KERATIN, TYPE I CYTOSKELETAL 20
465 Bladder	adder	0.0293408	0.420072	0.345338	0.21551153 X82634	at	Partial mRNA for hair keratin acidic 3-II
466 Bladder	adder	0.0291908	0.4200108	0.345302	0.21542443 t	AF001294_a t	PL (IPL) mRNA
467 Bladder	adder	0.0287948	0.4199694	0.345229	0.21532078 M21302_at		Small proline rich protein (sprll) mRNA, clone 174N
468 Bladder	adder	0.028752	0.419705	0.345162	RC_A 0.21512306 35_at	A4179	EST: zv94c08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 767438 3', mRNA sequence. (from Genbank)
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ORF for E6 protein gene extracted from Human papillomavirus 5b genome integrated into human carcinoma DNA	K+ channel beta 1a subunit mRNA, alternatively spliced	EST: zu42c09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 740656 5' similar to SW:BI3_MOUSE P28662 BRAIN PROTEIN	l3;, mRNA sequence. (from Genbank)	EST: ze91d10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 366355 3', mRNA sequence. (from Genbank)	EST; aa26h04,r1 NCI CGAP GCB1 Homo sapiens cDNA clone	IMAGE:814423 5', mRNA sequence. (from Genbank)	MYL4 Myosin, light polypeptide 4, alkali; atrial, embryonic		Crystallin, Beta B3 (Gb:X15145)	Enteric smooth muscle gamma-actin gene, 5' flank and	CRAT Carnitine acetyltransferase		HFL1 H factor (complement)-like 1	Folylpolyglutamate synthetase mRNA	Neuropilin 2	Putative envelope protein; orf similar to env of Type A and Type B	retroviruses and to class II HERVs gene extracted from Human	endogenous retrovirus HERV-K(HML6) proviral clone HML6.17	putative polymerase and envelope genes, partial cds, and 3'LTR	UMOD Uromodulin (uromucoid, Tamm-Horsfall glycoprotein)	3,5' cyclic nucleotide phosphodiesterase (HSPDE1C1A) mRNA	Sodium/Hydrogen Exchanger 5	<u> </u>	Neuronal PAS domain protein 2	0.21285224 U10690 f at MAGF-5a antigen (MAGF5a) gene	WT1 Wilms tumor 1	Laminin gamma2 chain gene (LAMC2)	ALDEHYDE OXIDASE	GLP1R Glucagon-like peptide 1 receptor		DLX-2 (DLX-2) gene	EPB42 Erythrocyte membrane protein band 4.2	Antisense mRNA for BCMA peptide
561_cds	at		AA478129_a		RC_AA0262 E		AA459155 a E	_	म	HG2191-			at at	M65292_s_a	-	at				U60269_cds	2_at	at	at	at .	559		U10690 f at 1	M60614 at \	spo		Ī.,	J51003_s_a			
D26 0.21497534 2_at	0.21493292 X83127			0.21472059		0.21464953 80_at		0.21448617	0.21431057 X52005		0.21412554 HT2261	0.21405894 D00654_at	0.21401396 X78706		0.21383993	0.21370876 M98045	0.21360534 N31684 at				0.21350056	0.213305 M15881	0.21327646 U40371	HG4194- 0.21311559 HT4464		0.21307544 67_at				0.21257673 L11005 at	0.2123044 U01157		0.21221857 t	0.21209788 M60298_at	0.21192634 Z29572_at
0.345037	0.344931			0.344806		0.344797		0.344426	0.344389		0.344342	0.344308	0.344261		0.344229	0.344007	0.343992				0.343946	0.343791	0.34375	0.343665		0.3435	0.343304	0.343301	0.343078	0.343078	0.342846		0.34279	0.342688	0.342606
0.4196658	0.4193523			0.4193309		0.4193172	the Pin at some in special dynamical lands of the pin state of the sta	0.4192931	0.4192291		0.4192033	0.4190671	0.418985			0.4185309	0.4185133					1	0.4181323	0.4179379		0.4178295	0.4176301	0.4176	0.4173596	0.4169847	0.4168963		0.4168408		0.4167408
0.0286433	0.0284737			0.0283879		0.0282716		0.0277701	0.0276949		0.0275428	0.0275347	0.0274612		0.0273511	0.0271896	0.0269445				0.0266457	0.0257196	0.0257014	0.025353		0.024638	0.0245341	0.0244112	0.0243394	0.0239442	0.0236619		0.0235036	0.0232202	0.0231249
469 Bladder	470 Bladder			471 Bladder		472 Bladder		473 Bladder	474 Bladder		475 Bladder	476 Bladder	477 Bladder		478 Bladder	479 Bladder	480 Bladder				481 Bladder	482 Bladder	483 Bladder	484 Bladder		485 Bladder	486 Bladder	487 Bladder	488 Bladder	489 Bladder	490 Bladder		491 Bladder	492 Bladder	493 Bladder

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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494 Bladder	0.0231141	0.4166007	0.342364	0.21187279 X75308_at	MMP13 Matrix metalloproteinase 13 (collagenase 3)
	100000		0.00	×	
495 Bladder	0.0229837	0.4165835	0.342346	0.211//591 1 at	Parvaibumin
496 Bladder	0.0229343	0.0229343 0.4164714	0.342058	0.21172091 U55209 at	Myosin VIIa transcript 2 mKNA
497 Bladder	0.0223716	0.4161491	0.341868	0.21164344 T83397_at	Homo sapiens peroxisomal phytanoyl-CoA alpha-hydroxylase (PAHX) mRNA, complete cds
	0.0212573	0.41609	0.341829	U32499_s_a 0.21149504 t	D3 dopamine receptor mRNA
499 Bladder	0.0211896	0.4158762	0.341796	0.21140356 L20861_at	WNT5A Wingless-type MMTV integration site 5A, human homolog
500 Bladder	0.0208589	0.4155853	0.341709	U88902_cds 0.2113415 1 f_at	U88902_cds Integrase gene extracted from Human endogenous retrovirus H clone 1 f at g10.34 integrase and putative envelope protein genes, partial cds
501 Bladder	0.0207751	1	0.341524	0.21124786 Z33905_at	43kD acetylcholine receptor-associated protein (Rapsyn)
502 Bladder		0.4155607	0.341481	0.21116468 X69878_at	FLT4 Fms-related tyrosine kinase 4
503 Bladder	0.02062	0.415351	0.341413	RC_AA4043 0.21099436 81 f at	EST: zw37a04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 772206 3', mRNA sequence. (from Genbank)
504 Bladder	0.0201105	0.4153276	0.341311	0.21092583 U48231_at	Bradykinin receptor B1 subtype mRNA
					DNA sequence from clone RP1-151B14 on chromosome 22 Contains SSTR3 (somatostatin receptor 3) gene, pseudogene similar to phosomal profesor 139, RAC2 (res-related C3 hot ulinum foxin
0 0 10 10 10	00000		0 201040	10 000307 k07370k0 0	substrate 2 (rho family, small GTP binding protein Rac2)) gene, ESTs,
ono biadder	0.0198045	0.4151385	0.341212	0.210/6/91 286000 at	S Los, Goos and Ope Islands, complete sequence
506 Bladder	0.0198612	0.4150705	0.341166	0.21062627 W39573 at	EST: zc20b05.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 322833 5', mRNA sequence. (from Genbank)
507 Bladder	0.0194261	0.4148907	0.341027	0.21056598 H04627 at	
508 Bladder	0.0190298	0.414712	0.340882	U64573_s_a 0.21039835 t	Connexin43 gap junction protein (connexin43) gene, exon 1 and promoter region
509 Bladder	0.0190044	0.4147117	0.340794	0.21032225 R14782 at	EST: vf93a01.r1 Homo sapiens cDNA clone 29972 5'. (from Genbank)
510 Bladder	0.0187181	0.4146773	0.340765	0.21021667 R51517_at	Yg72d11.r1 Homo sapiens cDNA clone 38889 5'. (from Genbank)
511 Bladder	0.0184996	0.4146741	0.340616	M13928_s_a 0.21019728 t	
512 Bladder	0.0180239	0.0180239 0.4145186	0.340493	0.21004976 M60331_at	PRM1 Protamine 1
513 Bladder	0.0176025	0.4143131	0.340331	0.20997985 M59911_at	ITGA3 Integrin alpha-3 subunit
514 Bladder	0.0174845	0.4143131	0.340303	HG3936- 0.20973095 HT4206 at	Interleukin 9 Receptor (Gb:S71404)

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Inventors: Sridhar Ramaswamy, et al.

'n	er 0.0174559	9 0.4139852	0.340278	0.20961878 M24248 at		MYL3 Myosin, light polypeptide 3, alkali: ventricular, skeletal. slow
, o Bladder	er 0.0173542	0.4137881	0.340195	RC_A 0.209517 64_at	(0	EST: aa31b10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814843 3', mRNA sequence. (from Genbank)
517 Bladder	er 0.017334	1 0.4136108	0.340025	0.20947352 t	U00803_s_a	Fvn-related kinase
518 Bladder	er 0.0172407	7 0.4134401	0.339856	0.20936738 U48807 at		Dual specific protein phosphatase mRNA
519 Bladder	er 0.0170615	5 0.4131798	0.339735	0.20925198 D86957 at		KIAA0202 gene, partial cds
520 Bladder	er 0.01695	0.4128612	0.339721	0.20919491 t	AA346065_a t	
521 Bladder	er 0.0166705	0.4128221	0.33964	HG2 HT2 0.2089954 t	HG2730- HT2827_s_a t	Fibrinogen, A Alpha Polvpeptide, Alt. Splice 2. E
522 Bladder	er 0.0164375	0.4126806	0330630	M63	362_ma	Control I / ATD A A TD A A A A A A A A A A A A A A
523 Bladder	T	1	0.339405	0.20876858 D14827 at		Gasuld H,N-A1 Pase catalytic subunit gene Tax helner profein 1
524 Bladder	er 0.015948	0.4122615	0.33938	0.20860969 U54804	\top	Has2 mRNA
525 Bladder	н 0.0157191	0.4120875	0.339378	0.20852247 1_at	ma	SCYA1 gene (secreted protein I-309) extracted from Human secreted protein (I-309) gene
526 Bladder	ır 0.0156512	0.4120398	0.339377	X134 0 20845494 t	X13451_s_a	B-CELL ANTIGEN RECEPTOR COMPLEX ASSOCIATED PROTEIN
527 Bladder	ır 0.0154402	0.4118176	0.339169	0.20838776 U67784 at		Orphan G protein-coupled receptor (RDC1) mRNA nartial cds
528 Bladder	ır 0.0153809	0.4117838	0.339033	0.20822155 55 s	AA2364 s at	EST: zr75g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669266 3', mRNA sequence, (from Genhank)
529 Bladder	ır 0.0152863	0.4115226	0.339024	RC_A 0.20817296175 at	AA0710	EST: zm58d10.s1 Stratagene fibroblast (#937212) Homo sapiens
530 Bladder	r 0.0151383	1	0.338979	0.20804358 D88532 at	1	Pospik
531 Bladder	r 0.0147889	0.411213	0.338945	HG1 HT18 0.20794643 t	HG1827- HT1856_s_a t	Cytochrome P450, Subfamily lic. Alf. Splice Form 2
532 Bladder	r 0.0147604	0.4107625	0.338885	0.20775723 \$81957	at ,	BMP-5=bone morphogenic protein-5 {promoter} [human, Genomic, 1116 nt]
533 Bladder	r 0.0146777	0.410709	0.338728	0.2075998 1_at)51_rna	G protein-coupled receptor (GPR4) gene
534 Bladder	r 0.0138417	0.4106537	0.338702	0.20747581 U51704 at		EST: Human mRNA sequence containing Alu repetitive elements. (from Genbank)
535 Bladder			0.338684	0.20728248 U49857	1	Transcriptional activator mRNA
536 Bladder	1		0.338646	0.20723127 X68314	at	GPX2 Glutathione peroxidase 2, gastrointestinal
537 Bladder	r 0.0131295	0.4101775	0.338527	0 20708442 162647	+0	Doors with council and a second secon

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Homo sapiens mRNA for zinc finger protein, complete cds		TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR	DTR Diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)	EST: ze28h05.s1 Soares retina N2b4HR Homo sapiens cDNA clone 360345 3', mRNA sequence, (from Genbank)	Interleukin 6 (interferon beta 2)	IL6 Interleukin 6 (B cell stimulatory factor 2)	· · · · · · · · · · · · · · · · · · ·	Nox2 gene (exon 2)	0.20388559 L20469 s at Truncated dopamine D3 receptor mRNA	AA188555_a EST: zp78e11.r1 Stratagene HeLa cell s3 937216 Homo sapiens to CDNA clone 626348 5' mRNA secilence (from Genhank)	PTPRM Protein forosine phosphatase recentor type mu polymortida	EYA1A gene		TAK1 binding protein 1 (TAB1) mRNA	0.20336822 L17326_s_at Human pre-T/NK cell associated protein (1F6) mRNA, 3' end	Glufathione S. transferaco M2 (musucla)	Estrogen sulfotransferase mRNA, partial cds	Golgin, 165 Kda Polypeptide	EST: zv92e06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 767266 3', mRNA sequence. (from Genbank)	AA018418_a EST: ze50a02.r1 Soares retina N2b4HR Homo sapiens cDNA clone t	EST: yf34c12.r1 Homo sapiens cDNA clone 128758 5'. (from
0.20475064 D45213_at	RC_AA1565 59959 32_at	153353 M31165 at	39062 M60278 at	RC_AA0132	X04602_s_a t-2	X04602_s_a t	HG2987- HT3136_s_a	0.20397389 X93017 at	L20469 s at	AA188555_a t	X58288 at	Y10260_at	M31520_ma 1_at	U49928_at	L17326_s_at	M63509_s_a t	U55764_at	#	A4183	AA018418_a t	71851 R14606 of
0.204/5064	0.20459959	0.20453353	0.20439062	0.20434543	0.20424682 t-2	0.20419681	0.2041304	0.20397389	0.20388559	0.203797791	0.20368409 X58288 at	0.20354605 Y10260_at	M 0.2034471	0.20342268 U49928	0.20336822	0.20328908	0.20320529 U55764	0.20302072	RC_A 0.20294668 94_at	0.202903211	0.20274854
0.330934	0.33688	0.336814	0.336689	0.336588	0.336515	0.336439	0.336385	0.336249	0.336192	0.336033	0.335958	0.335911	0.335899	0.33578	0.335678	0.33559	0.335516	0.335474	0.335442	0.335288	0 335045
607704.0	0.4077612	0.4076997	0.4076392	0.4074823	0.4073624	0.4072766	0 4072441	0.4069091	0.4068644	0.4068053	0.4067128	0.4065523	0.4062783	0.4062186	0.4058838	0.4056924	0.40569	0.4056819	0.4056769	0.4056769	0.4056633
0.000000.0	0.0063708	0.0060597	0.0058652	0.0056581	0.0054524	0.0054524	0.0054254	1 1	0.0052947	0.0051277		0.0048514		0.0044372	0.0043853	0.0041493	0.0041047	0.0038496	0.0037646	0.0034687	0.0033625

Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

Subject Inc.. 2023.2020-002

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583 Bladder	lder	0.0022909	0.4056633	0.335105	0.20258886 K00629_f_at	00629_f_at	Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end
584 Bladder	der	0.0021413	0.4056353	0.335019	0.20258497 t	U05012_s_a t	NTRK3 Neurotrophic tyrosine kinase, receptor, type 3 (TrkC)
585 Rladder	lder	0.0020917	0.4056081	0.334994	0.20228115 a	A424381_s l	AA424381_s EST: zv90g12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone at 767110 5', mRNA sequence. (from Genbank)
586 Bladder	Ider	0.0020461		0.334881		म	COL4A6 Collagen, type IV, alpha 6
587 Bladder	lder	0.0019807	0.4052483	0.334872	0.20219491 L41607_at		GCNT2 Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
588 Bladder	lder	0.0019386		0.334754	A/ 0.20212647 t	A085059_a	AA085059_a clone 547369 5' similar to gb:M26880 UBIQUITIN (HUMAN);, mRNA sequence. (from Genbank)
589 Bladder	ider	0.0016093	0.4051888	0.334483	0.20199428 S72503_s	72503_s_at	at HRK1
590 Bladder	der	0.0015221	0.4051793	0.334442	0.20188577 U43843_at		H-neuro-d4 protein mRNA
		2000	0 4000.44	0.004400	A 000175707 t	AA074933_a	Zm85b07.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544693 5' similar to gb:J04794 ALCOHOL.
os i biaddei	ogei	0.0011404	0.4030311	0.334400	A 20101102.0	641	EST: x83g04.s1 Soares ovary tumor NBHOT Homo sapiens cDNA
592 Bladder	dder	0.0011096	0.0011096 0.4049275	0.334242	U.20160204 88 s at	8 s at A285229 a	88 s at crone 810390 3, mRNA sequence. (iloni Genbailk) AA285229 a PMY0709 KG1-a Lambda Zap Express cDNA library Homo sapiens
593 Bladder	der	8.49E-04	0.404859	0.334139	0.20151573 t	I	cDNA 5', mRNA sequence. (from Genbank)
594 Bladder	dder	8.17E-04	0	0.334067	0.2014302 U58130_at		Burnetanide-sensitive Na-K-2Cl cotransporter (NKCC2) mRNA
595 Bladder	der	7.92E-04	7.92E-04 0.4048312	0.333876	0.20133114 t	AF000562_a t	Uroplakin II mRNA, partial cds
596 Bladder	dder	7.44E-04	7.44E-04 0.4048144	0.333754	0.20125984 X13839 at	13839 at	LCAT Lecithin-cholesterol acyttransferase
597 Bladder	dder	4.26E-04	0.4045939	0.333694	0.20115615 X89426	89426_at	ESM-1 protein
0		I c			A	AA167340_a	
598 Bladder	dder	3.76E-04	3.76E-04 0.4043819	0.33362	0.2009895/1	1- 000007	609112 5', mKNA sequence. (from Genbank)
599 Bladder	doer	3.2/E-04	3.27 E-04 0.4043563	0.33333	0.20095226 U/2209 at	722043 at	TITESSOCIATED TAGEOR 2 (TAFZ) HINNA Enthalial macific transcription factor ESE 14 (ESE 1) mDNA
ooo biadaga	מתפו	1.02.L.0.1	-	0.000000	R CZC7000000	RC_D59630	EST: Human fetal brain cDNA 3'-end GEN-052F04, mRNA sequence.
602 Bladder	dder	-6.02E-04		0.333167		U46461 at	Dishevelled homolog (DVL) mRNA
0		0000	1		0 2006507 1 07504		TGFBR3 Transforming growth factor, beta receptor III (betaglycan,
603 Bladder	dder	-0.001185	0.4039462	0.333110	U.20005.U 吊	RC D12031	EST: Human HepG2 3'-directed Mbol cDNA, clone s14g02, mRNA
604 Bladder	dder	-0.001562	-0.001562 0.4038779	0.	0.20054983	ਰ	sequence. (from Genbank)
605 Bladder	dder	-0.001612	-0.001612 0.4038751	0.332966	0.20040289 U90716_at	J90716_at	Cell surface protein HCAR mRNA

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606 Bladder	-0.001721	0.4038679	0.332934	0.20023473	HG2936- HT3080 at	Immunodlohulin Heavy Chain Enhancer Flement
607 Bladder	-0.001765	0.4038679	0.332928		4.	CD4 CD4 antigen (p55)
					AA059287_s	EST: zf65e02.r1 Soares retina N2b4HR Homo sapiens cDNA clone
608 Bladder	-0.001997	- 1	0.3329		at	381818 5', mRNA sequence. (from Genbank)
609 Bladder	-0.002165	0.4034976	0.332767	0.20002142 U39840_at	39840_at	Hepatocyte nuclear factor-3 alpha (HNF-3 alpha) mRNA
610 Bladder	-0.002394	0.4032889	0.332649	0.19995838	00951 at-2	0.19995838 U00951 at-2 Himan clone A9A2BR11 (CAC)n/(GTG)n reneat containing m DNA
611 Bladder	-0.002394	0.4032842	0.332649	0.19992596 U00951	00951 at	Clone A9A2BR11 (CAC)n/(GTG)n repeat-containing mRNA
		1		A	11	EST: zu67c08.r1 Soares testis NHT Homo sapiens CDNA clone
612 Bladder	-0.00249		0.332635	0.19982278 t	1	743054 5', mRNA sequence, (from Genbank)
613 Bladder	-0.003573	0.4030942	0.33262	0.19968727 M99063_at	99063_at	KERATIN, TYPE II CYTOSKELETAL 2 ORAL
614 Bladder	-0.003698	0.4029892	0.332328	A/ 0.19958569 t	AA488505_a t	Human placenta (Diff33) mRNA complete cris
615 Bladder	-0.004628	0.4028657	0.332274	0.19952804 M10943 at	10943_at	Metallothionein-If gene (hMT-II)
);	105626 122	Ccr2 gene (ccr2a) extracted from Homo sapiens ccr2b (ccr2), ccr2a
616 Bladder	-0.004662	0.4028616	0.332263	0.1994643		(עטרב), עסיט (עסיט) and כסיט (כסיט) genes, and lactorerrin (lactorerrin) gene, partial cds, complete sequence
617 Bladder	-0.00467	0.4028103	0.332095	M 0.19938204 1	M77348_ma 1 s at	Pmel 17 mRNA
618 Bladder	-0.004929	0.4027283	0.332083	0 10032640 67882	70075 21	ID1 Inhibitor of DNA binding 1, dominant negative helix-loop-helix
619 Bladder	-0.004992		0.332083	0.19924726 722780	2780 at	NIOTALIA CVI ICIN
				R		EST WORLD of Source countillier !!
620 Bladder	-0.005389	0.4026367	0.331958	0.1992314 51_at	at	con 7, 2720074-31, 30ales 07al y tufflof NDHOT Homo sapiens cDNA clone 754950 31, mRNA sequence. (from Genbank)
621 Bladder	-0.005719	0.4026367	0.331891	VC 0 19904143/2	ша	Interferon beta 1 gene extracted from Gene for human fibroblast
		1		S 2 OFT FOCULO	RC 447577	Interest of the state of the st
622 Bladder	-0.005925		0.331843	0.19900347 09_at	770	cs r. zboguo.s1 Soares NnHMPu S1 Homo sapiens cDNA clone 668120 3', mRNA sequence, (from Genbank)
523 Bladder	-0.006015	0.4025945	0.331716	0.19896111 M94055	at	SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT
624 Bladder	-0 006144	0.4025404	0.334552	RC RC RC	AA0016	EST: zh85b09.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
625 Bladder	0.0000-	0.4023968	0.334432	AE	000584_a	CDINA Glone 428057 3', mKNA sequence. (from Genbank)
Transaction and the second			2011000	V. 13002,000 L	AAAGU2	Prostate differentiation factor mRNA EST: vx67407 e1 Soores total fetus Nh3UE9 0 112
626 Bladder	-0.006568	0.402238	0.331396	0.1986566 57	at	cone 796525 3', mRNA sequence. (from Genhank)
627 Bladder	-0.006643	0.4021483	0.331396	0.19847181 91	_AA4417 at	EST: zw62c02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774626 3, mRNA sequence (from Genhank)
628 Bladder	-0.007003	0.4021237	0.331287	0.19844111162435	2435 at	Cholinordic rocentor notional pioeticis, alabo noticis, and of

The stands of th

soo Bladder		-0.007142	0.4021064	0.331182	0.19837402 U03735 f at	0.19837402 U03735 f at MAGE-3 antigen (MAGE-3) gene
630 Bladder			0.4020942	0.331057	0.1982545 X98253 at	ZNF183 genre EST: zw63b06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
631 Bladder		-0.007542	0.4020822	0.331042	t t	clone 774707 3', mRNA sequence. (from Genbank) FST: vb96h08.r1 Homo sapiens cDNA clone 79071 5'. (from
R32 Rladder		-0.008052	0.402003	0.330863	0.19803475 T61992 at	General Society of Society NHHMPU S1 Homo sapiens cDNA clone
200	-	008352	0.4015873	0.330778	0.19795163 53_at	753044 3', mRNA sequence. (from Genbank)
633 Bladder	+	-0.008408	0.4015569	0.330644	0.19783106 M31651_at	SHBG Sex hormone-binding globuliff
635 Bladder		-0.008503	0.4014916	0.330377	0.19770393 X82324 at	POUSF4 FOU dollidii, class of dansorpros
636 Bladder		-0.00858	0.4013344	0.330336	0.1975626 t-2	KIAA0316 gene product
637 Bladder		-0.00858	1 [0.330265	0.197480981	KIAA0316 gene M5 muscarinic acetylcholine receptor gene
638 Bladder		0.008913	0.4012493	0.330188	0.19/3/300 Mousss at	
639 Bladder		-0.008955	0.4012289	0.33012	0.1972677 1 at	
640 Bladder	+	-0.009156	0.400803	0.329999	- 11	at EDNKB Ellucinelli receptor type and thrombonoietin receptor) extracted from Human
641 Bladder		-0.009259	0.4007721	0.329843	0.19712663 1 s. at	thrombopoietin receptor (MPL) gene
			1	l	M91368_s_a	Na+/Ca+ exchanger (CNC) mRNA
642 Bladder	1	-0.009677	0.4005682	0.329809		RC AA2428 EST: 265e10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
643 Bladder		-0.010218	0.4003349	0.329765	0.19699791 23 at	668298 3', mRNA sequence. (from Genbank)
644 Bladder		0.010399	-0.010399 0.4001721	0.		Dystrobrevin isoform DTN-3 (DTN) gene, exon 11B and complete cds
645 Bladder		0.010399	-0.010399 0.4000874	0.32966	0.19683957 M34715 at	Pod I Fredhall of the Control of the
646 Bladder		-0.010495	0.3998658	0.329531	0.19673371 J02947 s	s at SOD3 Superoxide dismutase 3, extracellular
647 Bladder		-0.010526	5 0.3998479	0.329392	0.1965774 N32716 at	EST: yx74h12.r1 Homo sapiens cDNA clone 267527 5' similar to PIR:S45251 S45251 SNF2alpha protein - human ;. (from Genbank)
648 Bladder		-0.010583	3 0.3997595		İ	0.19651204 L27671 s. at Intercellular adhesion molecule 4, Landsteiner-Wiener blood group
649 Bladder	der	-0.01127	7 0.3997316	5 0.329308	0.196438U3 X66839 at	
650 Bladder		-0.011684	-0.011688 0.3997071		0.19629197	
651 Bladder		-0.01172	-0.011726 0.3996856	6 0.329158	0.19624645 M99564_at	PROTEIN

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

FIG. 1B2

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652 Bladder		-0.0125	0.3996109	0.329063	A 0.19618687	AB000114_a t	Osteomodulin
653 Bladder		-0.0125	0.3995068	0.329017	AB 0.1961066 t-2	AB000114_a t-2	Osteomodulin
654 Bladder		-0.012651	0.3994813	0.329003	X967 0.19597839 1_at	X96783_rna 1_at	Syt V gene (genomic and cDNA sequence)
655 Bladder		-0.012887	0.3994667	0.328917	0.19588974 H11788_at	111788_at	EST; ym11b06.r1 Homo sapiens cDNA clone 47577 5'. (from Genbank)
656 Bladder		-0.013006	0.3990419	0.328917	Δ 0.195705581	AA393318_a t	EST: zt70d02.r1 Soares testis NHT Homo sapiens cDNA clone 727683 5'. mRNA sequence. (from Genbank)
657 Bladder		-0.013401	0.398884	0.328766	0.1955738 Y08134_at	'08134_at	ASM-like phosphodiesterase 3b
658 Bladder		-0.013401	0.3988671	0.328623	0.19554159 Y08134_at-2		H.sapiens mRNA for ASM-like phosphodiesterase 3b
659 Bladder		-0.013852	0.3988458	0.328581	A 0.1954427811	\A203274_a	AA203274_a cDNA clone 446465 5' similar to contains element MER27 repetitive element: mRNA sequence (from Genhank)
660 Bladder	19	-0.014469	0.3988446	0.328581	0.19530731 U07139	J07139 at	CAB3b mRNA for calcium channel beta3 subunit
661 Bladder		-0.014503	0.3987374	0.328479	0.19524048 X51602 at		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECIESOR
662 Bladder		-0.014829		0.32836	0.19514215 U51334 at	151334 at	Putative RNA binding protein (RBP56) mRNA
663 Bladder		-0.015127	0.3985746	0.328318	0.19502036 U09860	J09860_at	PRSS7 Protease, serine, 7 (enterokinase)
							EST: zr49c02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
664 Bladder		-0.015148	0.3984816	0.32823	0.19493929 99_at	AZ338	boo722 3 similar to 1R:G469478 G469478 SM-20.;, mRNA sequence. (from Genbank)
							EST: zv63f03.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
		-			<	0.00	clone 758333 5' similar to TR:G1050752 G1050752
665 Bladder		-0.015468	0.3984666	0.328219	0.19485556 t	V-4401236_8	AA401230_8 NTNUKENINE/ALPHA-AMINOADIPALE AMINOTKANSPEKASE;; t
666 Bladder		-0.015874	0.3983022	0.327967	0.19475098 D61391	at	Phosphoribosypyrophosphate synthetase-associated protein 39
667 Bladder		-0.016048	0.3981427	0.327907	RC_A 0.19456865 18 at	A4497	EST: zx09b07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785941 3', mRNA sequence, (from Genbank)
668 Bladder		-0.01669	0.3975521	0.327902	0.19452329 W04902	at	EST: za43a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 295292 5', mRNA sequence, (from Genbank)
669 Bladder		-0.016695	0.3974719	0.327892	0.19443734 2_at	U43753_cds 2_at	Frataxin (FRDA) gene, promoter region and
670 Bladder		-0.016758	0.3973807	0.327852	Q 0.1943273†	\A024428_a	AA024428_a EST: ze73e12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
671 Bladder		-0.016795	0.3973601	0.327779	0.19419599 U46767_at	146767 at	Monocyte chemoaltractant protein-4 precursor (MCP-4) mRNA
672 Bladder		-0.016861	0.3971088	0.327724	0.19414152 t	AB000462_a t	SH3 binding protein, clone RES4-23A

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Chromosome 1q subtelomeric sequence D1S553	sapiens cDNA, mRNA sequence. (from Genbank)	sho leither and (ondo) and o	Orphan receptor GPR9 (GPR9) gene, panda cus	CSNKZAZ Casein Killase Z, alpria primo porpopraco	Homo sapiens cell cycle-regulated factor p78 mRNA, complete cds	Cytochrome P-450IID (clone pMP33)	EST: EST82450 Homo sapiens cDNA 5' end similar to None. (from	Genbank)	AA248587_a EST: csh0559.seq.F Human Tetal nearly, Latinuda ZAT Lypross Tromband	sapiens cUNA 5, mkinA sequence. (Indin deliberin)	CALMODULIN-KELAIED FROIEIN IND-1	Putative G-protein (GP-1) IIIKINA	IL1B Interleukin 1, beta	EST: Human Filbo 3 dilected Misot cerve, 110m/355 1154, 554.	Inputed, Interview Sequence: ("Single Consult.")	sapiens cDNA, mRNA sequence. (from Genbank)	Growth hormone-releasing hormone receptor form b gene extracted	from Human growth hormone-releasing hormone receptor gene,	alternatively spliced forms a, b, and c, partial cds	protein gene encoding beta 3 subunit exon 1 and promoter	Receptor protein tyrosine kinase	AA203501 a EST: zx59a01.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	cDNA clone 446760 5', mRNA sequence. (from Genbank)	EST: hbc3204 Homo sapiens cDNA clone hbc3204 5'end. (from	Genbank)	EST: zw55d04.s1 Soares total fetus NDZHF8 9w Homo saplens CDINA	clone 773959 3', mRNA sequence. (from Genbank)	MAT8 protein	EST: 17a9 Human retina cDNA randomly primed sublibrary Homo	apiens curve, intrive sequence. (non consum)	EST: XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	EST: Human aorta cDNA 3'-end GEN-354C01, mRNA sequence.	(from Genbank)
क्र	ä	U32674_s_a			A4889	ti	5	35288 at G	\A248587_a E		at	at	ä	D20728	at E	ă		U17579 rna fr	i		at	AA203501 a E	1		äţ,	RC_AA4366 E		at		-	_AA4599	D58185	at_
0.1941271 006155	0.19406258 W27099		0.19401053 t	0.19378962 M55268 at	RC_A 0.19369626 79 at	0 40364406 X16866	001100010	0.1935521 T35288_at		0.19348507 t	0.1933749 M58026	0.19327982 U87964	0.19324511 X04500		0.1931399	0.1930074 W28931			0.19289848 1 at	0.19282453 Y14140 at	0.19273911 X74764		0.19267961		0.19261755 T48536		0.19253203 19_at	0.19241257 U28249		0.19231294	0 19227564 49	0.1322.00	0.19218242
0.327532	0.327525		0.327431	0.327425	0.327413	000200	0.321200	0.32698		0,326855	0.326837	0.326812	0.326635	1 0	0.326605	0.326596	200		0.326594	0.326589	0.326388		0.326211		0.32619		0.326186	0.326078		0,325988	0.325056	0.020300	0.325728
0.3970419	0.3970003		0.396916	0.3966488	0.3966376	0.000000	0,3905800	0.3961862	The state of the s	0.396161	0,3961282	0,3960434	0.3960353		0.3959516	0 3050152	0,0000102		0.3958722	0.3957672	0.395692		0.3954331		0.3953917		0.3953916	0.3953075		0.3952483	7000084		0.3950855
-0.017018	0.017086	i	-0.017145	-0.017254 (-0,017352	-0.017499		-0.018183	-0.018255	-0.018479	-0.018564		-0.019007	0.049035	-0.019000		-0 019274	-0.01928	-0.019426		-0.019641		-0.019692		-0.019931	-0.020105		-0.020349	0370000	-0.020458	-0.020494
673 Bladder	674 Bladder		675 Bladder	676 Bladder	Dodoor	piaduei	678 Bladder	679 Bladder		680 Bladder	681 Bladder	682 Bladder	Bladder		684 Bladder	Diodolor	Bladdel		GRE Bladder	687 Bladder	688 Bladder		880 Bladder	חומחתכו	690 Bladder		Bladder	Bladder		Bladder		694 Bladder	695 Bladder
673 E	674	5	675	676	2 2	1/0	678	679		680	681	682	683		684	i.	င္အ၀		686	687	688		880	200	069		691	692		693		769	969

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Crystallin, beta B2	EST: zu18b03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 738317 3', mRNA sequence. (from Genhank)	Melanocortin-4 receptor flurman. Genomic 1671 ntl	Alpha1-fetonrotein transcription factor (hETE) mDN/A	אוועות ביישור וומויז פרוליות ומכופון וומויז פרוליים וויישור וויישור וויישור וויישור וויישור וויישור וויישור וויישור וויישור ויישור וויישור ווישור וויישור וויישור וויש	0.19186023 U93553 at-2 Fetoprotein-alpha 1 (AFP) transcription factor	APEH N-acylaminoacyl-peptide hydrolase	Messenger RNA for human leukocyte (alpha) interferon. (from Genbank)	Human DNA from chromosome 19-specific cosmid F25965, genomic	AC002398 c F25965, genomic sequence::Hirman DNA from chromosome 19-	specific cosmid F25965, genomic sequence	Neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds	C00038_s_a EST: HUMGS0003443, Human Gene Signature, 3'-directed cDNA	sequence, mRNA sequence. (from Genbank)	Asialod/scoprotein recentor 2	33 KD HOUSEKEEPING PROTFIN	Macrophage lectin 2	EST: ym96h06.r1 Homo sapiens cDNA clone 166811 5' similar to	gb:X07290_cds1 ZINC FINGER PROTEIN HF.12 (HUMAN);. (from Genbank)	SHC (Src homology 2 domain-containing) transforming protein 1 pseudogene 1	TOOL AND THE TOTAL OF THE TOTAL	AHSC Alaba 2 US almontation clashed and the state of the	EST: yx81c11.r1 Homo sapiens cDNA clone 268148 5'. (from Genbank)	EST: aa35b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	AA130284_a EST: zl29d04.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA	delic access of mixing sequence. (Horn Genbank)
AA367473_a t	RC_AA4166 01 s at	0.19204307 S77415 at	U93553 at		U93553 at-2	0.1917311 J03068_at	क्र		AC002398 c	ds4_at		C00038_s_a		3 ma		T			m	2293_a	<u>+</u>		_AA4812 at	AA130284_a	
0.192152381	0.19210674 01	0.19204307	0.19196393 U93553		0.19186023	0.1917311	0.19171514 J00214 f	_		0.19152829 ds4_at	0.19138749 L07615 at		0.19126/22	X5528; 0.19121084 s at	0.1911793	0.19111119 D50532 at		0.19102716 R88880 at	0.1909511	0.10085656	0.19072703 M16961	0.19059922 N34697 at	0.19053024 66	0.190432891	
0.325687	0.325676	0.325581			0.325488	0.325313	0.32518			0.324955	0.324906	770700	0.324011	0.324772	0.324642	0.324625		0.324604	0.324479	0.324472	0.324467	0.324322	0.324285	0.324281	
0.3950675	0.3949988	0.3947264	0.3946935	1	0.3944264	0.3943677	0.3942698			0.3942502	0.3942059	0 2044 20	0.334133	0.394081	0.3940115	0.3938853		0.3938128	0.3937911	0.3934037	0.3933395	0.3931407	0.3931174	0.393047	
-0.020686	-0.020779	-0.020972	-0.020973		-0.020973	-0.021106	-0.021225			-0.021422	-0.021755	0.024706	-0.02.17.30	-0.021852	-0.022063	-0.022398		-0.022716	-0.022777	-0.023046	-0.023377	-0.023552	-0.023763	-0.02385	-
696 Bladder	697 Bladder	698 Bladder	699 Bladder		700 Bladder	701 Bladder	702 Bladder			703 Bladder	704 Bladder	705 Bladder	חממממ	706 Bladder	707 Bladder	708 Bladder		709 Bladder	710 Bladder	711 Bladder	712 Bladder	713 Bladder	714 Bladder	715 Bladder	

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						EST: zf50b08.s1 Soares retina N2b4HR Homo sapiens cDNA clone
716 Bladder	-0.023852	0.3929791	0.324155	RC 0.19034865 76	RC_AA0478 76_at	380343 3' similar to contains Alu repetitive element; contains element L1 repetitive element; mRNA sequence. (from Genbank)
717 Bladder	-0.024469	0.3929719	0.324041	0.1902926 U52100	U52100_at	XMP mRNA
718 Bladder	-0.024848	0.3929131	0.323925	0.19021156 M97496	M97496_at	GUCA2 Guanylate cyclase activator 2 (guanylin, intestinal, heat-stable)
719 Bladder	-0.024857	0.3928742	0.323863	HG4243 0.19015184 HT4513	HG4243- HT4513_at	Zinc Finger Protein Znf155
720 Bladder	-0.025077	0.3928663	0.323777	0.19005889 1 at	U33317_ma 1 at	Defensin 6 (HD-6) gene
721 Bladder	-0.025122	0.392821	0.323752	0.18996385	R02207_s_a t	
722 Bladder	-0.02519		0.32374	0.18992423	AA018887_a t	
723 Bladder	-0.025327	0.3924997	0.323687	0.18986525 U02082 at	U02082 at	Guanine nucleotide regulatory protein (tim1) mRNA
724 Bladder	-0.025577	0.3924233	0.323526	0.18977955 X07696 at	X07696 at	KRT15 Keratin 15
725 Bladder	-0.025611	0.3924211	0.323446	0.18969487 M20137_at	M20137_at	Interleukin 3 (IL-3) mRNA
726 Bladder	-0.025949	0.3923743	0.323428	0.18966202 R11248 at	R11248 at	EST: yf41c02.r1 Homo sapiens cDNA clone 129410 5'. (from Genbank)
727 Bladder	-0.026125	-0.026125 0.3923549	0.323322	0.18955627 U50929 at	U50929 at	Betaine:homocysteine methyltransferase mRNA
728 Bladder	-0.026255	0.3922236	0.323103	0.18953861 U26914 at	U26914 at	Ras-responsive element binding protein (RREB-1) mRNA
729 Bladder	-0.0267	0.3922088	0.322989	0.18935868 U80457 at	U80457_at	Transcription factor SIM2 long form mRNA
					000000	EST: zu55b03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
730 Bladder	-0.026902	0.3919809	0.322869	0.18927269 00 at	NC_A44020	done 741869 3' similar to 1 R:G452270 G452270 2-19 PROTEIN PRECHRSOR : mRNA seguence (from Conhad)
731 Bladder	-0.027084	0.3918091	0.322867	0.18922588 U12140 at	U12140 at	Tyrosine kinase recentor o 145TRK-R (TRK-R) mony
732 Bladder	-0.027725	0.3917496	0.322761	0.18916056 L31573 at	L31573 at	Sulfite oxidase mRNA
733 Bladder	-0.027825	0.3916795	0.422730	M 1880027	M24351_cds	M24351_cds PTHLH gene (parathyroid hormone-like protein A) extracted from
		}	0.012100	1000001.0	zpo_/	TTR gene extracted from Human mutant preallumin gene
734 Bladder	-0.028417	0.3916368	0.322684	0.18891996 3_s_at		linked to familial amyloidotic polyneuropathy (FAP)
i so pianuel	-0.020301	0.3916368	0.3226	0.18887882 M32053	M32053_at	H19 RNA gene
736 Bladder	-0.028745	0.3916183	0.322572	HG2365- 0.18874364 HT2461	. at	Glyceraldehyde-3-Phosphate Dehydrogenase (Gh-K03121)
737 Bladder	-0.028766	0.3915584	0.322522	0.18868731 t		DAF Decay accelerating factor for complement (CD55, Cromer blood group system)
738 Bladder	-0.029168	0.3915509	0.322458	0.18860404	U61276_s_a t	Transmembrane protein Jacqed 1 (H.I1) mRNA
739 Bladder	-0.029489	0.3915392	0.32233	0.18855678 U18549 at		PROBABLE G PROTEIN-COUPLED RECEPTOR GPR6

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

-0.03001 0.3913489 0.322553 0.18843356 X05997 at -0.03001 0.3913737 0.32245 0.18827498 M74096 at RC_AA3496 0.030116 0.3913126 0.322045 0.1882763 12 s at -0.030116 0.3911068 0.321948 0.18811071 X04707 at H63242 s at -0.030421 0.391068 0.321948 0.18711071 X04707 at H63242 s at -0.030754 0.3909387 0.321824 0.18773443 W28045 at -0.031396 0.3908784 0.321489 0.1877443 W28045 at -0.031997 0.3907873 0.321489 0.18774843 W28045 at -0.03199 0.3907473 0.321486 0.18774651 M91487 at -0.03199 0.3907473 0.321486 0.1877469 t M81780 cds -0.032694 0.3907473 0.321056 0.18728555 D84307 at -0.033267 0.3907405 0.321032 0.18702558 at -0.033267 0.3903749 0.320463 0.18702558 at -0.033267 0.3903749 0.320463 0.18702558 at -0.033267 0.3903749 0.320463 0.18702558 at -0.033689 0.3904705 0.320463 0.18702558 at -0.033689 0.3907574 0.320455 0.18688573 X76383 at -0.033689 0.3902574 0.320455 0.186881037 75 at -0.033855 0.3901519 0.320455 0.186881037 75 at -0.033855 0.3901519 0.320455 0.186881037 75 at -0.033855 0.3901519 0.320455 0.186881037 75 at -0.03385771 a	-
-0.03001 0.3913737 0.322245 0.18827498 M74096 at PC_AA3496 -0.030012 0.3913126 0.322045 0.18827498 M74096 at PC_AA3496 -0.030116 0.3911068 0.321948 0.18871071 X04707 at HG3242-PG32042 0.3910789 0.321781 0.187895589 t H74231 s at -0.030754 0.3909387 0.321624 0.18777561 M91487 at -0.031396 0.3907894 0.321489 0.18773443 W28045 at -0.03199 0.3907697 0.321499 0.18773443 W28045 at -0.03199 0.3907473 0.321404 0.18773443 W28045 at -0.03199 0.3907473 0.321404 0.1877565 D84307 at -0.03199 0.3907473 0.321404 0.1877565 D84307 at -0.0332874 0.3907697 0.321056 0.18728565 D84307 at -0.032694 0.3907429 0.320446 0.1870559 at -0.0332879 0.3904705 0.320463 0.18702558 at -0.0332879 0.3904705 0.320463 0.18702558 at -0.033689 0.3902574 0.320455 0.18693897 at -0.033689 0.3902574 0.320455 0.18681037 75 at -0.033855 0.3901519 0.320455 0.18681037 75 at -0.033855 0.3901519 0.320455 0.18681037 75 at -0.03385771 a	គ
COMPANDED COMPANDD COMPANDD	827498 M74096_at ACADL Acyl-Coenzyme A dehydrogenase, long chain
-0.03012	496
-0.030116 0.3911068 0.321948 0.18811071 X04707_at H74231_s_a = -0.030421 0.391081 0.321806 0.18795699 t H74231_s_a = -0.030552 0.3910789 0.321781 0.18789558 t X95463_s_a = -0.0313 0.3909387 0.321524 0.18777561 M91487_at -0.031396 0.3907697 0.3215489 0.18773443 W28045_at -0.031974 0.3907697 0.321489 0.187747565 M81780_cds -0.031974 0.3907697 0.321404 0.1874765 45_at -0.032992 0.3907723 0.321056 0.18721075_at -0.032694 0.3907523 0.321032 0.1870886 L40992_at -0.032694 0.3907527 0.3200499 0.18702558 at -0.032699 0.3904705 0.3200459 0.18702558 at -0.033689 0.3902574 0.320455 0.18693897 at -0.033689 0.3902574 0.320455 0.1868103775_at -0.033855 0.3901519 0.320455 0.1868103775_at -0.033855 0.3901519 0.320455 0.1868103775_at -0.033855 0.3901519 0.320455 0.1868103775_at -0.033855 0.3901519 0.320455 0.1868103775_at -0.03385771_a	882263 12_s_at KIAA0305 gene product
-0.030421 0.391081 0.321806 0.18795699 HT4231_s_a	at
-0.030421 0.391081 0.321806 0.18795699 t	
-0.031652 0.3910789 0.321781 0.18789558 t -0.030754 0.3909631 0.321624 0.18777561 M91487 at -0.03130 0.3908387 0.32164 0.18774561 M91487 at -0.031862 0.3908784 0.321486 0.1877443 W28045 at -0.031862 0.3908784 0.321404 0.1874765 45 at -0.03274 0.3907723 0.321404 0.1874765 45 at -0.032894 0.3907723 0.321056 0.18721075 5 at -0.033267 0.3904705 0.320463 0.18702558 at -0.033267 0.3902574 0.320465 0.18693897 at -0.033855 0.3901519 0.320455 0.18681037 75 at -0.033855 0.3901519 0.320455 0.18681037 75 at	H14231_s_t
-0.030552 0.3910789 0.321781 0.18789558 t -0.030754 0.3909337 0.321624 0.18777561 M91487 at -0.03139 0.3908387 0.32154 0.18773443 W28045_at -0.031862 0.3908848 0.321489 0.1876421 S78653 at -0.031862 0.3908784 0.321486 0.18754499 t -0.031974 0.3907697 0.321404 0.1874765 45 at -0.032274 0.3907473 0.321404 0.18728565 D84307_at -0.032274 0.3907123 0.321056 0.18721075 5 at -0.032694 0.3905223 0.321032 0.18710886 L40992_at -0.032867 0.3903749 0.320463 0.18693897 at -0.033869 0.3902574 0.320455 0.1868573 X76383 at -0.033855 0.3901519 0.320455 0.18681037 75_at -0.033855 0.3901519 0.320455 0.18681037 75_at	w
-0.0313	789558 t FMR2 Fragile X mental retardation 2
-0.0313	777561 M91487_at EST: HUMRTPGEAF Homo sapiens cDNA. (from Genbank)
-0.031396 0.3908848 0.321489 0.1876421 S78653 at AA452625 at -0.031862 0.3908784 0.321486 0.18754499 t	T73443 W28045 at sapiens cDNA, mRNA sequence, (from Genhank)
-0.031862 0.3908784 0.321486 0.18754499 t -0.031974 0.3907697 0.321404 0.1874765 45 at -0.032274 0.3907123 0.321056 0.18721075 5 at -0.032694 0.3905223 0.321056 0.18721075 5 at -0.032267 0.3904705 0.320649 0.18702558 at -0.033267 0.3903749 0.320463 0.18693897 at -0.033855 0.3901519 0.320455 0.18681037 75 at -0.033855 0.3901519 0.320455 0.18681037 75 at -0.033855 0.3901519 0.320455 0.18681037 75 at	#
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-0.031974 0.3907697 0.321404 0.1874765 45 at -0.03199 0.3907473 0.321372 0.18728565 D84307 at -0.032274 0.3907123 0.321056 0.18721075 5 at -0.032694 0.3905223 0.321032 0.18710886 L40992 at -0.033267 0.3904705 0.320649 0.18702558 at -0.033689 0.3902574 0.320463 0.1868573 X76383 at -0.033855 0.3901519 0.320455 0.18681037 75 at AA236771 a	
-0.031974 0.3907697 0.321404 0.1874765 45 at -0.032274 0.3907473 0.321372 0.18728565 D84307 at M81780 cds -0.032694 0.3907123 0.321056 0.18721075 5 at -0.032699 0.3904705 0.320649 0.18702558 at -0.033689 0.3902574 0.320463 0.18693897 at -0.033689 0.3902574 0.320455 0.1868573 X76383 at -0.033855 0.3901519 0.320455 0.18681037 75 at AA236771 a	
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-0.032274 0.3907123 0.321056 0.18721075 5 at -0.032694 0.3905223 0.321032 0.18710886 L40992 at -0.032992 0.3904705 0.320649 0.18702558 at -0.033267 0.3903749 0.320463 0.18693897 at -0.033689 0.3902574 0.320455 0.1868573 X76383 at -0.033855 0.3901519 0.320455 0.18681037 75 at AAZ36771_a	780_cds
-0.032694 0.3905223 0.321032 0.18710886 L40992_at -0.032992 0.3904705 0.320649 0.18702558_at -0.033267 0.3903749 0.320463 0.18693897_at -0.033689 0.3902574 0.320455 0.1868573 X76383_at -0.033855 0.3901519 0.320455 0.18681037 75_at AA236771_a	
-0.032992 0.3904705 0.320649 0.18702558 at L41668 ma1 -0.033267 0.3903749 0.320463 0.18693897 at -0.033689 0.3902574 0.320455 0.1868573 X76383 at -0.033855 0.3901519 0.320455 0.18681037 75 at AA236771 a	
-0.032992 0.3904705 0.320649 0.18702558 at L41668 rna1 -0.033267 0.3903749 0.320463 0.18693897 at -0.033689 0.3902574 0.320455 0.1868573 X76383 at -0.033855 0.3901519 0.320455 0.18681037 75 at AA236771 a	Zm63c02.r1 Stratagene fibroblast (#937212) Homo sapiens cDNA
-0.032855 0.3901519 0.320455 0.18702558 at L41668 rna1 c.0.033855 0.3901519 0.320455 0.18681037 75 at AAZ36771_a	
-0.033267 0.3903749 0.320463 0.18693897 at -0.033689 0.3902574 0.320455 0.1868573 X76383 at -0.033855 0.3901519 0.320455 0.18681037 75 at AA236771_a	_at
-0.033855 0.3901519 0.320455 0.18681037 75 at AA236771_a	L41668_ma1
-0.033855 0.3901519 0.320455 0.18681037 75_at	at X76383_at
-0.033855 0.3901519 0.320455 0.18681037 75_at	1
-0.033855 0.3901519 0.320455 0.18681037 75 at AA236771_a	
AA236771_a	
-0.033876 0.3900421 0.320433 0.18678343 t	AA236771_a EST: zr99e10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 678343 t IMAGE:683850 5', mRNA sequence, (from Genbank)
760 Bladder -0.034205 0.3900045 0.320416 0.18664177 L42354 at (clone 48E	ä

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Docket No.	2825.2020-002
Title: Gen	etic Markers for Tumors
Inventors: S	Sridhar Ramaswamy, et al.

761 Bladder	-0.034385	0.3899595	0.320403	0.18657228 t	U19145_s_a t	G antigen 4
762 Bladder	-0.034771	0.38993	0.320403	0.1865496	L78833_cds 4_at	Ifp35 gene extracted from Human BRCA1, Rho7 and vatl genes, and ipf35 gene, partial cds
763 Bladder	-0.035006	0.3897993	0.320322	0.18653668	.47125 s at	0.18653668 L47125_s_at EEF1A1 Translation elongation factor 1-alpha-1
764 Bladder	-0.03503	0.389783	0.320302	0.1864109	A310850_a	AA310850_a EST: EST181766 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA t sequence. (from Genbank)
765 Bladder	-0.035159	0.3897465	0.320166	HG668- 0.18624996 HT4793 at		T-Cell Factor 1, A/B/C, Alt. Splice 1, A
766 Bladder	-0.035343	0.3897402	0.319963	0.18613453 35 at	A4494	EST: zx05c11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785588 3', mRNA sequence, (from Genbank)
767 Bladder	-0.035349	0.3896959	0.319923	0.18603286	RC_D59362 at	EST: Human fetal brain cDNA 3'-end GEN-023A02, mRNA sequence. (from Genbank)
768 Bladder	-0.035574	0.3895944	0.319876	RC 0.18597053 64	AA1279 at	EST: zl13g07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 501852 3', mRNA sequence, (from Genbank)
769 Bladder	-0.035596	0.38957	0.319827	RC 0.18594567 55	RC_AA4560 55_at	EST: aa03f02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 812187 3', mRNA sequence. (from Genbank)
770 Bladder	-0.035655	0.3	0.319756	0.18587051 S49592	49592 s at	at Transcription factor E2F like protein Ihuman, mRNA, 2492 ntl
771 Bladder	-0.03572	0.38953	0.319691	0.18582466 X52011 at	52011 at	MYF6 Muscle determination factor
772 Bladder	-0.035772	-0.035772 0.3893506	0.319637	RC 0.18578549 48	1	EST: zx68b07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796597 3' similar to SW:BTD_HUMAN P43251 BIOTINIDASE PRECURSOR: mRNA sequence. (from Genbank)
773 Bladder	-0.03581	0.3892865	0.319609	0.18569428 U53786 at		EVPL Envoplakin
774 Bladder	-0.035854	0.3892196	0.319568	X0788 0.18563591 1_f_at	X07881_rna 1_f_at	Human gene PRB3L for proline-rich protein G1
775 Bladder	-0.036148	0.3891827	0.319542	0.18548931 t	A443437_a	AA443437_a EST: zw94b07.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA tolone 784597 5', mRNA sequence. (from Genbank)
776 Bladder	-0.036155	0.3891742	0.31951	HG1098 0.18534674 HT1098	at .	Cystatin D
777 Bladder	-0.036159	0.3891442	0.31939	0.18522803 K	03183 f at	0.18522803 K03183 f at Chorionic gonadofronin beta subunit gene
778 Bladder	-0.036347	0.389093	0.319212	0.1851617 U37707_at	37707_at	DLG3 Homolog 3 of Drosophila large discs
779 Bladder	-0.036462	0.38901	0.319197	0.18507805 L	11238 s at	0.18507805L11238 s at GP5 Glycoprotein V (platelet)
780 Bladder	-0.036479	0.3889986	0.319159	0.18501881 X98176	98176_at	MACH-alpha-2 protein
781 Bladder	-0.037156		0.319064	0.18497732 U36221	ät	Pancreatic zymogen granule membrane protein GP-2 mRNA
/82 Bladder	-0.03/168	0.3889706	0.319039	0.18496111 J05037	at	L-SERINE DEHYDRATASE

- 0				0		EST: yi56g01.r1 Homo sapiens cDINA clone 162288 5. (from
/83 Bladder	adder	-0.03/352		0.31899	0.1848/U1/ HZ5982 at	ูบenbank)
784 Bladder	adder	-0.037433	0.3888803	0.318978	0.18473051 D87449_at	KIAA0260 gene, partial cds
					HG3288-	
785 Bladder	adder	-0.037499	0.3888392	0.318944	0.1846395 HT3465_at	Xanthine Dehydrogenase (Gb:U06117)
786 Riadder	ndder	-0.037582	0.3888254	0 318744	AA043894	AA043894_a EST: zk57b05.r1 Soares pregnant uterus NbHPU Homo sapiens
787 Bladder	adder	-0.037757	١.		0.18454467177564 54	DGS D mRMA 3' and
101	ianna	0.007		0.01010		טומילי ליינים לי
788 Bladder	adder	-0.037985	- 1	0.318692	0.18448463 Y11416 at	P73
789 Bladder	adder	-0.038096	0.3885346	0.318689	0.18445788 X52008_at	GLRA2 Glycine receptor, alpha 2
790 Bladder	adder	-0.038301	0.3884737	0.318592	0.18441501 1 at	Platelet-derived growth factor (PDGFA) A chain gene
791 Bladder	adder	-0.038347	0.3884653	0.318587	0.18422878 U64197 at	CC chemokine LARC precursor
					AFFX-BioB-	
792 Bladder	adder	-0.038464	0.3884125	0.318456	0.18417145 5_at-2	AFFX-BioB-5_at (miscellaneous control - 11k chips)
0		4			AFFX-BioB-	
793 Bladder	adder	-0.038464		0.318448	0.1841414 5_at	AFFX-BioB-5_at (endogenous control)
794 Bladder	adder	-0.038474	- 1	0.318267	0.1840723 X04571_at	EGF Epidermal growth factor
795 Bladder	adder	-0.038671	0.3883067	0.318238	0.18396977 S81944_at	GABRA6 Gamma-aminobutyric acid (GABA) A receptor, alpha 6
796 Bla	Bladder	-0.038671	0.3882187	0.318157	0.18393171 S81944 at-2	 Gamma-aminobutyric acid (GABA) A receptor, alpha 6
797 Rladder	ıdder	-0 039458	0.3881823	0.318016	M16707_rna	1
798 Bladder	nddar	-0.039879				DDL14 Define debudences 4 (44 cie.)
200 000	SOOK	4.00000	- 1	0.011043	0.10302302 009/1/ dt	RUTI Retiilol deflydiogenase 1 (11-cis)
/ 99 Bladder	adder	-0.040094	0.3880022	0.317844	0.18379784 U06088 at	N-ACETYLGALACTOSAMINE-6-SULFATASE PRECURSOR
		0			D83017_s_a	
800 Bladder	adder	-0.040261	9	0.317769	0.183646 t	Nel-related protein
801 Bla	Bladder	-0.040266		0.317669	0.18359812 U29607_at	EIF-2-associated p67 homolog mRNA
802 Bladder	adder	-0.04041	0.3879417	0.317593	0.18359652 X80878_at	R kappa B mRNA
803 Bladder	ndder	-0.040444	0.3878776	0.317503	Z35402_rna	
804 Bladder	ıdder	-0 040452	. 1		-' ്× +	-
805 Bladder	ıdder	-0.040502	_Li		0.18332963 U90910_at	Clone 23564 mRNA sequence
806 Bladder	ıdder	-0.040502	0.3874456	0.317393	0.18323557 U90910 at-	0.18323557 U90910 at-2 Human clone 23564 mRNA sequence
807 Bladder	adder	-0.040935	0.3874282	0.317386	0.18320854 U13219_at	Forkhead protein FREAC-1 mRNA
808 Bladder	dder	-0.041346	-0.041346 0.3873323	0.317278	H89896_s_a	EST: yw29e12.r1 Homo sapiens cDNA clone 253678 5'. (from

809 Bladder	-0.041386	0.3872941	0.317151	0.1830505 W56463	N56463 at	EST: zc57h06.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 326459 5', mRNA sequence. (from Genbank)
					RC_AA1913	EST: zp83b09.s1 Stratagene HeLa cell s3 937216 Homo sapiens
810 Bladder	-0.041622	0.3871705	0.317042	0.1829702 23	23_at	cDNA clone 626777 3', mRNA sequence. (from Genbank)
811 Bladder	-0.041659	0.3871328	0.317018	0.18292162 D83657	083657_at	Calcium-binding protein in amniotic fluid 1
812 Bladder	-0.041729	0.3870957	0.317	0.18282989 U51127	J51127_at	IRF5 Interferon regulatory factor 5
813 Bladder	-0.041926	0.3870679	0.316944	0.1826882 X70340	X70340_at	TGFA Transforming growth factor, alpha
					HG1227-	
					HT1227 s_a	
814 Bladder	-0.042023	0.3869889	0.316873	0.18257338 t		Collagen, Type Ii, Alpha 1
815 Bladder	-0.042134	0.3869088	0.316808	0.18247803 L49054_at	-49054_at	T(3;5)(q25.1;p34) fusion gene NPM-MLF1 mRNA
816 Bladder	-0.042295	0.3868925	0.316481	0.18235354 D13305 at	713305_at	CCKBR Cholecystokinin B receptor
147 Dioddor	0.049442	7200000	740464		U08198_ma	
o 17 biaddel	-0.042412	0.36060/4	0.310431	0.18228452	l at	complement പ്ര gamma subunit precursor (പ്രദ്യേ) gene
818 Bladder	-0 042555	0.3867752	0.31645	10 18220404	RC_D20297 at	EST: Human HL60 3'directed Mbol cDNA, HUMGS01271, clone pm2024 mRNA seculance (from Genhank)
	200	100000	2	1	HC/185	לייוים מושלוים לייוים אין מילות אין מילות אין
819 Bladder	-0.042602	0.3864655	0.316264	0.18212236 HT4455	134165- 1T4455 at	Estroden Sulfotransferase. Ste
820 Bladder	-0.042682	0.3864215	0.316031	0.18209106 Z38026 at	238026 at	CAP-18 protein
821 Bladder	-0.042683	0.3864205	0.315881	0.18197083 X06985 at	₹06985 at	HMOX1 Heme oxygenase (decycling) 1
					M24736_s_a	
822 Bladder	-0.04293	0.386372	0.315732	0.18194029 t		SELE Selectin E (endothelial adhesion molecule 1)
2000	00000	0000	7			EST: zr51e07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
823 Bladder	-0.043024	0.386258	0.315646	0.18190604 41	11_at	
824 Bladder	-0.043058	0.3858043	0.315634	0.18172954 X97230 f at	x97230 f at	NK receptor, clone library 4M1#6
825 Bladder	-0.043284	0.3856897	0.315562	0.18171148 33_s_at	RC_AA2365 33_s_at	Ecotropic viral integration site 1
					U52077_s_a	
826 Bladder	-0.043347	0.3856251	0.315518	0.1816369 t		Mariner1 transposase gene, complete consensus sequence
897 Bladder	0.043547	0 3954014	0 245464	V 404 F0000	X14085_s_a	
828 Bladder	0.043594	0.385/128	0.315347	0.10130323	10.0000	GCTC Confession (1977)
820 Bladder	-0.0736AB	0.3853718	0.010047	0.10130303 002000 at	302000 at	UST US CYSTALII IVI
בט הומחתם	0+00+0.0-	0.36337 10	0.010042	0.10140073	J02392 at	Homo sapiens zinc linger protein mKINA, complete cds
830 Bladder	-0.043723	0.3852908	0.315283	0.18130343 t	D10537_s_a t	MPZ Myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)
831 Bladder	-0.043723	0.3852509	0.315166	D1 0.18123597 t-2	D10537_s_a t-2	Myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)
000					AA504736_a	

and plans also green green and send green green green and green green and green green and green green and green gr

835 Bladder -0.044235		1 0.315075 5 0.315052 8 0.314931	0.18099922 X00949 at 0.180990922 U47050 at 0.18091089 Z96810 at U58496 s a	Prepro-relaxin H1 Putative calcium influx channel (htrp3) mRNA DNA sequence from PAC 452H17 on chromosome X contains sodium and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs
-0.04433	1433 0.384841 1367 0.3848284	1 0.3148 4 0.314751	0.18087707 t 0.18077473 M35198_at	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1 Integrin B-6 mRNA
-0.04453	453 0.3848256	3 0.314651	AA046737_a	
-0.044571		0.3		
Bladder -0.045069	069 0.3844741	0.314585	0.18050249 X05615_at 0.18043184 S57296_at	Thyroglobulin HER2/neu receptor {3' region, alternatively spliced} [human, breast cancer cell line mRNA Partial 175 at
-0.045081	081 0.3844155	0.314583	0.1803542 J05253	
-0.045087	087 0.3843775 189 0.3840872	0.314393	RC_AA3502 0.18033373 68_at	
-0.045272	1 1		AA418320_a	(richoz) glucose transporter gene mRNA Homo sapiens mRNA for pre-mRNA cleavage factor I gula de
-0.045289	289 0.3837578	0.314275	0.18009719 W16486 at	EST: 2b11e11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 301772 5' mRNA seguence (from Conhock)
-0.045358	358 0.3836986	0.314254	0.18001667 74_at	EST: zs12f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685007 3', mRNA sequence, (from Genhank)
-0.046107	107 0.383659	0.314223	RC_AA0534 0.17997743 00_at	EST: 2/71b04.s1 Stratagene colon (#93/204) Homo sapiens cDNA clone 510031 3' mRNA sequence (from Generals)
-0.046137	37 0.383646	0.314133	X51362_s_a 0.179903 t	DRD2 Donamina D2 recentor
-0.046357		0.3141	0.17985399 90 at	EST: zx88c06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
-0.04644	344 0.3829775	0.313987	7651 at	MYOG Myogenin (myogenic factor 4)
-0.046661	161 0.3829162	0.313968	0.17971055 96 r at	Ferritin, light polynentide
-0.046761	61 0.3828282	0.313921	24_a	EST: zs53h10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701251 5' mRNA sequence (from Cont.)
-0.0467	-0.046776 0.3827492	0.313888	0.17958038 L23852 at	(clone Z146) retinal mRNA, 3' end and repeat region

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RENIN PRECURSOR, RENAL	Protein-tyrosine phosphatase	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3	PRECURSOR	Mitogen induced nuclear orphan receptor (MINOR) mRNA	PAH Phenylalanine hydroxylase	Agouti (mouse) related protein	P97 homologous protein	IKBL mRNA	EST: za85a06.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299314 5', mRNA sequence. (from Genbank)	Calcitonin	EST: aa70h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826343 3' similar to WP:C09F5.2 CE01774;, mRNA sequence. (from Genbank)	EST: zh93e03.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	CDINA CIONE 42880U 3', MKINA Sequence. (from Genbank)	(ciolle zap i i s) mKNA, 3 end or cds Cartilage-specific homeodomain protein Cart 4 mDNA	UMPS gene extracted from Human UMP synthase mRNA	Metabotropic dlutamate recentor 8 mRNA	EST: aa33b06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	MAGE-10 antiden (MAGE10) gene	0.17823903 U10685 at-2 Melanoma antigen, family A. 10	Glucose transporter (Gl 1/T4) gene	Solute carrier family 2 (facilitated alucose franchar) member 4	EST: yu11a03.r1 Homo sapiens cDNA clone 233452 5. (from Genbank)	EST: ze58g07.s1 Soares retina N2b4HR Homo sapiens cDNA clone 363228 3', mRNA sequence. (from Genbank)
M26901_s_a t	D64053 at		M35878 at	U12767 at	L47726 at	U88063 at	D85939 at	X77909_at	W05585_at		_AA5211 at	AA0047			7	AC000099_a t	A465262_a		C)	M91463_rna 1_at	3_rna		A0188
0.17950714	0.17949066 D64053		0.17941739 M35878	0.17930369 U12767 at	0.17921634 L47726 at	0.17918551	0.17913964 D85939	0.17903109 X77909	0.17901021 W05585	HG2290- 0.17898475 HT2386_at	RC 0.17886487 11	RC RC	0.17862274 A0400 at	0.17853734 U31986 at	0.17841299	0.17836724	0.178304481	0.17826846 U10685 at	0.17823903	0.17816487 1 at	M9146 0.17801975 1_at-2	0.1779619 H78886 at	RC_A 0.17791204 76_at
0.313812	0.313789		0.313772	0.313769	0.313733	0.31365	0.313637	0.31358	0.313358	0.313346	0.313266	0.3132748	0.313224	0.313171	0.313148	0.313064	0.313036	0.312796	0.312742	0.312664	0.312637	0.312524	0.312506
0.3826017	0.382595		- 1	0.3824896		0.3824306	0.3823082	0.3823004	0.38226	0.3821859	0.3821023	0 3820475	0.3820371		0.3819985	0.3819808	0.3819386	0.381879	0.381844	0.3818053	0.381739	0.3816713	0.3815118
-0.046844	-0.046941		-0.047023	-0.047073	-0.047356	-0.047482	-0.047599	-0.047623	-0.047636	-0.047699	-0.047809	-0.048048	-0.048208		-0.04829	-0.048471	-0.048607	-0.048809	-0.048809	-0.048856	-0.048856	-0.048856	-0.048939
855 Bladder	856 Bladder		857 Bladder	858 Bladder	859 Bladder	860 Bladder	861 Bladder	862 Bladder	863 Bladder	864 Bladder	865 Bladder	866 Bladder	867 Bladder	868 Bladder	869 Bladder	870 Bladder	871 Bladder	872 Bladder	873 Bladder	Bladder	875 Bladder	876 Bladder	877 Bladder
85	85		82	85	85	986	98	398	86;	864	865	866	867	398	398	870	871	872	873	874	875	876	877

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X11 protein mRNA, partial cds	EST: zs40a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clor	00/036 3, ITIKINA sequence. (Irom Genbank)	EST: zx76a07.s1 Soares ovary tumor NbHOT Homo sapiens cD	clone 809652 3', mRNA sequence. (from Genbank)	SCP1 protein		Kinase Inhibitor P27kip1, Cyclin-Dependent		C9 Complement component C9	EST: ze76a01.s1 Soares fetal heart NbHH19W Homo sapiens of clone 364872 31 mRNA sequence (from Genhank)	IL3RA Interleukin 3 receptor, alpha (low affinity)		Transcription factor TBX5 mRNA	EST: yf84f08.r1 Homo sapiens cDNA clone 29219 5'. (from Gen	EST: zv18a05.r1 Soares NhHMPu S1 Homo sapiens cDNA clon	733908 5, MKINA sequence. (from Genbank)	EST: zl71a06.r1 Stratagene colon (#937204) Homo sapiens cDN clone 510034 5', mRNA sequence. (from Genbank)	Transcription factor AP-2 alpha (activating enhancer-binding pro-	(mind)	TRANSCRIPTION FACTOR AP-2	Post-synaptic density protein 95 (PSD95) mRNA	Homo sapiens mRNA for ADP ribosylation factor-like LAK, comp	spo	IEX-1	EST: zu25e03.s1 Soares NhHMPu S1 Homo sapiens cDNA clon	TANIS Transpir I (skeletal fact)	CCND1 Cyclin D1 (PRAD1: parathyroid adenomatoric 4)	EST: zw02f08.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 768135 5; mRNA sequence (from Genhank)	Interleukin 10 (IL10) gene	
U79255_at	RC_AA2353	45 al	KC_AA4546	75_at	X95654_at	HG4258-	HT4528_at	X02176_s_a		RC_AA0244 82_at	D49410 at	U80987_s_a		R14545_at	AA479990_a	-	AA053052_a t	X52611_s_a t-2	X52611 s a	1	U83192_at		ਡ	S81914_at	RC_AA4215	121715 at	ज	25_a)_rna	
0.17778562	0.47773773	0.11.101.0		0.17768581	0.17761421		0.17754705		0.17747056	0.17738837	0.1773117		0.17726237	0.177218	7708497	0.11100121	0.17703103	0.17698587		0.17692783	0.17683215		0.17676586	0.17665437	0 17657328	0.17655952	0.17652261	0.17641869	0.17637491	
	0.312424	174710.0	0	0.312421	0.312421		0.312325	•	0.312167	0.31216	0.31207		0.312065	0.311922	0.311879	0.0110.0	0.311715	0.311532		0.3115	0.311436	000	0.311408	0.311378	0.311253	0.311236	0.311175	0.311081	0.310921	
0.3813945		- 1					- 1		l l	0.3812373	0.381231	1	0.3811915	0.3810056	0.3807295	0.0001	0.3806762	0.3806182		0.3804509	0.380384	2000000	0.3002907	0.3802084	0.3802191	0.3801958	0.3801661	0.3801507	0.3801491	
-0.049251	-0.04934	0.0	0,00	-0.049594	-0.049889	1	-0.050145	(((-0.050162	-0.050354	-0.050406		-0.05043	-0.050454	-0.050779		-0.050831	-0.051018		-0.051018	-0.051185	0.054445	0.051413	/001 co.u-		-0.051762	-0.051891	-0.052106	-0.052219	
879 Bladder	880 Bladder		777	881 Bladder	882 Bladder		583 Bladder	-	384 Bladder	885 Bladder	386 Bladder	207 Dlodder	oor Diaudei	888 Bladder	89 Bladder		890 Bladder	891 Bladder		92 Bladder	93 Bladder	94 Bladdor	05 Bladdor	30 Diaduei	896 Bladder	897 Bladder	898 Bladder	899 Bladder	900 Bladder	
	-0.049251 0.3813945 0.312483 0.17778562 U79255_at	-0.049251 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353	-0.049251 0.3813945 0.312483 0.17778562 U79255_at RC_AA2353 0.04934 0.3813911 0.312424 0.1777377343_at	-0.049251 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353	-0.049594 0.3813791 0.312427 0.17778562 U79255_at RC_AA2353	-0.049594 0.3813045 0.312483 0.17778562 U79255_at RC_AA2353	-0.049251 0.3813945 0.312483 0.17778562 U79255_at RC_AA2353	-0.049594	-0.049251 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353	-0.049251 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353	-0.049251 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353	-0.049251 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353	Bladder -0.05046 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353	-0.049251 0.3813945 0.312483 0.17778562 U79255 at e1.0.049251 0.3813911 0.312424 0.17773773 43 at e1.0.049889 0.3813791 0.312421 0.17768581 75 at e1.0.049889 0.3813083 0.312421 0.17768581 75 at e1.0.050145 0.3812536 0.312325 0.17754705 HT4528 at e1.0.050406 0.3812373 0.312167 0.17747056 t e1.0.050406 0.3812373 0.31216 0.17738837 82 at e1.0.050406 0.381231 0.31207 0.17738837 82 at e1.0.05043 0.3811915 0.312065 0.17726237 t	Bladder -0.049251 0.3813945 0.312483 0.17778562 U79255 at Bladder -0.04934 0.3813911 0.312424 0.17773773 43_at RC_AA4546 Bladder -0.049889 0.3813791 0.312421 0.17768581 75_at Bladder -0.050145 0.3812536 0.312421 0.17764705 HT4528_at Bladder -0.050162 0.3812413 0.312325 0.17747056 HG4258-at Bladder -0.050406 0.3812373 0.31216 0.17747056 HCAA0244 Bladder -0.050406 0.381231 0.31207 0.17738837 82_at Bladder -0.05043 0.381231 0.31206 0.17738837 Bat Bladder -0.050454 0.3811915 0.312065 0.17726237 H89987_s_a	-0.049251 0.3813945 0.312483 0.17778562 U79255 at -0.04924 0.3813911 0.312424 0.17773773 4.3 at RC_AA4546	Bladder -0.049251 0.3813945 0.312483 0.17778562 U79255 at RC_AA2353 Bladder -0.049594 0.3813911 0.312424 0.17773773 4.3 at RC_AA4546 Bladder -0.049889 0.3813791 0.312421 0.17768581 75 at HG4258- Bladder -0.050145 0.3812536 0.312325 0.17754705 HT4528 at HG4258- Bladder -0.050406 0.3812413 0.312167 0.17747056 t RC_AA0244 Bladder -0.050406 0.381231 0.31216 0.17738837 82 at Bladder -0.050436 0.381231 0.31206 0.17738837 82 at U80987 s at Bladder -0.050436 0.381231 0.31206 0.17738837 82 at U80987 s at Bladder -0.050436 0.3811915 0.312065 0.17726237 t A4479990 a Bladder -0.050779 0.3807295 0.311879 0.17708127 t	-0.049251 0.3813945 0.312483 0.17778562 U79255 at -0.049251 0.3813941 0.312424 0.17773773 43 at -0.049594 0.3813791 0.312421 0.17768581 75 at -0.049889 0.3813791 0.312421 0.17768581 75 at HG42580.050145 0.3812536 0.312325 0.17754705 HT4528 at HG42580.050406 0.3812413 0.312167 0.17747056 t HG42580.050406 0.3812373 0.312167 0.17747056 t U80987 s at -0.05043 0.3811915 0.312065 0.17726237 t H454545 at -0.050454 0.3811915 0.312065 0.17726237 t H454545 at -0.050831 0.3807295 0.311879 0.17708127 t HA4545 at -0.050831 0.3807295 0.311715 0.17708127 t HA455050 at -0.050831 0.3806762 0.311715 0.17703103 t	-0.049251 0.3813945 0.312483 0.17778562 U79255 at -0.049251 0.3813911 0.312424 0.17773773 43 at RC_AA4546 -0.049594 0.3813791 0.312421 0.17768581 75 at RC_AA4546 -0.050145 0.3812536 0.312421 0.17761421 X95654 at HG4258-0.050162 0.3812373 0.312167 0.17754705 HT4528 at X02176_s_a -0.050354 0.3812373 0.31216 0.17738837 82 at U80987_s_a -0.050406 0.381237 0.312067 0.1773177 D49410 at -0.050454 0.3811915 0.312065 0.17726237 t -0.050454 0.3807295 0.311879 0.17708127 t -0.050831 0.3806762 0.311715 0.17708127 t -0.050831 0.3806762 0.311715 0.17703103 t -0.05018 0.3806762 0.311532 0.17703103 t -0.051018 0.3806182 0.311532 0.17698587 t.2	Colored State Colored Stat	Colored Colo	Colored State Colored Stat	Colored Border Colo	Colored Colo	Courage Cour	Courage Cour	Columbation Columbation	Courage Cour	Court Cour	Columbia Columbia

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901 Bladder	-0.052241	9	0.310844	0.17628665 06_at	क	Biphenyl hydrolase-like (serine hydrolase)
902 Bladder	-0.05242	0.380094	0.310809	0.1762216 M19311	19311 at	CALM1 Calmodulin 1 (phosphorylase kinase, delta)
903 Bladder	-0.052562	0.38005	0.310767	0.17614442 U29091	9091_at	Selenium-binding protein (hSBP) mRNA
904 Bladder	-0.052612	0.3798863	0.310751	Ms 0.17608452 t	M98399_s_a t	a CD36 CD36 antigen (collagen type I receptor, thrombospondin receptor)
905 Bladder	-0.053404	0.3798255	0.310744	AB 0.17602567 t-2	AB000464_a t-2	Homo sapiens mRNA, exon 1, 2, 3, 4, clone:RES4-24A
906 Bladder	-0.053404	0.3798242	0.310695	AE 0.17585273 t	AB000464_a t	mRNA, clone RES4-24A, exon 1, 2, 3, 4
907 Bladder	-0.05352	0.3797001	0.31062	RC_A 0.17581442 79_at	AA2848 at	RC_AA2848 Homo sapiens incomplete cDNA for a mutated allele of a myosin 79 at class I, myh-1c
908 Bladder	-0.053525	0.3796234	0.31062	0.17570098 t	M86933_s_a t	AMFLY Amelogenin (chromosome Y encoded)
909 Bladder	-0.053631	0.3795871	0.310562	0.17562555 U25997	5997 at	Stanniocalcin precursor (STC) mRNA
910 Bladder	-0.053647	0.379577	0.31038	0.17554551 t	U31903_s_a t	CREB-RP (creb-rp) mRNA
911 Bladder	-0.05379	0.3794811	0.310354	X51758 0.17550051 5_s_at	spo_c	Ig light-chain, partial Ke-Oz- polypeptide; Author-given protein sequence is in conflict with the conceptual translation gene extracted from Human lambda-immunoglobulin constant region complex (germline)
912 Bladder	-0.053809	0.3794594	0.310343	RC_A 0.17545697 96 at	A0051	EST: zh95g08.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429086 31 mRNA sequence (from Garbank)
913 Bladder	-0.054179	0.3793585	0.310253	0.1754006 X97261 r at	7261 r at	
914 Bladder	-0.05418	0.3793045	0.310106	0.1753604 01	RC_AA4436 01 at	Ribosomal protein S6 kinase. 90kD. nolvnentide 4
915 Bladder	-0.05418	0.3792672	0.309962	0.17530957 D70830	0830 at	Doc2 beta
916 Bladder	-0.054438	0.3791232	0.309836	HG2320- 0.17524497 HT2416	, te	Integrin Beta 3 Subunit
917 Bladder	-0.054711	0.3790096	0.309822	0.17514394 X81788	ज्ञ	DS-1 mRNA
918 Bladder	-0.054745	0.3789618	0.309768	HG3104 0.17511037 HT3280	HG3104- HT3280 at	Serine Protease Met1
919 Bladder	-0.054884	-0.054884 0.3789519	0.30971	0.174969 Z22536		SERINE/THREONINE-PROTEIN KINASE RECEPTOR R2
920 Bladder	-0.055123	0.3788492	0.309659	0.17490895 U42359	2359 at	N33 protein form 1 (N33) dene exon 10 and complete ode
921 Bladder	-0.055216		0.309571	0.17488223 X59711	at	NFYA Nuclear transcription factor Y, alpha
922 Bladder	-0.055298	0.3787144	0 300571	0 47470882 1 24880		

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923 B	923 Bladder	-0.055363	-0.055363 0.3786407	0.309539	0.17470266 M23263_at		AR Androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)
924 B	924 Bladder	-0.055363	0.3785724	0.309519	0.1746403	M23263_at-2	Androgen receptor (dihydrotestosterone receptor; testicular 0.1746403 M23263_at-2 feminization; spinal and bulbar muscular atrophy; Kennedy disease)
						RC_AA6090	RC_AA6090 EST: af10e05.s1 Soares testis NHT Homo sapiens cDNA clone
925 B	925 Bladder	-0.055451	- 1	0.309518	0.17461504 46 at	46_at	1031264 3', mRNA sequence. (from Genbank)
926 B	926 Bladder	-0.055468	0.3784481	0.309517	0.17457187	0.17457187 M28210 at	GTP-binding protein (RAB3A) mRNA
						×	
927 B	927 Bladder	-0.056229		0.30948	0.17449811	1_at	Zinc finger protein, Hsal1
928 B	928 Bladder	-0.056404	0.3783108	0.309291	0.17445382 D63813_at	D63813_at	Rod photoreceptor protein
						U58675 cds	OR17-40 gene extracted from Human olfactory receptor gene cluster on chromosome 17. OR17-228 and OR17-40, and OR17-24 and
929 B	929 Bladder	-0.056584	0.378178	0.309255	0.17440191	2_at	OR17-25 pseudogenes
930 B	930 Bladder	-0.056686		0.309149	0.17429632	L27584_s_at	0.17429632 L27584_s_at CAB3b mRNA for calcium channel beta3 subunit
931 B	931 Bladder	-0.056927	0.3779717	0.309098	0.17425135	0.17425135 D21205_at	
9		1				AA249368_a	
932 B	932 Bladder	-0.05699	0.3779557	0.309027	0.17419182	-	sapiens cDNA 5', mKNA sequence. (from Genbank)
(0		0	1		J22961_s_a mRNA clone with similarity to L-glycerol-3-phosphate:NAD
933 B	933 Bladder	-0.057061		0.30902	0.1/4144	-	oxidoreductase and albumin gene sequences
934 B	ladder	-0.057316	0.3778359	0.309016	0.17404564 L20433 at	L20433_at	Octamer binding transcription factor 1 (OTF1) mRNA
						RC_AA2583	
935 B	935 Bladder	-0.057415	-	0.308978	0.1739985 83	83_at	Ash2 (absent, small, or homeotic, Drosophila, homolog)-like
936 B	936 Bladder	-0.057557	0.377759	0.308947	0.17399201	0.17399201 U03399_at	
						RC_AA0253	
937 B	937 Bladder	86760.0-	- 1	0.308836	0.1738913 52	52_at	clone 364 / 59 3', mRNA sequence. (from Genbank)
938 B	938 Bladder	-0.057623	0.3776443	0.308821	0.17383607	0.17383607 X02750_at	PROC Protein C (inactivator of coagulation factors Va and VIIIa)
000	1			, 0000	000000000000000000000000000000000000000	AC000115_c	AC000115_c WUGSC:H_GS188P18.1a gene extracted from Human BAC clone
939 E	939 bladder	97760.0-	0.3770403	0.308681	0.17378932 ds1_at	ds i_at	GS188P18
							Human DNA sequence from PAC 196E23 on chromosome Xq26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor
						1	TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-
	7	0		07.000.0	000000000000000000000000000000000000000	AC000115_c	AC000115_c 3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene
340 E	940 Bladder	01100.0-		0.300040	0.17376082 ds1_at-2	usi ar-z	couling for two isolottis, a predicted CpG island, ESTS and STS
941 E	941 Bladder	-0.057815	0.3776221	0.308509	0.17359714 M93311	M93311_at	GIF
a C/0	949 Bladder	-0.057903	-0.057903 0.3775278	0.308477	0 17354976	0.17354976 T23709 at	Seo545 Homo canions cDNA clone HY8cDNA2-4 5' (from Genhank)
775	opposition in the same of the	200.0	0.01	20000	70000	140100 00	

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		7	-					1					-	1		_	_		_					,	-			-					
G protein-coupled receptor GPR-NGA gene	HEPATOCYTE NUCLEAR FACTOR 4	TRANSCRIPTION FACTOR P65	AGTR1 Angiotensin receptor 1	CTSB Cathepsin B	EST: zc54a05.r1 Soares senescent fibroblasts NbHSF Homo sapiens	cDNA clone 326096 5' similar to contains element MER6 repetitive	element;, mRNA sequence. (from Genbank)	CMACA NATION	OREIN CAINIP responsive element modulator	EST: zk51a08.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486326 5', mRNA sequence. (from Genbank)	EST: 2485h01.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 648433 5' mRNA sectionse (from Gorbank)	Semanhorin III family homolog mRNA	Transcription factor E2F like protein Ihuman, mRNA, 2492 nfl	EST: zw23d05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 770121 3', mRNA sequence, (from Genbank)	REGULATOR OF G-PROTEIN SIGNALLING 2		Interleukin 9 receptor (IL9R) gene	EST: zp74c05.s1 Stratagene HeLa cell s3 937216 Homo sapiens	cDNA clone 625928 3', mRNA sequence. (from Genbank)	EST: zd50g02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 344114 5', mRNA sequence, (from Genbank)	CRKL V-crk avian sarcoma virus CT10 oncogene homolog-like	Homo coning alaka 9 (11) and	Gall Ac-T4 gene		Growth factor receptor-bound protein 14	Serine/threonine protein kinase, NIK	Glutamine cyclotransferase	EST: Homo sapiens thymus mRNA (randomly primed, normalized),	single-pass sequence, mRNA sequence. (from Genbank)	UBA52 Ubiquitin A-52 residue ribosomal protein fusion product 1	Cd4 Antigen
U64871_at	at	L19067_at	at				ਜ਼	D14826_s_a	1	AA044095_a t	AAZU9Z39_a t	1	at	RC_AA4304			L39064_rna1		AA1868	at		at	ਜ਼	//20778_s_a	1	-						at	_at
0.17349717 U64871		0.17340761 L19067	0.17323422 S77410	0.17322688 L22569_at			· 0.17310478 W52493	0.47304769	0.11 3047 00	0.17299914	0.17294106	0.17291485 U38276 at	0.17278095 U47677		0.17274654 66_at	0.17272046 L13391_at		0.17263705		0.17256323 97		0.17248246 W73805	0.17239277 X59656	0.172314261	0.17224173 Y08564 at		0.17220227 24 s at	0.17216259 Y10256	0.17213538 X71125_at		0.1720956 L44538_at	0.171912 M26880	HG3477 0.17185773 HT3670
		- 1	0.308247	0.30823		(0.308116	0 308064		0.307896	0.307697	0.307635	0.30757		0.307509	0.3075		0.307483		0.307462	004	0.307400	0.307406	0.307273	0.307194		0.307152	0.307081	0.307075	1	0.307026	0.307025	0.306999
				0.3770426			0.3770138	0.3769707		0.3769475	0.3769444	1	0.3768076			0.3766483		0.3766062	1	0.3765569	1007CC0	0.3765490	0.3/05489	0.3762352	1 :	0	0.3/59164	0.3758407	0.3757221		0.3757021	0.3755727	-0.06016 0.3754811
-0.057932	-0.058142	-0.058185	-0.058279	-0.058318		7	-0.058408	-0.058582	0.00000	-0.058627	-0.058834	-0.058922	-0.059008		-0.059211	-0.059263		-0.059276	0.00	-0.059444	0.050594	0.050804	-0.039004	-0.059808	-0.059829	0	-0.05983	-0.059907	-0.02993	0	-0.060048	-0.06014	-0.06016
943 Bladder	944 Bladder	945 Bladder	946 Bladder	947 Bladder			948 Bladder	949 Bladder		950 Bladder	951 Bladder	952 Bladder	Bladder		954 Bladder	955 Bladder		Bladder		bladder	058 Bladder	950 Bladdor	Diagrael	Bladder	961 Bladder	() () () () () () () () () ()	902 bladder	you bladder	964 Bladder		900 Bladder	966 Bladder	967 Bladder
945	944	945	946	947		, 	346	946		950	951	952	953		954	955		926	7	106	0,7,8	050	202	096	961	060	206	203	904	Ç	300	966	196

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

FIG. 1P

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

968 Bladder	-0.060167	0.375449	0.306919	0.17 173505 M84250 at		C CARACTER AND A CONTROLL VICINIA
	00000		0.306717	AFU 0 17169876 t	AF-000177_a t S	Sm-like protein CaSm (CaSm) mRNA
969 Bladder	-0.060292	0.3134232	0.30665	n 17160052 Z32684 at		XK mRNA for membrane transport protein
970 Bladder	-0.060331	0.3732740	0.0000	RC	8	EST: 2/29e12.s1 Soares pregnant uterus NbHPU Holniu Sapieris
7.4 Dloddor	9090 0-	0.3752392	0.306632	0.17154895 08		cDNA clone 503374 3', mRNA sequence. (mon Sensam)
97 I Bladder		0.3752141	0.306472	0.17148261 M35128 at	1	Muscarinic acetylcriolitie i eceptori gene
וממממו			02170000	AA2	AA233107_a	Homo sapiens Smad6 mRNA, complete cds
973 Bladder	-0.060818	0.3751358	0.300430	0.11.140130 N75	N75203 s a E	EST: yw33e05.r1 Homo sapiens cDNA clone 254048 5'. (from
974 Bladder	-0.0609	0.3750482	0.306445	0.17143147 t		Genbank)
				HG3921	HG3921- uT4101 f af F	f at Homeofic Protein C6, Class I
975 Bladder	-0.06095	0.3/4993		0,17129926 M62783	1	NAGA N-acetylgalactosaminidase, alpha-
976 Bladder	-0.060957	- 1	0.300343	0.17 123520 18021 33	i ta	Skeletal muscle 190kD protein
977 Bladder	-0.060983	- 1	0.30625	0.1712317 A03030	i to	DROTFIN PHPS1-2
978 Bladder	-0.06102	0.3747438	0.306225	0.171170	1050	FST: zw06a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
070 Bladder	-0.061163	0.3745751	0.306203	0.17107646 52 at		768470 3', mRNA sequence. (from Genbank)
		ł	0.206113	U22970 0 17107646 1 s at	_ma	6-16 gene (internet of Filtraducible popular program). Human interferon-inducible peptide (6-16) gene
980 Bladder	-0.061183		0.000.0	0 4709845 179205	#	Rihosomal protein L39
981 Bladder	-0.06128	0.3/44//2	0.30007	D. I. COOOLO	; , ,	
	9		0 308083	H1 H1 0 170802 t	s a	Olfactory Receptor Or17-201
982 Bladder	-0.061301	0.3/44003			BC AA4790	EST: zv17e07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
983 Bladder	-0.061365	0.374273	0.306063	0.17075153	at	753924 3', mRNA sequence. (from Genbank)
				0.1.4	4203285_a	AA203285_a EST: zx57e08.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
984 Bladder	-0.061386	-0.061386 0.3742026	0.305984	0.17071.0	N AA0252	FST: 2e81f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
985 Bladder	-0.06139	9 0.3741972		0.17065834	7 at	clone 365411 3', mRNA sequence. (from Genbank)
986 Bladder	-0.06140	-0.061409 0.3741908	0.30573	0.1705834	RC AA4614	EST: 2x68d02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
987 Bladder	-0.061466	6 0.3741314	0.305654	0.17054002	5 at	
988 Bladder	-0.061485	5 0.3740752	2 0.305547	0.17049176	61 at	
noo Bladder	-0.06168	8 0.374063	3 0.30554	0.17045891	KC_AA44314 61 at	

]	Dock Title: nven	C	enet	ic	Ma	ırkers	20-002 s for Tumors aswamy, et al.
EST: zw62c11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774644 3' similar to TR:G207250 G207250 RAT GROWTH RC_AA4417 AND TRANSFORMATION-DEPENDENT;, mRNA sequence. (from Genbank)	AA278413_a EST: zs81h05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t	U04636_rna Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase 1_at-2 and cyclooxygenase)	Cyclooxygenase-2 (hCox-2) gene	17019337 M37981_at CHRNA3 Alpha-3 neuronal nicotinic acetylcholine recentor subunit	RC_AA4547 EST: zx77b02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809739 3', mRNA seguence (from Genhank)	Short-chain dehydrogenase/reductase 1	0.16994397 S70348 at-2 erythroleukemia cell HEL mRNA Bartial 400 ctt	ITGB3 Integrin, beta 3 (platelet plyconmeterin IIIa antigen CD61)	Guanylate kinase associated protein (GKAP) mRNA	AA448460_a EST: zw79b12.r1 Soares testis NHT Homo sapiens cDNA clone t 782399 5', mRNA sequence. (from Genbank)	
A4417	AA278413_a E8 t	U04636_rna Pr 1_at-2 an	36_rna	W37981_at CF	२८_AA4547 ES 19 at clo	6999029 T68083 at Sh	370348 at-2 en	370348 at ITC	1	\A448460_a ES	
RC_A 0.17040685 98_at	0.17037009 t	0.17026342 1_at-2	0.17020734 1_at	0.17019337	RC_A 0.17012529 19 at	0.16999029	0.16994397	0.16984923 S70348 at	0.16980794 U67988 at	0.16972545	
0.305463	0.305277	0.30521	0.305062	0.305047	0.304825	0.304825	0.304813	0.304801	0.304775	0.304664	
0,373881	0.3737912	-0.061869 0.3737442	0.3736545	0.3736098	-0.061949 0.3734886	0.3733334	0.3733075	0.3733065	0.3732649	0.3732564	
-0.061822	-0.061832	-0.061869	-0.061869 0.3736545	-0.061889	-0.061949	-0.062022 0.3733334	-0.062104 0.3733075	-0.062104 0.3733065	-0.062136	-0.062189 0.3732564	
990 Bladder	991 Bladder	992 Bladder	. 993 Bladder	994 Bladder	995 Bladder	996 Bladder	997 Bladder	998 Bladder	999 Bladder	1000 Bladder	

=	T	 	Т			T	_		T		10	2		T
S70585_ma Thyroid-stimulating hormone alpha subunit [human, Genomic, 1327 nt]	0.43706787 J03460_s_at Prolactin-induced protein	AC002077_a GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 t			Prolactin-Induced Protein	AA059327_i EST: zf65e11.r1 Soares retina N2b4HR Homo sapiens cDNA clone at 381836 5', mRNA sequence, (from Genhank)		N-acetyltransferase 1 (arylamine N-acetyltransferase)	CYP2A6 Cytochrome P450, subfamily IIA (phenobarbital-inducible),	0.38979056 K03192_f_at polypeptide 6	K03192 f at-Cytochrome P450, subfamily IIA (nhengharhital-inducible), bolynentide	G G G G G G G G G G G G G G G G G G G	0.3807439 M81057 at CPB1 Carboxynentidase B1 (fissue)	0.37644237 M97815 at CRABP2 Cellular retinoic acid-binding profess 2
S70585_rna 1_at	J03460_s_at	AC002077_a t	HG1763-	HT1780 s a	 	AA059327_i at		D90041_s_a tt		K03192_f_at	<03192 f at-	1	M81057 at	M97815 at
S705 0.46934703 1_at		0.42199615		-	0.41081786	0.4027538 at		0.39607754 t	1	0.38979056		0.38526917 2	0.3807439	0.37644237
0.615615	0.57007	0.549476			0.538343	0.527243		0.51971	 	0.515125	-	0.509847	0.504484	0.501
0.7052603	0.6544581	0.6254832			0.6140406	0.601601		0.5946991	1	0.5911/45		0.583999	0.5778751	0.5733255
0.4144211 0.7052603	0.4051815 0.6544581	0.3902984 0.6254832			0.3692085 0.6140406	0.3573955		0.3370636 0.5946991	0 22000	0.3302206 0.5911/45		0.3302206 0.583999	0.3101546 0.5778751	0.3052343 0.5733255
Breast	2 Breast	3 Breast			4 Breast	5 Breast		6 Breast	0,000	/ DIEBSI		8 Breast	9 Breast	10 Breast
	~	(43)			4	5		9	^			8	တ	9

FIG. 2A

		1010000	0200723	7 407666	The state of the s		ing the first first the first first the first fi
11	11 Breast	0.30387.33	0.57 13078	0.497555	U.37.31300 LL		Uyloulillille F*+30 4 gene FET: #60k40 *4 Cooper facilis NLIT Homo capians c'INIA clone
12	12 Breast	0.3018422	0,5663985	0.494761	0.36980766 t	AA393009_a	727579 5', mRNA sequence. (from Genbank)
			1		The state of the s		CYP19 Cytochrome P450, subfamily XIX (aromatization of
13	13 Breast	0.301496	0.5648769	0.491622	0.36651027 X13589	at	androgens)
							EST: 40a4 Human retina cDNA randomly primed sublibrary Homo
14	14 Breast	0.301386	0.5610314	0.488126	0.3636768 W27961	ğ	sapiens cDNA, mKiNA sequence. (Irom Genoank)
15	Breast	0.3011417	0.5586313	0.485323	0.36068076 HT2461	ä,	Glyceraldehyde-3-Phosphate Dehydrogenase (Gb:K03121)
2							EST: zs53h01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701233 5' similar to TR:G1223890 G1223890 PUTATIVE
					₹	A287713_a	AA287713_a T1/ST2 RECEPTOR BINDING PROTEIN PRECURSOR.;; mRNA
16	16 Breast	0.2956604	0.5576914	0.483406	0.3586727 t	l	sequence. (from Genbank)
17	17 Breast	0.2954511	0.5521304	0.480035	0.35643905 D16583	at	HDC Histidine decarboxylasè
					<u> </u>	HG3236-	
18	Breast	0.2892586	0.5511941	0.477087	0.35386467 HT3413	بـ ۔¦	at Neurofibromatosis 2 Tumor Suppressor (Gb:L27065)
19	Breast	0.2879139	0.5490707	0.475087	0.35197905 U22029	fat	CYP2A7 Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 7
06	20 Broset	0.2857103	0 5785878	0.474104	HG880-		Mucin 6 Gaetric (Gb.) 07517)
3	1000	001.001.0	- 1		0.00	>	
21	Breast	0.2855561	0.5433092	0.471108	0.34810886 5	5_at	AFFX-DapX-5_at (endogenous control)
22	22 Breast	0.2855561	0.5397123	0.469333	AFFX-0.34622866 5 at-2	AFFX-DapX-5 at-2	AFFX-DapX-5 at (miscellaneous control - 11k chips)
					M	4 s a	
23	23 Breast	0.2817361	0.5391187	0.467654	0.3445486 t	****	polypeptide 6
24	24 Breast	0.2797567	0.53859	0.465246	0.3429625 X58072	at	GATA3 GATA-binding protein 3
25	25 Breast	0.272856		0.463567	0.3413686 U73330	at	PAC clone 85D2 from 13q12-13q13, complete sequence
26	Breast	0.2579279	0.5322417	0.462184	0.33994487 M14091	at	THYROXINE-BINDING GLOBULIN PRECURSOR
27	Breast	0.2570436	0.5311074	0.460936	0.33822918 T92512_at	92512_at	Ye24g11.r1 Homo sapiens cDNA clone 118724 5'. (from Genbank)
28	28 Breast	0.2555496	0.5289472	0.459658	X 0.33666405	X17059_s_a t	AAC1 Arylamine N-acetyltransferase, liver
		1				M63962_rna	
es 	29 Breast	0.2509626	0.5283092	0.458428	0.33551738 1	1_at	Gastric H,K-ATPase catalytic subunit gene
30	30 Breast	0.2476297	0.527762	0.456917	0.3340632 W07430_	V07430_at	EST: za96f10.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 300427 5', mRNA sequence. (from Genbank)
3	31 Breast	0.2458172	0.5273711	0.455669	0.3326946 N79354	179354_at	EST; yz73a08.r1 Homo sapiens cDNA clone 288662 5'. (from Genbank)

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32 Breast

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								7	Γitl	e:	t No.: Gene ors: S	etic N	1ar	ker	s fo									
and the first faith		III.T.V.A. Sequence, (from Genbank)	s. at (clone CTG-B37) mRNA sequence 469 EST: zl51g10.s1 Soares pregnant uterus NbHPU Homo saniens	cDNA clone 505506 3', mRNA sequence. (from Genbank) EST: Human fetal brain cDNA 3'-end GEN-020E05, mRNA sequence	(from Genbank)	AFFX-PheX-3_at (miscellaneous control - 11k chips)	AFFX-Phex-3 at (endogenous control)	Couragine syndrome complementation group A CSA protein (CSA)	Clone 23948 mRNA semience	PRM1 Protamine 1	Human cytochrome P450-IIB (hIIB3) mRNA, complete cds	EST: ae62a09.s1 Stratagene lung carcinoma 937218 Homo caniona	cDNA clone 951448 3', mRNA sequence. (from Genbank)	min. Class II HLA-DR-beta-1*09012 (HLA-DRB1*09012) gene, 3'end cds	YRRM1	DCC=deleted in colorectal cancer {alternatively spliced, exon 1A}	EST: zw76008.srf Soares testis NHT Homo sapiens cDNA clone	CYPAGE Cytochrome P450, subfamily IIA (phenobarbital-inducible).	o application of the contraction	0.31337/M31667 f at CYTOCHROME P450 IA2	NHA Ketohexokinase (fructokinase)	Low-Wir G I P-binding protein (RAB31) mRNA	RFC2 Renlication factor C (activator 4) a varia	P2X7 receptor
	AA478131_a	10.977	-\F	RC_D59354	AFFX-Phex-	3 at-2 AFFX-PheX-	3 at	U28413 at		M60331 at	M29873_s_a t	A6097		at	at		A4323	i d	Ď.	ਗੁੱ	ID.	\top		
	0.331441461	0 33004461 40577	RC A	0.9209409	0.021120.0	0.32679677/3 at-2 AFFX-I	U.3256697 3_at	0.3245835 U28413	0.32374018 U79293	0.32270935 M60331	0.32168627	70007000	0.5201 0001 95 at	0.31968847 M96132	0.31869397 X76059	0.31773603 S81294 at	0.31697726 78 at	0.31625086 M33318	1 004500	0.31431746 X78678 at	U 3135/462+	0.31298834 M19481 at	0.31211993 M87338 at	0.31118977 Y09561 at
	0.454783	0.452885	0.45194	0.450851	0.440047	0.449047	0.440400	0.448017	0.447233	0.446593	0.445578	0 444513		0.443448	0.442246	0.441581	0.440414	0.439703	0.439017	0.438184	0.437622			0.435751
	0.5269248	0.5260367	i.	0.5229325	1	J	0.000	0.5198922	0.5194382	0.010100	0.5172582	0.5166451		0.5148028	0.5139468	0.5127663	0.5122337	0.5119829	0.510178	1	0.5087296			0.5075588
	0.245815	0.2450795	0.2396013	0.2394474	0.2387956	0.2387956		0.236189	0.2339904		0.2294978	0.2275559		0.2262459		0.2216474	0.2207041	0.2167237	0.2138934	0.2089151	0.2072929 0	J		0.2054884 0
	1					ļ	1	- [-					+						1			#	4

38 Breast 39 Breast 40 Breast

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50 Breast 51 Breast 52 Breast 53 Breast

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5A Breact) act	0 2036483	0.507147	0.434863	RC_A 0.31047577 93_at	A0571	EST: zk79g01.s1 Soares pregnant uterus NbHPU Homo sapieris cDNA clone 489072 3', mRNA sequence. (from Genbank)
24 Dicast	Cast	0.2026314	0.5069917	0.433748	0.3098519 W07461_at	.61_at	EST: zag7f08.r1 Soares retal lung NuHL18W Torno saprens conscione 300519 5' similar to WP:B0491.7 CE02109 DIPHTHINE SYNTHASE;, mRNA sequence. (from Genbank)
56 Breast	east	0.2008918		0.433043	0.30905774 M27826_at		Endogenous retroviral protease mikinA
K7 Breact	pact	0 1930344	0.5063547	0.432044	0.30823	(00629 j at	0.30823 K00629_i_at Human kpni repeat mma (cdna clone pcd-kpni-4), 3' end
G Dropet	Gast	0.188382	- 1	0.431654	0.30751547 t	√A428090_a	AA428090_a EST: zw32a08.r1 Soares ovary tumor Nutrici i rouno sapiens com t t clone 770966 5', mRNA sequence. (from Genbank)
50 Breach	pact	0.1879053	- 1	0.430951	0.30678293 X71135	äţ	Sox3 gene
60 Breast	east	0.1877799	0.1877799 0.5042729	0.430504	0,30609787 L40396	at	(clone s22i71) mRNA tragment
61 Breast	east	0.1873657	0.1873657 0.5028442	0.430114	0.3054275 U33147_at		Mammaglobin IIIKINA
62 Br	62 Breast	0.1860077	0.5017778	0.429478	X0788 0.3047553 1_f_at	X07881_rna 1_f_at	Human gene PRB3L for proline-rich protein G1
63 Br	63 Breast	0.185097	0.5007832	0,428728	0.30425614 R82528	at	Genbank)
64 B ₁	64 Breast	0.1850751	0.5005295	0.428209	0.30378756	0.30378756 17_at	cDNA clone 502003 3', mRVI assertione (from Genbank)
65 Bi	65 Breast	0.1826687	0.5004	0.427635	RC_A 0.30302867 53_at	RC_AA4365 53_at	EST: zv08c11.s1 Soares Nilmirru ST Homo Saprats Socrations 753044 3', mRNA sequence. (from Genbank)
999 1999	66 Breast	0.1818307	0.5002153	0.426603	0.3025784	HG2566- HT4792 <u>r</u> at	HG2566- 0.3025784 HT4792 r at Microtubule-Associated Protein Tau, Alt. Splice 3, Exon 8
						YEL002c/W	
67 B	67 Breast	0.1809896	0.4988202	0.426546	0.3018145 BP1	ह्यू क	No into for gene
68 B	68 Breast	0.1806067	7 0.4987948		0.30131826t	703301_s_a	SMA5 mRNA
69 B	69 Breast	0.1776925	š		0.30063042	0.30063042 H18713 at	H.sapiens mKNA for aminopeptidase Frince
70 E	70 Breast	0.1762679	9 0.4966449	0.424616	0.3001228 875174	S75174 at	E2F4 E2F transcription factor 4, p107 p100 miles.
71 8	71 Breast	0.1761461	1 0.4966449			at	(from Genbank)
72 E	72 Breast	0.175442	2 0.4960552	0.42353	0.29917407 W03018	W03018 at	Glucocorticold receptor DINA bilitaling lactor
73 E	73 Breast	0.1742659	9 0.4955122	0.423282	0.298475921	HT4369_s_a	Adrenergic Receptor, Alpha 1b
74 E	74 Breast	0.1733242	2 0.4954579	0.422941		0.29794037 N29207 at	
751	75 Breast	0.1718145	5 0.4949794	0.422192	0.29747328 at	RC_Dooss4	
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77 Breast 0.1686359 0.4937092 78 Breast 0.1672696 0.4930089 79 Breast 0.1659615 0.4926859 80 Breast 0.1659615 0.4916681 81 Breast 0.1636634 0.4907536 83 Breast 0.163612 0.4897454 84 Breast 0.1580962 0.4897454 85 Breast 0.1580962 0.4874758 86 Breast 0.1575966 0.4874758 87 Breast 0.1575966 0.4874758 88 Breast 0.1575966 0.4874758 89 Breast 0.1575966 0.4874758 80 Breast 0.1575966 0.4874758 81 Breast 0.1575966 0.4874758 82 Breast 0.1575966 0.4874758 83 Breast 0.1575966 0.48765833	2 0.420646 9 0.420364 9 0.419925 2 0.419109 1 0.418326	0.2965633 M23263 at-2 RC_AA1916 0.29607454 47 at 0.2955664 U90910 at-2 0.29524457 U90910 at at 0.29421106 04 f at 0.29421106 04 f at 0.2936591 W31698 at at 0.2932521 D83913 at	0.2965633 M23263_at-2 feminization; spinal and bulbar muscular atrophy; Kennedy disease) RC_AA1916 Ceruloplasmin (ferroxidase) 0.2955664 U90910_at-2 Human clone 23564 mRNA sequence Homo sapiens mRNA for ADP ribosylation factor-like LAK, complete 0.2947381 W68464_at cds EST: zi74e11.s1 Stratagene colon (#937204) Homo sapiens cDNA
	0 0 0 0		Ceruloplasmin (ferroxidase) Human clone 23564 mRNA sequence Clone 23564 mRNA sequence Homo sapiens mRNA for ADP ribosylation factor-like LAK, complete cds EST: 2/74e11.s1 Stratagene colon (#937204) Homo sapiens cDNA
0.1659615 0.1659615 0.1644084 0.163634 0.163634 0.1580962 0.1580673 0.1580673 0.1580673 0.1580673 0.1580673 0.1580962 0.1580673 0.15809673 0.15809673	0 0 0		Human clone 23564 mRNA sequence Clone 23564 mRNA sequence Homo sapiens mRNA for ADP ribosylation factor-like LAK, complete cds EST: zi74e11.s1 Stratagene colon (#937204) Homo sapiens cDNA
0.1659615 0.1644084 0.1636634 0.1633128 0.1580962 0.1580673 0.1575966 0.1568142 0.1552809 0.1528014	0 0 0		Clone 23564 mRNA sequence Homo sapiens mRNA for ADP ribosylation factor-like LAK, complete cds EST: zl74e11.s1 Stratagene colon (#937204) Homo sapiens cDNA
0.1644084 0.1636634 0.1630412 0.1580962 0.1580673 0.158142 0.1552809 0.1528014 0.1486395	0.		Homo sapiens mRNA for ADP ribosylation factor-like LAK, complete cds EST: zl74e11.s1 Stratagene colon (#937204) Homo sapiens cDNA
0.1636634 0.1633128 0.1620412 0.1580962 0.1580673 0.1575966 0.1575969 0.1552809 0.1528014	0.	2554 at at xmf	EST: zl74e11.s1 Stratagene colon (#937204) Homo sapiens cDNA
0.1636634 0.1633128 0.1580962 0.1580673 0.1575966 0.1568142 0.1552809 0.1528014	0	at	clone 510380 3' similar to contains Alu repetitive element: mRNA
0.1633128 0.1620412 0.1580962 0.1575966 0.1568142 0.1552809 0.1528014		_ +	sequence. (from Genbank)
0.1580962 0.15809673 0.1575966 0.1568142 0.1552809 0.1528014	0	+	Zinc finger protein 42 (myeloid-specific retinoic acid- responsive)
0.1580962 0.1580673 0.1575966 0.1568142 0.1552809 0.1528014	0.416865		Genethonin 1
0.1580673 0.1575966 0.1568142 0.1552809 0.1528014 0.1486395	0.416215		Gag 2 protein from Human endogenous retrovirus HERV- K10./ntype=DNA /annot=CDS
0.1575966 0.1568142 0.1552809 0.1528014 0.1486395	0.416033	0.29236576 M333317 f et	CYP2A7 Cytochrome P450, subfamily IIA (phenobarbital-inducible),
0.1568142 0.1552809 0.1528014 0.1486395	0	5 .	AGTR1 Anglotensin recentor 1
0.1552809 0.1528014 0.1486395	<u> </u>	at	PDK1 Pyruvate dehydrogenase kinase isoenzyme 1
0.1528014	0.414581	0.29113963 U20325 at	Cocaine and amphetamine regulated transcript CART (hCART)
0.1486395	0.414185	σ.	Dents Disease candidate gene
	0.413004	0.29028687 73 at	RC_AA5210 EST: aa72a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 73 at IMAGE:826448 3', mRNA sequence, (from Genhank)
0 1 100		J32499_s_a	
92 Breast 0.1483/66 0.4848/22			D3 dopamine receptor mRNA
94 Breast 0.1473178 0.4840047	0.412473	0.28943676 U62435 at 0.28907865 L 10844 at 0.	Cholinergic receptor, neuronal nicotinic, alpha polypeptide 6
95 Breast 0.1472629 0.4839905			EST: 46g7 Human retina cDNA randomly primed sublibrary Homo sabiens cDNA, mRNA sequence, (from Genhank)
96 Breast 0.146634 0.4839169	0.411477	HG415- 0.2883357 HT415 at	Lectin. Galactoside-Binding Soluble 2
97 Breast 0.1462051 0.4833313	0.410845		GIF Polymeric immunoglobulin receptor

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			Annual Control of the			
98 Breast	0.1454632	0.4830362	0.410382	HG 0.28760898 HT	HG3731 ² HT4001 r at	HG3731* 0.28760898 HT4001 r. at Imminopolobidin Heavy Chain Vdire Regions (Ghd 23568)
99 Breast	0.1446769	0.4820118	0.410039		11661 at	PRLR Prolactin receptor
			* LIBERTING TO LIVE TO	AA		
100 Breast	0.142678	0.4817252	0.409762	0.28671452 t		Heat shock 40kD protein 2
				!		Zt80f04.r1 Soares testis NHT Homo sapiens cDNA clone 728671 5'
				AA	AA398863_a	similar to contains Alu repetitive element; contains element L.1
101 Breast	0.1425744	1	0.409464	0.286305 t		repetitive element;, mRNA sequence. (from Genbank)
102 Breast	0.1425183	- 1	0.408963	0.28593504 U60521_at		Cysteine protease ICE-LAP6 mRNA
103 Breast	0.1420439		0.408845	0.28553647 X66436_at		POSSIBLE GTP-BINDING PROTEIN HSR1
104 Breast	0.1404123	0.4797016	0.408685	0.28527972 X92475 at	1	ITBA1 protein
105 Breast	0.1404123	0.4786941	0.408089	0.28492057 X92475 at-2 ITBA1 gene	2475 at-2	ITBA1 gene
1				AA	AA447244_a	
106 Breast	0.1396912	0.478331	0.407545	0.284583541		KIAA0740 gene product
11	1			16X	780_ma	
107 Breast	0.1388565	0.4772545	0.407181	0.28430355 1_at		Cardiac troponin I gene, exons 1 to 5
108 Broast	0.1396660		400001	RC	9259	EST: zl70d10.s1 Stratagene colon (#937204) Homo sapiens cDNA
ומח חופשפו	0.1300000	0.477 1034	0.400837	0.28399804 47 r at		clone 509971 3', mRNA sequence, (from Genbank)
0	1			RC	A3992	Company of the control of the contro
109 Breast	0.1377513	0.4762728	0.406635	0.28356695 26 at		Homo sapiens chromosome 19, cosmid R28784
110 Breact	0.4365007		00000			EST: yu14a06.r1 Homo sapiens cDNA clone 233746 5' similar to
110 016091	0.1303307	0.4701049	0.40639	0.28320184 H66367	at	contains Alu repetitive element;. (from Genbank)
111 Broact	0.4964403		40770	X5£	X55037_s_a	
111 016451	0.1301492		0.405/2	0.282949751		GATA3 GATA-binding protein 3
112 Breast	0.136135	0.4749816	0.405224	0.28260452 U37519_at		ALDH8 Aldehyde dehydrogenase 8
113 Breast	0.1350118	0.4749779	0.405038	RC_A 0.2823362 39_at	A1923	EST: zp97g11.s1 Stratagene muscle 937209 Homo sapiens cDNA
		1		2000-0-1		GOTIE 020130 3, IIINNA Sequerice. (Irom Genbank)
114 Breast	0.1345174	0.4746602	0.404481	0.2817898 R33301 at		contains MSR1 repetitive element : (from Genhank)
Ĺ Į	(EST: yq30g06.r1 Homo sapiens cDNA clone 197338 5'. (from
115 Breast	0.1338865	0.4742993	0.404086	0.2813785 R86920	at	Genbank)
116 Breast	0.1333216	0.4734562	0.403847	0.28105938 D38024	to	Facioscapulohumeral muscular dystrophy (FSHD) gene region, D4Z4 tandem reneat unit
					1	EST: zn18b04.s1 Stratagene neuroenithelium NT2RAMI 937234
	0			RC	A0843	Homo sapiens cDNA clone 547759 3', mRNA sequence, (from
11/ breast	0.13306	0.4733514	0.403658	0.28065583 18_at		Genbank)
118 Breast	0 1304407	0.4730474	0.402953	RC_A	A0184	EST: ze50a08.s1 Soares retina N2b4HR Homo sapiens cDNA clone
252	10110010	11100110	0.707.0	0.400000104 41		302390 3, mKINA sequence. (from Genbank)

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119 Breast	ıst	0.1301951	0.4724207	0.402594	RC_AA2279 0.28009456 41_s_at	EST: zr56c12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667414 3', mRNA sequence. (from Genbank)
120 Breast	ast	0.1300902	0.4722814	0.402019	0.279751 S76978_s_at	Prostate-specific membrane antigen {alternatively spliced} [human, at primary prostatic tissues, mRNA Partial, 251 nt]
121 Breast	ıst	0.1299656	0.4716187	0.401658	0.27957845 30_at	EST: zs38b03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687437 3', mRNA sequence. (from Genbank)
122 Breast	ıst	0.1299156	0.4715659	0.401536	0.279199 L37378_at	Guanylyl cyclase (RetGC-2) mRNA
123 Breast	ıst	0.1296486	0.4713915	0.400846	0.2789851 J05200_s_at	0.2789851 J05200_s_at Ryanodine receptor 1 (skeletal)
					RC_D60715	EST: Human fetal brain cDNA 3'-end GEN-126H02, mRNA sequence.
124 Breast	ıst	0.1293121		0.400395	0.27856982_at	(from Genbank)
125 Breast	ıst	0.1284234		0.400225	0.2781939 U97188_at	Putative RNA binding protein KOC (koc) mRNA
126 Breast	ıst	0.1277191	0.4705171	0.399834	0.27790773 X59766_at	AZGP1 Zinc-alpha-2-glycoprotein 1
127 Breast	ıst	0.1249595		0,399515	0.2775942 Z21217_at	KIAA0008 gene product
128 Breast	ıst	0.1232011	0.4700199	0.399377	0.27723655 M13755 at	G1P2 Interferon, alpha-inducible protein (clone IFI-15K)
129 Breast	ıst	0.1224186	0.4695616	0.399132	0.2768773 M59815 at	C4A Complement component 4A
					RC_AA4769	EST: zu38c05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
130 Breast	ıst	0.1212664	0.1212664 0.4695155	0.398823	0.27644926 22_at	clone 740264 3', mRNA sequence. (from Genbank)
131 Breast	ıst	0.1196906	0.1196906 0.4694306	0.398724	0.27623805 U37221_at	
132 Breact		0 1187018	0.4690452	0.200070	AA203527_a	
133 Breast		0.1183818	0.4690452	0.39027.9	0.27002134 (0.27557287 M44324 at	Complete cas
134 Breast		0.1183761	0.4689992	0.397569	- 11	ACR Acrosin
						Information & recomforthme A (II ODDA) some manufactural
135 Breast	ıst	0.1180724	0.4679385	0.397387	0.2751059811 at	interreduir-o receptor type A (iLondA) gene, promoter and comprete
136 Breas	_	0.1146055		0.397198	0.27480546 U03399 at	T-complex protein 10A (TCP10A) mRNA
137 Breast	st	0.1143943	0.4674776	0.396417		TN Titin
138 Breast		0.114019	0.4667478	0.306255	. 4	EST: ye04h07.r1 Homo sapiens cDNA clone 116797 5' similar to
139 Breast	st	0.113987		0.396175	0.2738823 15702 at	Contains Alu repetitive element; (from Genbank) BF B-factor propertin
						EST: EST17092 Aorta endothelial cells, TNF alpha-treated Homo
700		0,000,000	000	1		sapiens cDNA 3' end similar to EST containing Alu repeat, mRNA
140 Breast		0.11338/6	0.11338/6 0.4663909	0.395823	0.27358848 44_f_at	sequence. (from Genbank)
141 Breast		0.1132141	0.1132141 0.4662151	0.395441	0.2732057 M84605 at	PUTATIVE TACHYKININ RECEPTOR
142 Breast		0.1129674	0.4661736	0.395316	0.27288175 R86180 at	EST: yp88g01.r1 Homo sapiens cDNA clone 194544 5'. (from Genbank)
143 Breast		0.1124377	0.4661096	0.395248	0 27254072 46 at	EST: aa93h11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
						HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(2) ALPHA
144 Breast		0.111//24	0.111//24 0.4658541	0.394866	0.27220443 M17236 at	CHAIN PRECURSOR

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147 Breast148 Breast149 Breast

150 Breast

145 Breast 146 Breast 151 Breast 152 Breast 153 Breast 154 Breast 155 Breast 156 Breast 157 Breast

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	43kD acetylcholine receptor-associated protein (Rapsyn)	Potassium Channel Protein (Gb:Z11585)	MYL4 Myosin, light polypeptide 4, alkali; atrial, embryonic	Zinc finger protein (SRE-ZBP) mRNA, 3' end	ous domain hinding profein 2	STIS-COLIGIES BLOCKIES			Cri-du-chat region mRNA, clone NIBB11	High-sulphur keratin	0.26953828 M64936 i at Homo sapiens retinoic acid-inducible endogenous retroviral DNA	CHGB Chromogranin B (secretogranin 1)	EST: zw24g07.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	AA434329 a clone 770268 5' similar to contains element TAR1 repetitive element ;,	mRNA sequence, (from Genbank)	Harakiri, BCL2-interacting protein (contains only BH3 domain)	EST: zx54g10.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	AA203236_a cDNA clone 446370 5' similar to contains element PTR5 repetitive	element ;, mRNA sequence. (from Genbank)	Homo sapiens mRNA for KIAA0746 protein, partial cds	 	Platelet-derived growth factor (PDGFA) A chain gene	0.26751587 Y00083 s. at TGFB2 Transforming growth factor, beta 2	3',5' cyclic nucleotide phosphodiesterase (HSPDE1C1A) mRNA	AA418143 a EST: zv97b09.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	767705 5', mRNA sequence. (from Genbank)		363596 3', mKNA sequence. (from Genbank)	+		Inositol polyphosphate 4-phosphatase type II-alpha mRNA
A0195	Z33905_at	HG2239-	X52005 at	0.271058 M88579 at	AB000463_s	al	AA203649_a	t	U52827_at	X63755_at	M64936 i at	,2692618 Y00064 at		AA434329 a		U76376 at		AA203236_a		RC_AA2783 73 at	M19989 cds	1_at	Y00083 s a	U40371 at	AA418143 a	4	RC_AA0200	05_at	X13930_f_at	D16593_at	1196922 at
RC_A 0.2720548 28_at	0.27181688 Z33905_at	0.9748054	0.27133763 X52005 at	0.271058	0202020	0.2707273		0.27037978	0.26987523 U52827_at	0.26973763 X63755_at	0.26953828	0.2692618			0.26902696	0.26873964 U76376			0.26849845	RC_A 0.26814502 73 at		0.26789686 1_at	0.26751587	0.26735756 U40371		0.26710793 t		0.26685247 05	0.2665116	0.26636195 D16593	0 26603657 196922
0.394259	0.394094	0 303000	0.393688	0.393578	70000	0.393291		0.392932	0.392676	0.392536	0.392379	0.392287		-	0.391921	0.391697			0.391248	0.391228		0.390739	0.390189	0.390136		0.390046		0.389661	0.389591	0.389387	0.389078
0.4645429	0.4644613	0700070	0.4033040	0.4637664		0.463425/		0.4623278	0.4623278	0.4622459	0.4622331				0.4619075	0.4616584		,	0.4614898	0.4614792		0.4613786	0.461143	0	1	0.4609028		- 1	0.4602697	0.4602091	0 4598492
0.1110564	1			0.101017		0.106184		0.1061657	0.1059116	0.1055779	0 1052419	0 1051398	222		0.1049577	0.1048			0.1046188	0.1034737		0.1033571	0 1029475	0.1025376		0.1023547		0.1014101	0.1013909	0.1010564	0 100846

164 Breast 165 Breast 166 Breast 167 Breast

161 Breast 162 Breast

163 Breast

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					A constant of the second of th	EST: zv39e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
168 Breast	0.10077	0.4594875	0,388973	AA 0.26585692 t	AA410925_a t	Gorle (39044 5 Sillilar to go.masa455 i transcoom Live. ENHANCER PROTEIN 1 (HUMAN);, mRNA sequence. (from Genbank)
169 Breast	0.1002694	1	0.388742	0.2655794 L36529 at	6529 at	(clone N5-4) protein p84 mRNA
170 Branet	0.0087009	0.4586633	0.388/19	M14	M14123_xpt	Neutral protease large subunit from Human endogenous retrovirus HERV-K10 /ntvna=DNA /annot=CDS
I / U DIEGS!	7001060'0		0.300413	4.20000002.0	מונים של שלים	11Live-1/10.111ype-Diva Guinot-ODO
171 Breast	0.0983236	0.4585121	0.388281	0.26500675 t	U1UZ16_s_a t	POU domain, class 1, transcription factor 1 (Pit1, growth normone factor 1)
				H		
172 Breast	0.0980842		0.388186	0.26479006 HT4687	- 1	f_at Homeotic Protein Hpx-2
173 Breast	0.0980702		0.387885	0.26460913 X53331	53331_at	MGP Matrix protein gla
174 Breast	0.0978578	0.4568232	0.387839	0.26442334 C14915_at	14915_at	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12
175 Breast	0.0970478	0.456665	0.387323	HG4258 0.26423895 HT4528	HG4258- HT4528_at	Kinase Inhibitor P27kip1, Cyclin-Dependent
176 Breast	0.0954316	0.456665	0.386864	0.264032 U23070	23070_at	Putative transmembrane protein (nma) mRNA
				A	4021124_a	EST: ze67f10.r1 Soares retina N2b4HR Homo sapiens cDNA clone AA021124_a 364075 5' similar to contains Alu repetitive element;contains element
177 Breast	0.0942793		0.386723			L1 repetitive element ;, mRNA sequence. (from Genbank)
178 Breast	0.0933483		0.38664	0.26351067 ME	M62400_at	GABRR1 Gamma-aminobutyric acid (GABA) receptor, rho 1
179 Breast	0.0931456	0.4559138	0.386298	0.26323184 M20137	20137_at	Interleukin 3 (IL-3) mRNA
0	1 100000		000100	D2	D26561_cds	ORF for L1 protein gene extracted from Human papillomavirus 5b
180 Breast	0.0928915		0.385822	0.26303378 T at		genome integrated into human carcinoma DINA
181 Breast	0.0918815	0.4554118	0.38558	0.26274347 U13369	13369_at	Ribosomal DNA complete repeating unit
· · · · · · · · · · · · · · · · · · ·			_			EST: zc20b05.r1 Soares senescent fibroblasts NbHSF Homo sapiens
182 Breast	0.0915385	0.4554013	0.385333	0.2625152 W39573	39573_at	cDNA clone 322833 5', mRNA sequence. (from Genbank)
0,000	700000		000		RC_D20426	EST: Human HL60 3'directed Mbol cDNA, HUMGS01400, clone
log Breast	0.0906031	0.45533909	U.3851/1	0.2623259/ at	1t	pm2/64, mKNA sequence. (from Genbank)
184 Breast	0.0904789	0.4550578	0.385048	HG742- 0.2621092 HT742_at	HG742- HT742_at	Latent Membrane Protein Lmp1
185 Breast	0.0901848	0.4549179	0.384871	D268	D26561_cds	ORF for E7 protein gene extracted from Human papillomavirus 5b
186 Breast	0.0901116		0.384438	0.26171422 T83444	33444 at	Homo sapiens mRNA for KIAA0887 protein, partial cds
187 Breast	0.0894928	0.4542728	0.384292	RC_AA4 0.26138297 09 s at	RC_AA4046 09 s at	EST: zt43h04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725143.3', mRNA sequence, (from Genbank)
188 Breast	0.089386	0.454048	0.383972	0.26089674	HG3286- HT3463 at	Crystallin, Albha A
1000000		1	1	ı	30.00	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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Title:	Genet	ic Markers for Tumors
Invent	ors: Sri	idhar Ramaswamy, et al.

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189 Breast		0.089384 0	0.454038	0.383734	0.2607195	AA491376_a t	AA491376_a EST: aa65e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
190 Breast	st 0.0887464		0.4539805	0.383516	0.26041833 T47519	T47519 at	Genethonin 1
191 Breast	34 0.0887102		0.4536992	0.383402	HG3987 0.26013142 HT4257	HG3987- HT4257_at	Cpg-Enriched Dna, Clone E06
192 Breast	st 0.0884397	4397	0.45333	0.383212	RC_A 0.25995356 06_at	RC_AA0020 06_at	
193 Breast	it 0.0883572	1	0.4527864	0.383177	HGZ5930- 0.25966272 HT26386	HG25930- HT26386_at	Estradiol 17-beta dehydrogenase 1
194 Breast		2548 0.4	0.0882548 0.4525867	0.382907	0.25936133		AA136315_a EST: zn82e03.r1 Stratagene lung carcinoma 937218 Homo sapiens t
195 Breast		1491 0.4	0.0881491 0.4525816	0.382771	0.25924832 U43843	U43843_at	H-neuro-d4 protein mRNA
196 Breast			0.4524845	0.382335	0.25912717 J04621	J04621 at	SDC2 Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
197 Breast	0		0.4523321	0.381941	0.25873658 Z83805 at	Z83805 at	Axonemal dynein heavy chain (partial, ID hdhc8)
198 Breast	t 0.087352		0.4521794	0.381668	0.25856188 M63896 at	M63896_at	Transcriptional enhancer factor (TEF1) DNA
199 Breast	t 0.0868997		0.4520838	0.381586	0.05830814	HG3729- HT3000 f at	HG3729-
200 Breast		ł	0.4548669	000000	100000	RC_AA4646	EST: 2x82a10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
	+	_1_	0000	0.301404	0.2301062.90 at		clone 810234 3', mRNA sequence. (from Genbank)
201 Breast		3226 0.4	0.0858226 0.4518275	0.381089	0.2580243	X/2304_s_a t	Corticotronin releasing hormone recentor 1
202 Breast		5196 0.4	0.085196 0.4518275	0.380869	0.25784394 R22178 at		Homo saniene CAGE28 mBNA nartial ada
203 Breast	0.084483	483 0.4	0.4511711	0.380622	0.25766003 L02840	T	Potassium channel Kv2.1 mRNA
204 Breast	0.084328		0.4510919	0.380434	0.05742084	AA495729_a	EST: zw04a10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
205 Breast			0.45093	0.380043	0.2571851 H66279 at	H66279 at	7772b07,r1 Homo saniens cDNA clone 210805 5' (from Canbonk)
	***************************************					AA421370 a	EST: zu06e06.r1 Soprements NHT Homo sapiens CDNA done
206 Breast	0.0832062	062 0.4	0.4509069	0.37974	0.25698048	f	mRNA sequence. (from Genbank)
207 Breast	0.0829828		0.450154	0.379476	1 25673324	J24488_s_a	CYP21 Cytochrome P450, subfamily XXI (steroid 21-hydroxylase,
208 Breast	0.0820699		0.450076	0.379348	0.2563814 X16662	(16662 at	ANX8 Annexin VIII
209 Breast	0.0811764		0.4498118	0.379243	0.25612888 M35198 at	\top	Integrin B-6 mRNA
210 Breast	0.0809659		0.4497008	0.378673	HG3513- 0.25604665 HT3707	at	Myosin, Heavy Polypeptide, Light Meromyosin
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214	244 Breast	0.0806473	0.4494901	0.378617	0.25580257 R81217	j e	Yj03b09.r1 Homo sapiens cDNA clone 147641 5' similar to gb:X54156_ma1 CELLULAR TUMOR ANTIGEN P53 (HUMAN):contains Alu repetitive element:. (from Genbank)
			1		HG	и •	
212	Breast	0.0795012	0.4492681	0.378224	0.25556183 HT3441	3441_at	Af-6 (Gb:U02478)
							(clone cD24-1) Huntington's disease candidate region mRNA
213	213 Breast	0.0794716		0.378136	0.25532648 L37199	äţ	fragment
214	214 Breast	0.0788738	0.4490815	0.37803	0.25504974 U07225	7225_at	P2U nucleotide receptor mRNA
7,0	Droact	0.0785072	0 7700170	137760	HG2530-	, †	Adamyly Cyrlace Accordated Protein 2
C17	ZIO DI EGSI	0.01003912	- 1	0.3//01	0.23403001	ซี ู	Audilyly Cyclase-Associated Hotelinz
216	216 Breast	0.0782644	0.4489539	0.377537	0.25459158 U85265	5265_at	Down syndrome candiate region 1 (DSCR1) gene, alternative exon 1
217	217 Breast	0.0780549	0.4486558	0.377337	0.25433654 U33920	3920_at	Clone lambda 5 semaphorin mRNA
218	218 Breast	0.077293	0.4483567	0.377062	0.25409475 R93659	3659_at	Homo sapiens mRNA for KIAA0871 protein, complete cds
							Homo sapiens brain expressed ring finger protein mRNA, complete
219	219 Breast	0.0762319	0.4482782	0.376916	0.25394967 Z21244_at	244_at	cds
					HG. HT4	HG3242- HT4231 s a	
220	220 Breast	0.075748	0.4476327	0.37681	0.25383845 t		Calcium Channel, Voltage-Gated, Alpha 1e Subunit, Alt. Splice 3
221	221 Breast	0.0751439	0.4469373	0.376733	X16 0.25367084	X16666_s_a t	HOXB1 Homeo box B1
777	Droot	0.0754.490	0.4489566		X16	X16666_s_a	20 mg
777	777 DI Edsi	0.0731439		0.370301	0.2333031 F-2		Tiomeo box B1
					RC	RC A40478	EST: zf50b08.s1 Soares retina N2b4HR Homo sapiens cDNA clone 380343 3' similar to contains Alu repetitive element:contains element
223	223 Breast	0.0744652	0.4465658	0.376361	0.253102 76	_at	L1 repetitive element;, mRNA sequence. (from Genbank)
Č		0170010					EST: yw69g06.r1 Homo sapiens cDNA clone 257530 5'. (from
477	774 bi east	0.0743978	0.4402/4/	0.373912	0.2529T53ZIN4ZUZZ	2022 at	Genbank)
225	225 Breast	0.0741908	0.4457812	0.375763	0.25279006 H81340_at	1340_at	EST: yu /4d04.r1 Homo sapiens cDNA clone 239527 5. (from Genbank)
226	226 Breast	0.0738568	0.4453105	0.375614	HG2465- 0.25244242 HT4871_at	HG2465- HT4871_at	Dna-Binding Protein Ap-2, Alt. Splice 3
227	227 Breast	0.0738299	0.4452643	0.375241	0.25228813 W36279 at	6279 at	EST: HFBEST-56 Human fetal brain QBoqin2 Homo sapiens cDNA, mRNA sequence. (from Genbank)
					MS	M57506_ma	SCYA1 gene (secreted protein I-309) extracted from Human secreted
228	228 Breast	0.0728815	0.4451951		0.25211945 1 at	# E	protein (I-309) gene
229	229 Breast	0.0728505	0.4448771	0.375194	0.25192085 M34041 at	4041 at	Alpha-2-adrenergic receptor (alpha-2 c2) gene
230	230 Breast	0.0722495	0.4446217	0.375006	AA3 0.25160065_at	AA383703_i _at	EST97119 Testis I Homo sapiens cDNA 5' end similar to similar to zinc finger protein ZNF2, mRNA sequence. (from Genbank)

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

-	0.074043	0.4442764	0.374782	0.25141132 D85939_at	gert ann gir, gire gree gree gree gree gree gree gree
231 Breast	1			σ,	Documine D2 receptor, mRNA
232 Breast	0.0712931	0.4433541	0.374466	0.251183 t	KIAA0032 gene
233 Breast	0.0708416	0.4429643	0.374334	at .:	L-SERINE DEHYDRATASE
234 Breast		0.4426800	0.373929	0.25060964 L36644 at	Receptor protein-tyrosine kinase (HEN/) Illinvin, 3 cms
235 Breast	0.07.00300	0.4466.101	200		Special of Special Announce of the Spiens
			7010	o 55033116\W23474 at	EST; zb33d08.r1 Soares paraulylors among from Genbank) cDNA clone 3053915', mRNA sequence. (from Genbank)
236 Breast			0.3/3/1	0.25035110 W2547 ; at	AAC2 Arylamine N-acetyltransferase, liver
237 Breast	0.0701355	0.4417023	0.373493		Cardiac tetrodotoxin-insensitive voltage-dependent sodium criamies
238 Breast	0.0698778	0.4415626	0.373388	0.25010458 M77235_at	alpha subunit (HH1) mKNA EST: 51a1 Human retina cDNA randomly primed sublibrary Homo
1000	0.0692833	0.4412475	0.373298		sapiens cDNA, mRNA sequence. (from Genbank)
239 Diedal	0.0889706	1	0.373272	0.24972571 U54804 at	Hasz mrna
Z40 Diedat		1	0000	RC_AA256/	Interferon (alpha, beta and omega) receptor 2
241 Breast	0.0678918	0.4411619	0.372733	0.24928777 X03635_at	ESR Estrogen receptor
242 Breast	0.0077000	To coot to		HG3517-	1 1
242 Breast	0.0675199	0.4407296	0.372691	0.24901806 HT3711_at	Alpha-1-Antitrypsin, 5' End
742 016634				em 447744	
		0,000	1850700	0.24878873 1 at	
244 Breast	0.0664876	0.0664876 0.4403650			NOS1 Nitric oxide synthase 1 (neuronal)
245 Breast	0.0662882	0.0662882 0.4401030	-	AFFX-BioB-	(oxido 144)
246 Breast	0.0660346	3 0.4401118	0.37189	0.24857435 M st-2	AFFX-BioB-M_st (miscellaneous control - 11k Chips)
		\$	0.374650	AFFX-5105 0 24838617 M st	AFFX-BioB-M st (endogenous control)
247 Breast	0.0660346				EST: yv72a02.r1 Soares fetal liver spleen 1NrLS hullio saprens
248 Breast	0.0659636	6 0.4400162	2 0.371623	0.24821983 N78064_at	cDNA clone 246254 3, Illians 30400000 (LIV-1) mRNA, partial Breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial
	0.0658123	2 0 4399824	4 0.371388	0.248083 U41060_at	
249 Breast	0.000012	1			S CDI anchored malecule-like protein
250 Breast	0.0651987	7 0.4396983	3 0.371382	0.24775968 at	UNA Idi GFT-allonota motosa a marting a martin
E	0.005400	0.4306083	3 0 371102	0 24764815	KIAA0683 gene product
Zon Breast	0.0031003	38 0.4396549		0.24739484	Tyrosine kinase (Tnk1) mkivA
1000 IO 707		1		AA167043	AA167043_a EST: zo86d03.r1 Stratagene ovarian cancer (#937219) Homo sapiens
253 Breast	0.0648255	0.43942	52 0.370813	0.24703103	cDNA clone 583/65 5, mixtor sequence (included to the control of t

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254 Breast	0.064351	0.4391809	0.37063	0.24686624 t	AA167824_a t	Cell division cycle 27
255 Breast	0.0639453	0.4385929	0.370405	A 0.24679068 t	AA401575_a t	EST: zu62b07.r1 Soares testis NHT Homo sapiens cDNA clone 742549 5', mRNA sequence. (from Genbank)
256 Breast	0.0636319	0.4385899	0.370254	0.2466424 M31606	₩,	PHKG2 Phosphorylase kinase, gamma 2 (testis)
257 Breast	0.0635282	0.0635282 0.4383332	0.370114	0.2463483 U47050_at		Putative calcium influx channel (htrp3) mRNA
258 Breast	0.0632544	0.4382424	0.369904	0.24618948 D79995_at		KIAA0173 gene
				×	X00371_rna	
259 Breast	0.0631949	0.4379791	0.369622	0.24601673 1	1_at	Myoglobin gene (exon 1) (and joined CDS)
260 Breast	0.0631807	0.4376267	0.369486	HG273- 0.2458327 HT273 at	************	I vmphocyte Antigen Hla-G3
						EST: ab40g02.s1 Stratagene HeLa cell s3 937216 Homo sapiens
1			1	<u> </u>	A4859	cDNA clone 843314 3' similar to SW:SOH1 YEAST P38633 SOH1
261 Breast	0.0622801	0.4371998	0.36945	0.24569954 45 at		PROTEIN. [1];, mRNA sequence. (from Genbank)
262 Breast	0.0618249	0.437025	0.369222	0.2455889 t	U145//_s_a t	MAP1A Microtubule-associated protein 1A
263 Breast	0.0615094	0.4367154	0.36913	0.2452498 M60614	äŧ	WT1 Wilms tumor 1
264 Breast	0.0614224	0.4366623	0.369032	0.2451102 X87870_at	87870_at ·	HEPATOCYTE NUCLEAR FACTOR 4
265 Breast	0.0612097	0.436333	0.368989	0.24490054 X87767	at	CD89 gene, exon S1
				2	A4959	EST: zw05h01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
266 Breast	0.0611846	0.4362189	0.368713	0.24461812 26_at		768433 3', mRNA sequence. (from Genbank)
<u>.</u>			6	<u>ac</u>	A1768	EST: zp11f06.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
267 Breast	0.0608841	0.4361712	0.368417	0.24444053 67_at	7 at	clone 609155 3', mRNA sequence. (from Genbank)
268 Breast	0.0608838	0.0608838 0.4361123	0.368366	0.24417712	79301 at-2	0.24417712 U79301 at-2 Human clone 23842 mRNA sequence
269 Breast	0.0608838	0.4359367	0.368173	0.24408029 U79301	79301 at	Clone 23842 mRNA sequence
						EST: yv37b01.r1 Soares fetal liver spleen 1NFLS Homo sapiens
						cDNA clone 244873 5' similar to contains Alu repetitive element;,
270 Breast	0.0600718	0.4357036	0.367956	0.24391416 N76208 at		mRNA sequence. (from Genbank)
	7000		1		AA3985	EST: zt73b05.s1 Soares testis NHT Homo sapiens cDNA clone
zi Breast	0.0599743	0.4354258	0.367793	0.24376059 33	3 at	
272 Breast	0.0594209	0.4353869	0.367737	A 0 2/25/15/50 +	AA476704_a	EST: zw87h02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
273 Breast	0.0583071		0.367392	0.24339215 D12485	12485 at	Plasma cell membrane alvoprotein (PC-1) mRNA
274 Breast	0.0581647	0.4349373	0.367376	0.24315822 HT961		Guanine Nucleotide Exchange Factor 2
	1000	1	0.00	R 200001	A4537	EST: aa19f07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
Z/o Breast	1969/60.0		0.30/333	0.24302986 94 at		813/33 3, mKNA sequence, (Irom Genbank)
Z/b Breast	0.05/404/	0.4347637	0.36699	0.24288869 L13436	13436_at	Guanylate cyclase mKNA, complete mature peptide

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RC_AA0585 EST: zf56d07.s1 Soares retina N2b4HR Homo sapiens cDNA clone 32 at 380941.31 mRNA sequence (from Genbank)	CARBOXYPEPTIDASE N 83 KD CHAIN			Protocadherin 9		Homo sapiens mRNA for KIAA0684 protein, partial cds	TRANSCRIPTION INITIATION FACTOR TFIID 250 KD SUBUNIT	Dotaceium channal KCNO4 mDNA	6-16 gene (interferon-inducible peptide precursor) extracted from	nuitati iiterieloi-iitaucible pepude (o-10) gerie	Uual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1	Of cardiac alpha-myosin heavy chain gene	at Mariner2 transposable element, complete consensus sequence	ADP-ribosyltransferase fruman skeletal muscle mRNA 1334 ntl	fur por hannu forom more formation for the first forma	CYP3A3 Cytochrome P450 IIIA3 (nifedipine oxidase chain 3)	RPE-retinal G protein-coupled receptor (rgr) mRNA	EST: ae57c05.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950984 3', mRNA sequence. (from Genbank)	a EST: ze72g05.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364568 5', mRNA sequence. (from Genhank)	Ig light-chain, partial Ke-Oz-polypeptide; Author-given protein	Sequerice is in conflict with the conceptual translation gene extracted from Human lambda-immunodishilin constant region consist	(germine)	COL11A1 Collagen, type XI, alpha 1		Nel-related protein	EST: zu08e03.r1 Soares testis NHT Homo sapiens cDNA clone 731260 5', mRNA sequence, (from Genbank)	Unknown protein mRNA within the p53 intron 1
RC_AA0585 32_at	19	: ·	146353 at	0.24203654 W27720 at	AA128724 a	•	0.2417678 D90359_at	U90065_s_a t	U22970_rna	U58496_s_a		/20656_rna 1_s_at		S74683 at	D00003_s_a	1	U14910_at	RC_AA6203 95_at	AA022985_a t		X51755 cds	1	J04177_at	D83017_s_a	ţ	AA416829_a t	U58658_at
0.24273749	1	HG862-	0.24216034 46353 at	0.24203654		0.24187939	0.2417678	0.24159676		U58496	0.24118869	0.24102162	0.24071202 U49974 f	0.24060303 S74683 at	0.00	0.24048653	0.24030784 U14910	RC_A 0.24019569 95_at	0.23997691			0.23974888 5 s at	0.23960805 J04177		0.2394968 t	0.23934166	0.23911104 U58658 at
0.366675	0.366623	0.366476	0.3664	0.366241		0.366168	0,365815	0.365773) (C	0.000.0	0.305142	0.365029	0.364834	0.364589	10000	0.36427	0.364101	0.363995	0.36396			0.363931	0.363878		0.363852	0.363752	0.363719
0.4346257		0 4344572	0.0565533 0.4340626	0.0564789 0.4340217			0.4336168	0.4335797	1	4	0.4334755	0.4332961	0.4329981	0.4329616	07.00		0.4322473	0.0526866 0.4320349	0.4317145			0.4316921	0.4314752		0.4312466	0.4312331	0.4311984
0.0572155	0.0572026	0.0570774	0.0565533	0.0564789		0.0563111	0.0556628	0.0551652	A KOOTITO O	1.000000	0.0548055	0.0533756	0.0531498	0.052965	0.0500000	0.0529083	0.0527766	0.0526866	0.0526438			0.0521825	0.0515696		0.0514911	0.0513471	0.0508588 0.4311984
277 Breast	278 Breast	270 Breast	280 Breast	281 Breast		282 Breast	283 Breast	284 Breast	100	Diedal	700 DIESSI	287 Breast	288 Breast	289 Breast	Droop t	Zau Dieasi	Breast	292 Breast	293 Breast			294 Breast	295 Breast		Breast	297 Breast	298 Breast
27.7	278	27.0	280	281		282	283	284	200	2 2	707	287	288	285	000	787	291	292	293			294	295		296	297	298

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299 Breast		502055	0.0502055 0.4310185	0.363266	0.23897916 U09278_at	U09278_at	Fibroblast activation protein mRNA
300 Breast	_	0.0488758	0.4309234	0.363095	0.23889045 t	AA085696_a t	AA085696_a EST: zl83a10.r1 Stratagene colon (#937204) Homo sapiens cDNA to clone 511194 5', mRNA sequence. (from Genbank)
301 Breast		0.0479617	0.4307557	0.362373	0.2387299 \$85963	S85963_at	Insulin receptor substrate-1 [human, skeletal muscle, mRNA, 5828 nt]
302 Breast		0.0476915	0.4306579	0.362356	. 0.2385545 at	W92242_s_at	EST: ze14b12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358943 5' similar to PIR:A49128 A49128 cell-fate determining gene Notch2 product;, mRNA sequence. (from Genbank)
303 Breast		0.0473838	0.4300758	0.362329	0.2384059	X02761_s_a t	FN1 Fibronectin 1
304 Breast		473665	0.0473665 0.4300495	0.362237	RC_AA 0.23825729 96 r at	RC_AA4304 96 r at	Ferritin, light polypeptide
305 Breast		465526	0.0465526 0.4300495	0.361832	0.23810378 D38128	D38128_at	PTGIR Prostaglandin I2 (prostacyclin) receptor (IP)
306 Breast				0.361756	0.23784631 M14113	M14113_at	F8C Coagulation factor VIIIc (hemophilia A)
307 Breast		0.0455725	0.4297436	0.361555	0.23775874 U32907	U32907_at	P37NB mRNA
308 Breast		0.0454797	0.4297331	0.361199	0.23755975 L32137	L32137_at	COMP Cartilage oligomeric matrix protein
309 Breast		0.0454438	0.429525	0.360914	0.23737626 M29335_at	M29335_at	MHC class II DO-alpha mRNA, partial cds
310 Breast		0.0453906	0.4294729	0.360901	0.23717825	Y08417 s at	0.23717825 Y08417 s at CHRNB3 Cholinerdic receptor, nicotinic, beta polypeptide 3
311 Breast		0.0453211	0.428889	0.360804	0.23707376 U40215 at	U40215 at	SYNZ Synapsin IIb
312 Breast		0.0447517	0.4288699	0.36077	0.23698239	AA059287_s at	
						AA287815 a	AA287815 a EST: zs50g04.r1 NCI CGAP GCB1 Homo sapiens cDNA clone
313 Breast		0.0447441	0.4284469	0.360739	0.23673148	ţ	IMAGE:700950 5', mRNA sequence, (from Genbank)
044			0000000				
3 14 Dieasi		0.04444.17	0.4283626	0.36061	0.23664106 H11098	H11098_at	
315 Breast	•	0.0436385	0.4283383	0.36046	0.23649785	AA149560_a t	EST: zo29d07.r1 Stratagene colon (#937204) Homo sapiens cDNA
316 Breast		0.0429564	0.4283285	0.360242	0.23635894 Z34975 at	Z34975 at	LDLC mRNA
347 Broom		V 00000 V 0	4204007	0.000	00000	AA443479_a	
318 Breag		122024	0.0420004 0.4281007	0.360067	0.23620261 1	1	Nuclear restricted protein, BTB domain-like (brain)
319 Breast	İ	120966	0.0420966 0.4277256	0.35998	0.23589963 M94167	M94167 at	Hours I gene for E-type calcium channer, exon 1
320 Breast		0.0412446	0.4276507	0.359764	0.23580083 H47945		Lysozyme (renal amyloidosis)
321 Breast		0.0409508	0.4274165	0.359641	0.23560052 R80351	R80351_at	EST: yi96e02.r1 Homo sapiens cDNA clone 147098 5'. (from Genbank)
322 Breast		0.0409182	0.4274137	0.359524	M11 0.23549774 1 at	M11973_cds 1_at	Gamma-B-crystallin gene (gamma 1-2)
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323	323 Breast	0.0407245	0.4272869	0.359415	0.23519807 W16700	W16700_at	EST: zb07e12.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 301390 5', mRNA sequence. (from Genbank)
324	324 Breast	0.040571	0.4272169	0.35934	0.23503631	RC_D19756 _at	EST: Human HL60 3'directed Mbol cDNA, HUMGS00712, clone mm0970, mRNA sequence. (from Genbank)
325	Breast	0.0405646	0.4269071	0.359249	0.23489252	S69369_at	PAX3 Paired box homeotic gene 3 (Waardenburg syndrome 1){alternative products}]
						AA074897 a	Zm85a05.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544688 5' similar to SW:ANRE_MOUSE P15267 KIDNEY ANDROGEN-REGULATED PROTEIN PRECURSOR;; mRNA
326	326 Breast	0.0404366	0.0404366 0.4268203	0.359135	0.23464967	1	sequence. (from Genbank)
327	327 Breast	0.0401511		0.358894	0.23449679 X72308	X72308_at	MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR
328	328 Breast	0.0401511	0.4262991	0.358715	0.2343904 X72308		at-2 Small inducible cytokine A7 (monocyte chemotactic protein 3)
329	329 Breast	0.0399904	0.4257574	0.358466	0.2343198 D21239	D21239_at	C3G protein
330	330 Breast	0.0397158	0.4256842	0.358429	0.23412012	AA081995_a	AA081995_a Zn26d06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 548555 5', mRNA sequence. (from Genbank)
331	331 Breast	0.0396951	0.0396951 0.4256407	0.358341	0.23407412 D14827_at	D14827_at	Tax helper protein 1
332	332 Breast	0.0396004	0.4253073	0.358213	AFFX-0 23386289 3 at-2	AFFX-LysX-	AFFX-1 vs X-3 at (miscallaneous control _ 11k chins)
333	333 Breast	0.0396004	1	0.358204	AFE) 0 23363796 3 at	AFFX-LysX-	AFFX-I vs X-3 at (endocemons control)
334	334 Breast	0.0394851		0.358092	0.23358318 D84424	D84424 at	Fetal brain mRNA for hvaluronan svnthase
335	335 Breast	0.0394712	0.4248546	0.358007	0.23343225 U20362	U20362_at	Tg737 mRNA
336	336 Breast	0.0394526	0.4247103	0.357475	0.23330581 80_at	RC_AA0262 80_at	EST: ze91d10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366355 31 mRNA sequence (from Genhank)
337	337 Breast	0.0394317		0.357429	0.23319118 W40374	W40374 at	DiGeorge syndrome critical region gene 2
338	338 Breast	0.0393458	0.424216	0.357374	0.23299167	S73885 c at	TFAP4 Transcription factor AP-4 (activating enhancer-binding protein
339	339 Breast	0.0388353	0.4242154	0.357075	0.2328101 U48807	a l	Dual specific protein phosphatase mRNA
340	340 Breast	0.0388174		0.356852	0.23268871 U36501	U36501_at	SP100 Nuclear antigen Sp100
341	341 Breast	0.0386099	0.4239275	0.356795	0.2325892 U03877	U03877_at	HEAT SHOCK 70 KD PROTEIN 1
342	342 Breast	0.0379743	0.4235694	0.356711	0.23248078 83	RC_AA5995 83_at	Homo sapiens mRNA for HIS1 protein, complete cds
343	343 Breast	0.0377849		0.356475	0.23232062 H16876	H16876_at	Ym34f05.r1 Homo sapiens cDNA clone 50123 5' (from Genbank)
344	344 Breast	0.037663	0.4235247	0.356319	0.23208803 X52011	X52011_at	MYF6 Muscle determination factor
345	345 Breast	0.0366197	0.4234619	0.3561	0.23193462	X87871_s_a t	HEPATOCYTE NUCLEAR FACTOR 4
346	346 Breast	0.0364763	0.4233822	0.355739	0.231781331	\A075998_a	Zm89b09.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545081 5' similar to gb:M15887 ACYL-COA-BINDING PROTEIN (HUMAN);, mRNA sequence. (from Genbank)

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					H. Amfridate R. Bade Sast	Spail Same Seeds	પાનામે 'મૃત્યત' ત્યાની લાક્ષ્ય પેતાની 'માતા' માતા કે મ
347	347 Breast	0.0363521	0.423366	0.355707	0.23166208 S66896 at	l	SCCA1 Squamous cell carcinoma antigen 1
						U08191_s_a	
348	348 Breast	0.0360756		0	0.23153605 t		R kappa B mRNA
345	349 Breast	0.0359579	9 0.4232217		0.23138444 U19180	at	BAGE B melanoma antigen
350	350 Breast	0.0358032		0.355297	0.2312569 Y00503	क्र	KRT19 Keratin 19
351	351 Breast	0.0355254	0.4230037		0.2311542 U60319	at .	HLA-H MHC protein HLA-H (hereditary haemochromatosis)
352	352 Broom	0.0252024			1 000		
200	חוכמאו	0.000000	- 1		0.2310241 2.48519		s_at XG gene (clone RACE5)
353	353 Breast	0.0353715	0.4227985	0.355041	0.23095721 S79267	at	CD4 CD4 antigen (p55)
354	354 Breast	0.0350129	0.4226657	0.35504	0.23072314 U699	61 at-2	0.23072314 U69961 at-2 Paired-like homeodomain transcription factor 2
355	355 Breast	0.0350129	0.4226657	0.35504	0.23061174 U69961	61 at	RIEG Rieger syndrome (solurshin)
57.0		000			AA41	02_a	EST: zv03b02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
220	300 breast	0.034632	0.4225272	0.354839	0.230449131		752523 5', mRNA sequence. (from Genbank)
357	357 Breast	0.0343895	0.42246	0.354758	RC_A 0.23033246 85_at	A2564	EST: zr81e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682126 3', mRNA sequence, (from Genbank)
040	<u> </u>				RC_A	A3427	EST: EST48360 Fetal spleen Homo sapiens cDNA 3' end, mRNA
200	338 Breast	0.0343283	0.4221102	0.354568	0.23021527 80_at		sequence. (from Genbank)
359	359 Breast	0.0341753	0.4218956	0.354511	RC_A 0.23003007 21 at	A6101	EST: af19h05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 1032153.3, mRNA segmence (from Genhank)
360	360 Breast	0.0333477	0.4217951	0.354484	U82108 0.22997577 1- 2	s_a	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 3
					U82108 s	n c	כשמומנטן ז ומנינטן ג
361	361 Breast	0.0333477	0.4212153	0.354359	0.22977675	5.	SIP-1 mRNA
362	362 Breast	0.0329759		0.354019	0.22964463 U09770 at		Ovsteine-rich heart protein (hCRHP) mRNA
363	363 Breast	0.032789	0.4207739	0.353884	0.22948655 U31628		IL15RA Interleukin 15 receptor alpha chain
364	364 Breast	0.0316908	0.420764	770000	RC_A	A2812	EST: zt08g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
	1000	0.001.0000	Ì	0.333041	0.22928058 95 at		IMAGE:712560 3', mRNA sequence. (from Genbank)
365	365 Breast	0.0316539	0.4205315	0.353408	AA197 0.22914945 t	AA197134_a E t	EST: zq11b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 629373 5', mRNA sequence, (from Genbank)
366	366 Breast	0.0314347	0.420473	0.353212	AA378316 0.228995261	ro,	Homo caniene clone 24738 mDNA sequence
367	367 Breast	0.030838	0.4204419	0.353157	0.22876112 U40223 at		Uridine nucleotide receptor (UNR) gene
368	Breast	0.0307915	0.420296	0.353041	M86757_s 0.2286301 t	σ,	S100A7 S100 calcium-binding profein A7 (psoriasin 1)
369	Breast	0.0306809	0.4202093	0.352829	0.22857477 D31417	न्न	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)
370	370 Breast	0.0304438	0.4199431	0.352616	D13666_s_0.228424491	'a	Cetanhlast sporific forter 2 (OCT 200)
		1		2.222	10117107	1	Secondar specific raciol 2 (OSF-208)

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							GCP-2 gene (granulocyte chemotactic protein-2) extracted from
974	974	0.0297859	0.4198474	0.35261	0 22825827 2 a	U83303_cds 1	Human line-1 reverse transcriptase gene, partial cds, and granulocyte chemotactic protein-2 (GCP-2) gene
1/0	Dicasi	0.0231000	1		AB)0464_a	ANC ASTRICTAL CO.
372	372 Breast	0.029558	0.4197755	0.352539	0.22816657 t-2	T	Homo sapiens mKIVA, exon 1, 2, 3, 4, clorie: KE34-24R
l i	-	0.000	0.4405445	0.252365	0.22809042 t	AB000464_a	mRNA clone RFS4-24A. exon 1, 2, 3, 4
3/3	373 Breast	0.029558	i	0.302303	0.22003072		FST: ve43c01 r1 Homo sapiens cDNA clone 120480 5'. (from
374	374 Breast	0.02903	0.4194021	0.352144	0.22790742 T95377	at	Genbank)
					AA	AA203513_a	EST: zx56b11.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
375	375 Breast	0.0283808	0.4192353	0.35209	0.22772473 t		cDNA clone 446493 5', mRNA sequence. (from Genbank)
376	376 Breast	0.0282599	0.4189481	0.352088	0.22761236 L15309	.at	ZNF141 Zinc finger protein 141 (clone pHZ-44)
377	377 Breast	0.0278669		0.351993	0.2274913 M32373	äţ.	ARSB Arylsulfatase B
378	378 Breast	0.0278168	0.4182043	0.351864	0.22730185 X51602_	at	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 PRECURSOR
379	Breast	0.0277125	0.4181201	0.351772	0.22718252 U85267	15267_at	Down syndrome candidate region 1 (DSCR1) gene, alternative exon 1
380	380 Breact	0.027534	1	0.351692	0.22712643 HT759	s at	Adrenergic Receptor, Beta 1
3	2000	20.1]	EST: aa55c10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
				-	AA	\488935_a	AA488935_a IMAGE:824850 5' similar to TR:G1167506 G1167506 PROTEIN
381	381 Breast	0.0268083	0.4180588	0.35164	0.22694637 t		KINASE.;, mRNA sequence. (from Genbank)
	(0,000	0.4470944	0.054004	RC_AA	RC_AA4357	Homo sapiens (cione ch13/ambda/) alpria-tubuiin IIIRNA, coi iipiete
382	382 Breast	0.0264018	0.0264019 0.4175409	0.331324	0.22001004 20 1 at	17/66 of	E12 Coadulation factor XII (Hademan factor)
28	383 Breast	0.0201934	0.0201934 0.4173403	707166.0	NI 16+1022.0	1112700 at	MA112700 at FST: zn62h02 r1 Stratagene muscle 937209 Homo sabiens cDNA
384	384 Breast	0.0261083	0.4175363	0.351205	0.2266237 t	B_6613116	clone 562803 5', mRNA sequence. (from Genbank)
385	385 Breast	0.0259383	0.0259383 0.4174866	0.350984	0.22649984 US)3553_at-2	0.22649984 U93553_at-2 Fetoprotein-alpha 1 (AFP) transcription factor
386	386 Breast	0.0259383	0.0259383 0.4174105	0.350956	0.22634694 U93553	93553_at	Alpha1-fetoprotein transcription factor (hFTF) mRNA
	-	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	2070770	0.05000	0 22640707 N26467 of	75467 of	Homo sapiens mRNA for DEPP (decidual protein induced by prodesterons)
388	388 Breast	0.0252955		0.350811	0.22608559 U15590 at	15590 at	Heat shock protein 27 (HSP27) mRNA
386	389 Breast	0.0251769	0	0.350803	0.22598173 73_at	RC_AA6098 73_at	EST: af08c07.s1 Soares testis NHT Homo sapiens cDNA clone 1031052 3', mRNA sequence. (from Genbank)
			i .	<u> </u>	6	D13814_s_a	
39(390 Breast	0.0250039	9 0.4169912	0.350739	0.22580901	A C 454 E 7 . 0	t A6012157 of 2008 1 Society precipital Intensity NNHPH Homo saniens CDNA
39.	391 Breast	0.0248178	8 0.4169903	0.350411	0.22566435 t	A043131_a	clone 486083 5', mRNA sequence. (from Genbank)

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CHRNA5 Cholinergic receptor, nicotinic, alpha polypeptide 5	EST: aa70h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826343 3' similar to WP:C09F5.2 CE01774;, mRNA	sequence, (from Genbank)	EST: yo07h11.r1 Homo sapiens cDNA clone 177285 5'. (from Genhank)	Forkhead protein FREAC-2 mRNA, partial cds	APEH N-acylaminoacyl-peptide hydrolase	EST: zh81d12.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	RC_AA0018 cDNA clone 427703 3' similar to contains Alu repetitive element;	IIIKNA sequence. (Irom Genbank)	PEPSINOGEN A PRECORSOR	Potassium Channel (Gb:L02752)	EST: zh51h04.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 415639 5', mRNA sequence. (from Genbank)	EST: 12f7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)	RC_AA4355 EST: zt85g06.s1 Soares testis NHT Homo sapiens cDNA clone 97 at 729178 3', mRNA sequence, (from Genbank)	C5R1 Complement component 5 receptor 1 (C5a ligand)	EST: zt18d04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713479 3', mRNA sequence, (from Genbank)	Carbonic anhydrase XII	Homo sapiens DNA sequence from Fosmid 27C3 on chromosome AA007583 a 22q11.2-ater. Contains two possibly alternatively spliced unknown	genes, one with homology to a worm protein. Contains ESTs	EST: zw24g05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770264 3', mRNA sequence. (from Genbank)	AA046737 a 380154 5' similar to contains Alu repetitive element: mRNA	sequence. (from Genbank)	Methylenetetrahydrofolate Reductase	GDI-dissociation inhibitor RhoGDIgamma mRNA
M83712_s_a t	A5211	11_at	H41895 at		J03068 at	1	RC_AA0018	1	JUU28/ at	псвз1- HT831_at	W78726_at	0.22420205 W26719 at	RC_AA4355 97_at	0.2238072 M62505 at	A2837	AA171913_a t	AA007583 a	1	1342	AA046737 a		at	0.22302984 U82532_at
N 0.22558725 t		0.22543037 11_at	0 22531524 H41895	0.22518136	0.22500269 J03068 at		0 00 477 404	0.22477461 00 at	0.2240484 JU0287	0.22456974 HT831_at	0.22449318 W78726	0.22420205	RC_A 0.2239583697 at	0.2238072	RC_A 0.22366253 74 at	0.22353487		0.22341135 t	RC_AA 0.22338043 45_r_at		0.22324742	HG4234-0.22316793 HT4504	0.22302984
0.350195		0.350134	0.350125	0.349987	0.349947		710067	0.049637	0.349/58	0.349684	0.349574	0.349547	0.349475	0.34942	0.349384	0.349378		0.34919	0.349146		0.349084	0.348608	0.348604
0.4169742		0.4164135	0 4164081	0.4163954	0.4163598		07063770	0.022320 0.4103070	0.0223644 0.4161504	0.4160872	0.416043	0.4158326	0.4158122	0.415485	0.4150932	0.02109 0.4149379		0.4148989	0.4148851		0.4148843	0.4147914	0.4146491
0.0247007		0.0243905	0.0237124	0.0234328	0.0232614		000000	0.0223320	0.0223844	0.0222027	0.0219029	0.0217941	0.0216546	0.0212416	0.0211948	0.02109		0.0208901	0.0208811		0.020606	0.0204034	0.0203722
392 Breast	-	Breast	Breast	395 Breast	396 Breast		200	SS/ Dieds	390 Dreast	399 Breast	400 Breast	401 Breast	402 Breast	403 Breast	404 Breast	405 Breast		406 Breast	407 Breast		408 Breast	409 Breast	410 Breast
392		393	394	395	396		706	300	286	399	400	401	402	403	404	405		406	407		408	409	410

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

411 Breast	0.0197804	0.414447	0.348522	0.2228833 2_s_at	s Paired box homeotic protein (PAX3) gene
412 Breast	0.019492	0.4143775	0.34837	AA431603_a 0.22280656 t	
413 Breast	0.018997	0.4142608	0.348266	RC_AA0341 0.22261675 79 at	
414 Breast	0.0183599	0.414243	0.347872	0.22255002 1178166 at	Human Ras-like small GTPase RIBA mRNA, alternatively spliced,
415 Breast	0.0183175	0	0.347631		IEX-1
416 Breast	0.0182602	0.414025	0.347608		HSPA6 Heat shock 70kD protein 6 (HSP70B)
417 Breast	0.0182602	0.4139094	0.347427	0.22224224 X51757 at-	0.22224224 X51757 at-2 Heat shock 70kD protein 6 (HSP70B1)
418 Breast	0.0182514	0.4136716	0.346928	0.2220524 53 i at	EST: zr79a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681880 31 mRNA sequence (from Genhank)
419 Breast	0.0180122	0.4135433	0.34677	HG2271- 0.22198065 HT2367 at	Profilanarin
420 Breast	0.0176827	0.0176827 0.4135337	0.346748		NDP Norrie disease (neamboniome) protoin
421 Breast	0.0174744	0.0174744 0.4133748	0.346619	0.22175573 X76383 at	HE3(alpha)
				HG3044-	
422 Breast	0.0172671	0.4132845	0.37658	HT3742_s_a	
	107100		0.0+0.0	U.ZZ 17 U0Z 1	
423 Breast	0.0172473		0.346399	0.22152884 37_at	IEST: 2894g02.31 NOT_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705170 31, mRNA sequence. (from Genbank)
424 Breast	0.0163557	0.4130339	0.346391	· 0.22143744 U28055 at	MST1 Macrophage stimulating 1 (hepatocyte growth factor-like)
425 Breast	0.0163481	0.4129909	0.34627	AA165144_i 0.2213406	EST: zo94e09.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 594568 5', mRNA sequence. (from Genhank)
426 Breast	0.016178	0.4129804	0.346263	0.22125793 t	
427 Breast	0.0160547	0.0160547 0.4126453	0.346189	0.2211309 W17400 at	EST: 2b15b10.r1 Sources fetal lung NbHL19W Homo sapiens cDNA
428 Breast	0.015821	0.4125003	0.346134	0.22097512 M14306 at	Beta-03/01 christollin (CVDDA2/A1) men A month of
429 Breast	0.0157	0.4123595	0.346113	0.22088304 L77563 at	DGS-F partial mRNA
430 Breast	0.0152924		0.346081	0.22075565 U82306 at	Unknown protein mRNA, partial cds
431 Breast	0.0144867	0.4120733	0.34601	0.22062117 L35854 at	Dystrophin (dp140) mRNA, 5' end
432 Breast	0.0144322	0.4120116	0.345968	0.22045566 N75646_at	EST: yv29a08.r1 Homo sapiens cDNA clone 244118 5'. (from Genbank)
433 Breast	0.0142941	0.4117874	0.345957	HG3495- 0.22032975 HT3689_at	Collagen, Type Ix, Alpha 1

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			2 -	15. That's that's 15 will not	
	07077070	0.444894	0 345843	0 22013435 84 at	
434 Breast	0.0141940	170117	0.00	11 %	co,
435 Breast	0.0135345	0.4111601	0.345695	0.21997169 t	758089 5', mRNA sequence. (from Genbank)
				HG3187-	
436 Droast	0.0134053	0.4410372	0.345647	0.21981709 t	
430 DI Edsi	0,010,0				EST: yx51d01,r1 Homo sapiens cDNA clone 265249 5. (from
437 Breast	0.0133904	0.4109576	0.345536	0.21976164 N31013	
		1		X00368_xpl	
438 Breast	0.0131763	0.4106325	0.345492	0.21968429 2_at	/annot=mRNA
				AA45916	AA459160_a EST: aa26h10.r1 NCI_CGAP_GCB1 Homo sapiens culvA clorie
439 Breast	0.0131511	0.4105138	0.345208	0.21950255 t	
440 Breast	0.0128706	0.4104281	0.345046	0.2194169 U53442 at	
441 Breast	0.0127012	0.4101566	0.344949	0.21936236 L07592_at	T
A42 Breast	0.0127012	0.4101006	0.344907	0.21919642 L07592 at-2	Human peroxisome proliferator activated feception in N.Y., compress at-2 cds
					EST: zs5zf04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
				AA2873	AA287308_a IMAGE:701119 5' similar to contains Alu repetitive element;confains
443 Breast	0.012679	0.4100905	0.344813	0.2191365 t	element MER1 repetitive element;, mRNA sequence. (from Genbank)
444 Breast	0.0124688	0.0124688 0.4100214	0.344664	0.21904598 U26403 at	at EPLG7 Eph-related receptor tyrosine kinase ligand /
				AFFX-BioC	
445 Breast	0.0120718	0.4099689	0.344567	0.21892244 3_st	AFFX-BioC-3_st (endogenous control)
				AFFX-BioC	
446 Breast	0.0120718	0.0120718 0.4096865	0.344257	0.21883304 3_st-2	AFFX-BioC-3_st (miscellaneous control - 11k chips)
447 Breast	0.0119039	0.4096225	0.344122	0.21864054 J05068	at TCN1 Transcobalamin
					EST: aa43a01,r1 Soares NhHMPu S1 Homo sapiens cDNA clone
				AA4897	AA489/16 a 823656 5 Similar to comains element wenter repetitive elements.
448 Breast	0.0118772	0.0118772 0.4094398		0.21856806 t	
449 Breast	0.0116967	7 0.409404	0.343898	0.21847437 U05227	at Rar protein mRNA
1000	000000000000000000000000000000000000000			AA406087	87_s TA14 (SCL) interrupting locus
430 Breast	0,0110000		0.04000		AAA17340 a EST: 7:07c02 r1 Soares testis NHT Homo sapiens cDNA clone
451 Breast	0.0115896	0.0115896 0.4093473	0.343743	0.21822464 t	731138 5', mRNA sequence. (from Genbank)
452 Breast	0.0108785	0 0108785 0 4092896	0	0.21807055 X16866 at	
453 Breast	0.0108434	4 0.4092376		0.21796383 L23852_at	at (clone Z146) retinal mRNA, 3' end and repeat region
AEA Dropet	0.010512	0 0105127 0 4091721	0.343412	HG4749- 0.21776974 HT5197 at)- at Calmitine Calcium-Binding Protein, Mitochondrial
434 Breast	0.010014	2110011			1

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

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0.0057106 0.4072251 0.341131 0.21533148 L38820 at	0.21533148 L38820 at

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478 E	478 Breast	0.0056493	0.4072181	0.341131	0.21517509 M33882	äţ	MX1 Myxovirus (influenza) resistance 1, homolog of murine (interferon inducible protein p78)
479	479 Breast	0.0055227	0.4071741	0.341103	0.21508758 U89717	at	RDH1 Retinol dehydrogenase 1 (11-cis)
1007	1007	0.0054338	0.407045	0 34405	RC 0.24401111 47	_AA4279	EST: zw50e09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
400	Diedst	0.0004320	0.40704.0	0.04	11116412.0	490685 a	EST; aa45b03.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
481 E	Breast	0.0050569	0.4069941	0.341034	0.21490355 t	1	823853 5', mRNA sequence, (from Genbank)
		The state of the s	1				CSF2RB Colony stimulating factor 2 receptor, beta, low-affinity
482	482 Breast	0.0050467	0.4069175	0.34068	0.21482638 M59941	äţ	(granulocyte-macrophage)
483 1	483 Breast	0.0049541	0.4067849	0.340611	0.21457182 H52378	ġ,	Spectrin, alpha, erythrocytic 1 (elliptocytosis 2)
484	484 Breast	0.0046402		0.34054	0.21441376 X56667	at	CALB2 Calbindin 2, (29kD, calretinin)
485	485 Breast	0.0045265		0.340332	0.21434543 U30930	ä,	CGT UDP-galactose ceramide galactosyl transferase
486	486 Breast	0.004522	0.4066148	0.340278	0.21423616 L41351	ä,	Prostasin mRNA
487	Breact	0.0044954	0.4065344	0.340149	RC_A	A5212	MAGE:827178 3' mRNA sequence (from Genhank)
P	Ol Gast	10010		01000	0.41117	70 at	
488	Breast	0.0041656	0.4065344	0.340109	0.21397248 S80905_f_at		PRB2 locus salivary proline-rich protein mRNA, clone cP7
	Administration to the second s	THE PARTY OF THE P				RC_AA6096	EST: af15h11.s1 Soares testis NHT Homo sapiens cDNA clone
489	489 Breast	0.0039722	0.4065061	0.339895	0.21390572 35_at		1031781 3', mRNA sequence. (from Genbank)
490 E	490 Breast	0.0036419	0.406475	0.33983	0.21379013 W28510_at		Calmodulin 1 (phosphorylase kinase, delta)
491	491 Breast	0.0036291	0.4062729	0.339828	0.21371846 U28131_at		HMGI-C chimeric transcript mRNA, partial cds
			1		1	14402121_a	AA402121_a EST: zt67e02.r1 Soares testis NHT Homo sapiens cDNA clone
4921	492 Breast	0.0027202	0.4061568	0.339806	0.21361004 t		727418 5', mRNA sequence. (from Genbank)
493 E	Breast	0.0025829	0.4061568	0.339632	0.21351214 U13044	J13044 at	GABPA GA-binding protein transcription factor, alpha subunit (60kD)
494	Breact	0.0024218	0.4059742	0 339487	0.21336308 NA820A	, VV820V at	EST: yv22a08.r1 Homo sapiens cDNA clone 243446 5'. (from
1	חבמפו	0.0044610		0.00000	0.50000012.0		OCHIDALIN)
	,				union when	4G1827- 4T1856_s_a	
495	495 Breast	0.0022413		0.339421	0.2131124 t		Cytochrome P450, Subfamily lic, Alt. Splice Form 2
4961	496 Breast	0.0016266	0.4058759	0.339319	0.21307735 U12139_at	J12139_at	Alpha1(XI) collagen (COL11A1) gene, 5' region and exon 1
497	497 Breast	0.0015754	0.405842	0.339132	0.21292847	4A282944_a	AA282944_a EST: zt15g08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
007	1	0		700000	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	00000	HRAR- beta 2=retinoic-acid-receptor beta/suspected tumor suppressor {5' region, transcription control region} [human, mRNA
480	490 breast	0.00 109		0.339124	0.21201194	287207 s at	0.21261194502302 s at Parta, 1730 ftg
499	499 Breast	0.0010207	0.4053617	0.339031	0.21276698 L32164	.32164_at	Zinc finger protein mRNA, 3' end
200	500 Breast	9.71E-04	0.4051561	0.338897	0.21268353 M37981	M37981_at	CHRNA3 Alpha-3 neuronal nicotinic acetylcholine receptor subunit
501	501 Breast	7.13E-04	0.4050444	0.338766	0.21263252 U82303	J82303_at	Unknown protein mRNA, partial cds

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502 Breast	2.19E-05	2.19E-05 0.4050356	0.338622	U83598_s_a	Death domain receptor 3 soluble form (DDR3) mRNA, partial cds
503 Breast	-4.57E-05	0.404849	0.338375	0.2123711 H11788_at	EST: ym11b06.r1 Homo sapiens cDNA clone 47577 5'. (from Genbank)
504 Breast	-3.96E-04	0.4047111	0.338312	M27533_s_a 0.21227753 t	Ig rearranged B7 protein mRNA VC1-region
505 Breast	-4.18E-04	0.404682	0.338305	RC_AA4339 0.21217075 51_at	RC_AA4339 EST: zw52h03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 51 at clone 773717 3', mRNA sequence. (from Genbank)
					Human DNA sequence from clone 522J7 on chromosome 22q13.3.
506 Breast	-6.52E-04	-6.52E-04 0.4043935	0.338228	RC_AA1942 0.21205503 57 r at	Contains part of a 60S Ribosomal protein L5 pseudogene and a Peregrin (BR140) LIKE gene downstream of a putative CpG island. Contains ESTs, STSs and GSSs
507 Breast	-0.001026	-0.001026 0.4043892	0.338161	0.21197373 L11372_at	Protocadherin 43 mRNA, 3' end of cds for alternative splicing PC43-12
508 Breast	-0.001101	0.4042602	0.33796	0.21185085 W51743_at	EST: zc48f12.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325583 5', mRNA sequence. (from Genbank)
509 Breast	-0.001213	0.4041543	0.33794	0.21173644 R46311_at	EST: yj53f04.r1 Homo sapiens cDNA clone 152479 5'. (from Genbank)
510 Breast	-0.001466	0.4041159	0.337509	0.21166414 L11238 s at	0.21166414 L11238_s_at GP5 Glycoprotein V (platelet)
511 Breast	-0.001939	0.4041023	0.337475	M58509_cds 0.21154357 1 s_at	M58509_cds_FDXR gene (adrenodoxin reductase) extracted from Human 1_s_atadrenodoxin reductase gene
512 Breast	-0.002216	0.404023	0.337361	0.21151799 D10656_at	CRK V-crk avian sarcoma virus CT10 oncogene homolog
513 Breast	-0.002298	-0.002298 0.4038912	0.337325	0.21140918 W27076 at	EST: 22g11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genbank)
514 Breast	-0.002486	-0.002486 0.4037237	0.33732	RC_AA3988 0.21122555 92_at	RC_AA3988 EST: zt62g12.s1 Soares testis NHT Homo sapiens cDNA clone 92_at 726982 3', mRNA sequence. (from Genbank)
515 Breast	-0.002519	0.4035768	0,3372	0.21118708 M19045_f_at LYZ Lysozyme	LYZ Lysozyme
516 Breast	-0.00258	0.4035298	0.337119	0.21098429 1 f at	Antigen (MAGE-1) gene
517 Breast	-0.002677	-0.002677 0.4032174	0.337049	L00137_cds 0.21089697 1_at	L00137_cds GHRF gene (growth hormone releasing factor) extracted from Human 1_at growth hormone-releasing factor (GRF) gene, exon 1 (

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					Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene,
518 Breast	-0.002713	0.002713 0.4028361		0.21082246 R67702_at	part of the KIAAV447 gene, a novel alternatively spliced gene similar to many (archae)bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STss and GSSs
500 Breast	-0.00283	0.00283 0.4028219		0.21072227 X73501 at-2	at-2 KERATIN, TYPE I CYTOSKELETAL 20
521 Breast	-0.00283 -0.002967	-0.00283 0.4027551 0.002967 0.4027481	0.336844	0.21064727 X73501 at 0.2104736 D50923 at	KERATIN, TYPE I CYTOSKELETAL 20
522 Breast	-0.00311	0.4026403	0.336636		
523 Breast	-0.003626	0.4025314	0.336635	0.2102628 J02963 at	ITGA2B Integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B)
524 Breast	-0.003913	0.4023718	0.336497	AA249119_a	AA249119_a Ec0276.seq.F Human fetal heart, Lambda ZAP Express Homo t sapiens cDNA 5', mRNA sequence. (from Genbank)
525 Breast	-0.00414	0.4023425	0.33645	AA075427_a	AA075427_a EST: zm87a05.r1 Stratagene ovarian cancer (#937219) Homo
526 Breast	-0.004198	0.4021739	0.336181	RC_AA4789 0.20996502 67 at	EST: zv18e03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754012 3', mRNA seguence (from Genhank)
527 Breast	-0.004209	0.4021293	0.336062	0.20990698 62_at	EST: zr79b07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681877 3', mRNA sequence. (from Genbank)
528 Breast	-0.004343	0.4021145	0.335997	HG870- 0.20980309 HT870 at	Golgin, 165 Kda Polynentide
529 Breast	-0.004345	0.4019598	0.335815	0.20973794 J05480_s_at	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform at (calcineurin A alpha)
530 Breast	-0.004866	0.4019173	0.33564	RC_AA4910 0.20961753 01 f_at	RC_AA4910 IMAGE:824614 3' similar to TR:G1293732 G1293732 O3625P: ,, mRNA sequence, (from Genbank)
531 Breast	-0.00499	0.4018627	0.335563	HG3934- 0.2095269 HT4204 at	G1 Phase-Sperific Gene
532 Breast	-0.005561	0.4016674	0.335514	0.20946161 X96754 at	GLUL Glutamate-ammonia ligase (glutamine synthase)

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					HG4113- HT4383 s a	
533 Breast	-0.005562	0.4016433	0.335492	0.20928715		Olfactory Receptor Or17-201
534 Breast	-0.005663	0.4015656	0.335262	0.20918314 X77753	77753_at	M1S1 Membrane component, chromosome 1, surface marker 1 (40kD glycoprotein, identified by monoclonal antibody GA733)
535 Breast	-0.005824	0.4014216	0.335199	0.2090622 S81243_	တ	at Mitogen induced nuclear orphan receptor (MINOR) mRNA
536 Breast	-0.0061	0.4014216	0.33513	0.20887616 X67594	ä	MC1R Melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)
537 Breast	-0.006865	-0.006865 0.4013628	0.335097	0.20877592 Z00010 at	30010 at	Germ line pseudogene for immunoglobulin kappa light chain leader peptide and variable region (subgroup V kappa I)
538 Breast	-0.006932	-0.006932 0.4013168	0.334864	0.2085361 X52008	52008_at	GLRA2 Glycine receptor, alpha 2
539 Breast	-0.007039	0.4008135	0.334489	0.20852098 S77812 at	77812 at	FLT1 Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
540 Breast	-0.007125	0.4006445	0.334404	RC_A 0.20844536 29_at	RC_AA2848 29_at	H.sapiens mRNA for Zinc-finger protein (ZNFpT7)
541 Breast	-0.007137	0.4006213	0.334356	0.20821393 U69114	69114_at	EST: Human Down syndrome region, YAC 152F7, mRNA sequence. (from Genbank)
542 Breast	-0.007167	0.4005706	0.334349	0.20809577 t	X78416_s_a t	CSN1 Casein, alpha S1
543 Breast	-0.007179	0.4004878	0.33416	0.20803538 H17239 at	17239 at	EST: ym42f05.r1 Homo sapiens cDNA clone 50975 5'. (from Genbank)
544 Breast	-0.007273	0.4004105	0.334138	AFF; 0.20793584 3_at	AFFX-CreX- 3_at	AFFX-CreX-3 at (endogenous control)
545 Breast	-0.007273	-0.007273 0.4003306	0.334113	0.20786817 3 at-2	X-CreX-	AFFX-CreX-3 at (miscellaneous control - 11k chins)
546 Breast	-0.007329	0.4003102	0.333913	0.20751318 L15296 s	aţ	Clone hRCNC2b retinal rod cyclic nucleotide-gated cation channel gene
547 Breast	-0.00735	0.4003039	0.333825	RC_A	A0197	VIA A OZZOF
548 Breast	-0.007536		0.333683	0.20738943 Z15005 at	5 at	CENPE Centromare protein E (312kD)
549 Breast	-0.007571	0.4001838	0.333417	0.20728518 X07696 at		KRT15 Keratin 15
550 Breast	-0.007576	0.4001827	0.333377	0.2071896 2 at	385_rna	GL105 gene (histone H2B) extracted from H.sapiens genes for histones H2B.1 and H2A
551 Breast	-0.007581	0.4000622	0.333334	0.20710509 89_at	A6208	EST: af95g10.s1 Soares testis NHT Homo sapiens cDNA clone 1055586 3', mRNA sequence. (from Genbank)
552 Breast	-0.00775	0.4000337	0.333331	0.20702955 U59057_at		CRYBA4 Beta-A4 crystallin
553 Breast	-0.00793	0.3999725	0.333312	RC_A 0.2069242 34_at	A2370	Golgi SNAP receptor complex member 2

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554	554 Breast	-0.008101	0.3999223	0.333172	0.20689984 T70856 at		EST: yd15f04.r1 Homo sapiens cDNA clone 108319 5' similar to SP:ME18_MOUSE P23798 DNA-BINDING PROTEIN ;, (from Genbank)
555	555 Breast	-0.008164	i	0.33296	0.20680106 99	9	EST: ag10h08.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1069983 3', mRNA sequence. (from Genbank)
556	556 Breast	-0.008488	0.3998312	0.332933	0.2065969 L12060 s	1	at RARG Retinoic acid receptor, gamma 1
557	557 Breast	-0.008644	0.3997046	0.332903	0.20652814 U13948	i të	Zinc finger/leucine zipper protein (AF10) mRNA
558	558 Breast	-0.008802	0.3995789	0.332877	0.20647828 N32716_at	32716_at	EST: yx74h12.r1 Homo sapiens cDNA clone 267527 5' similar to PIR:S45251 S45251 SNF2alpha protein - human ;. (from Genbank)
559	559 Breast	-0.008831	0.399577	0.332776	0.20638831 t	A076003_a	AA076003_a Zm89c09.r1 Stratagene ovarian cancer (#937219) Homo sapiens t cDNA clone 545104 5', mRNA sequence. (from Genbank)
560	560 Breast	-0.008894	0.3995217	0.332724	0.20635384 HT3621	HG3432- HT3621_at	Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 4, K-Sam Iv
561	Breast	-0.009085	0.3994748	0.332559	0.20627391 t	U20536_s_a	Cysteine protease Mch2 isoform alpha (Mch2) mRNA
562	562 Breast	-0.009642		0.33248	0.20620906 U27185 at	27185 at	RAR-responsive (TIG1) mRNA
563	563 Breast	-0.009689	0.3993699	0.332388	0.20605153 t	A233236_a	AA233236_a Human clone p4betaGT/3 beta-1,4-galactosyltransferase mRNA, t partial cds
564	564 Breast	-0.009812	0,3993147	0.332314	0.20596744 t	117446_s_a	M17446_s_a FGF4 Fibroblast growth factor 4 (heparin secretory transforming t
C L		0000		00000	X	X60299_s_a	מיסמווסקמו ואידדסמק דווסמקוואיס ואואנו ווא
202	505 Breast	-0.00985	0.3989676	0.332196	1 16167602.0	10000	KALLIMANIN SYNDROME PROTEIN PRECORSOR
567	566 Breast	-0.009934	0.3988/19	0.332023	0.205/3328 M6239/ 0.205/3328 M6239/	162397_at	MCC Mutated in colorectal cancers
568	568 Breast	-0.010371		0.331969	0.20551108 Z80777		H2A/k gene
569	569 Breast	-0.010508		0.331845	0.20542865 X60487	60487_at	H4/h gene for H4 histone
570	570 Breast	-0.010621	0.398646	0.331742	0.20533364 U16261	16261_at	MDA-7 (mda-7) mRNA
571	571 Breast	-0.01107	0.3986287	0.331568	0.2052397 74 s at	RC_AA4121 74 s at	Nucleoporin 88kD
572	572 Breast	-0.011111	0.3985811	0.331383	0.2051698 42	960	EST: af16a06.s1 Soares testis NHT Homo sapiens cDNA clone 1031794.3', mRNA sequence, (from Genbank)
573	573 Breast	-0.011919	0.3985346	0.33131	0.20504439 D13305	13305_at	
574	574 Breact	-0.011953	0 398/317	0.331051	D 20408066+	D31833 s_a	AVDD 4 Arraining and and a reconstruction of the
575	575 Breast	-0.012176		0.331175	0.20497473 L26953 at	26953 at	RMSA1 Regulator of mitotic spindle assembly 1
576	576 Breast	-0.012189	0.398048	0.331033	0.2048766 t	AA280228_a t	EST: zt04c11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA done IMAGE:712148 5', mRNA sequence. (from Genbank)
577	577 Breast	-0.012202	0.3979125	0.330916	0.20468736 U90304	190304_at	Iroquois-class homeodomain protein IRX-2a mRNA

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Hair keratin, hHb6 Homo sapiens mRNA for zinc finger protein, complete cds	EST: zr65e10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668298 3', mRNA sequence. (from Genbank)	SERUM AMYLOID A-4 PROTEIN PRECURSOR	(clone JJ1a) cadherin mRNA fragment	0.20409729.103778 s. at MICROTI IRIII E-ASSOCIATED BROTEIN TALI	מין אייביים אומיים מיטרים	DGS-D MKINA, 3' end	0.20395581 Y08134_at-2 H.sapiens mRNA for ASM-like phosphodiesterase 3b	ASM-like phosphodiesterase 3b	DNA sequence from PAC 453A3 contains EST and STS	Calbindin 27 nene exons 1 and 2 and Alu reneat	Histo-blood group AB0 gene, exon 1	EST: zr77e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669432 3', mRNA sequence. (from Genbank)			Fibrinogen, A Alpha Polypeptide, Alt. Splice 2, E	EST: zr48f03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666653 3', mRNA sequence. (from Genbank)	IF156 Interferon-induced protein 56	EST: zw11g07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	769020 5', mRNA sequence. (from Genbank)	EST: EST52587 Fetal heart II Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)	EST: zp83b09.s1 Stratagene HeLa cell s3 937216 Homo sapiens	cDNA clone 626777 3', mRNA sequence. (from Genbank)	EST; ze57h12.r1 Soares retina N2b4HR Homo sapiens cDNA clone	EST: zr72g02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 668978 5'. mRNA sequence (from Genhank)	AA085138 a clone 546132 5' similar to gb:M34539 FK506-BINDING PROTEIN	(HUMAN);, mRNA sequence. (from Genbank)	Fas, Apo-1 gene (promoter and exon I)
	82	at	at	103778 c at	177E64 of	, di	Y08134 at-2	Y08134 at		M19878_s_a	1	A2534		HT2827_s_a		AA2333 at	1	<u>ا</u> ـــ		_AA3464 _at	A1913		A018847_a	253330_s	085138_a		x82279_s_a
0.20455948 X99142 at 0.20444581 D45213 at	RC_A 0.20436706 23 at	0.20426139 M81349	0.20418884 L43338	0.20409729	0.0040447177564	0.20401117	0.20395581	0.20383477 Y08134 at	0.20375353 Z83745_at	0.2036282	0.20353736 X84746 at	RC_A 0.20345484 19 at			0.20330955	RC 0.20321149 71	0.20315346 M24594 at		0.20311978	0.20299536 07		0.2029343 23_at	0.20280564	0.20274048 at		0.2026461	0.20260999
0.330832	0.330618	0.330616	0.330457	0.330309	0 330750	0.300239	0.330007	0.329982	0.329902	0.329823	0.329795	0.329633		(0.329594	0.329499	0.329487		0.329235	0.329221		0.329121	0.329072	0.32896		0.328906	0.328906
-0.01241 0.3977047 -0.012689 0.3976834	0.3976801	0.3976657	0.3976527	-0.013949 0.3975537	0011151 03075315	0.081 0040	0.3973927	0.3973286	0.3973022	0.3973016	0.3973016	0.3971769		0.00	0.39/1318	0.3970318	0.3970246		0.3969408	0.3969314	6	0.3969139	0.3968759	0.3968066		0.3965611	0.3965053
-0.01241	-0.013411	-0.013466	-0.013784	-0.013949	-0.014154	-0.0-4134	-0.014178	-0.014178	-0.014269	-0.014396	-0.014603	-0.015383		1	-0.015565	-0.015592	-0.015713	1	-0.0158	-0.016186	(-0.016188	-0.016196			-0.016304	-0.016367
578 Breast 579 Breast	580 Breast	1 Breast	582 Breast	583 Breast	584 Broact	חומשאו	585 Breast	586 Breast	587 Breast	588 Breast	589 Breast	590 Breast			ogri breast	592 Breast	593 Breast		og4 breast	595 Breast	C C	590 Breast	597 Breast	598 Breast	(599 Breast	600 Breast
57	28	58	28	58	22	3	58	58	58	58	58	59		ŗ	ति	59	29	í	25	59	Č	25	59.	59(SS	09

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601	601 Breast	-0.016658	0.3964541	0.32868	RC 0.20253317	C_AA3994 2_at	RC_AA3994 EST; zt53e07.s1 Soares ovary tumor NbHO I Homo sapiens cUNA 72_at clone 726084 3', mRNA sequence. (from Genbank)
602	602 Breast	-0.016681	0.3964232	0.328519	A. 0.20238371 t	AC002450_a t	BAC clone GS244B22 from 7q21-q22, complete sequence
		Person of the Control					EST: zq50h02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 645075 5' similar to contains Alu repetitive
603	603 Breact	-0.016723	0.396422	0 328416	0.202180681	AA206983_a	element;contains element MER22 repetitive element;, mRNA
604	604 Breast	-0.017051	0	0	0.2021114 M21188 at	121188 at	INSULIN-DEGRADING ENZYME
				1	<u> </u>	U86755 s a	
605	605 Breast	-0.017133	0.3960699	0.328285	0.20206255 t	l I	TNF-alpha converting enzyme mRNA
909	606 Breast	-0.017432		0.328159	0.2019909 U76369	76369_at	Cationic amino acid transporter-2B (ATRC2) mRNA, partial cds
607	607 Breast	-0.017527	0.3959732	0.327911	0.20188579 X81637	81637_at	CLTB Clathrin, light polypeptide (Lcb)
809	608 Breast	-0.017668	0.3959027	0.327909	0.20182575 D88667	88667_at	Cerebroside sulfotransferase
					R	RC_AA2243	EST: zr12f12.s1 Stratagene hNT neuron (#937233) Homo sapiens
609	609 Breast	-0.017948		0.327818	0.2017172 51_f_at	1_f_at	cDNA clone 648623 3', mRNA sequence. (from Genbank)
610	610 Breast	-0.018025	0.3957652	0.327752	0.20162672 X00540	.00540_at	PRL Prolactin
					R	RC_AA4373	EST: zv62f11.s1 Soares testis NHT Homo sapiens cDNA clone
611	611 Breast	-0.018058	0.3957646	0.327647	0.20145844 23_at	3_at	758253 3', mRNA sequence, (from Genbank)
(0			<u>x</u>	RC_D59856	EST: Human fetal brain cDNA 3'-end GEN-071B10, mRNA sequence.
612	612 Breast	-0.018071	- 1	0.327481	0.20132859	at	(from Genbank)
613	613 Breast	-0.018516	0.3956075	0.327403	0.2011978 X59798	.59798_at	CCND1 Cyclin D1 (PRAD1; parathyroid adenomatosis 1)
7	1	07000		0000		1	
014	Breast	-0.018/42	0.3954774	0.327229	0.20115829 K18154 at	18154 at	ES1: yf9/d10.r1 Homo sapiens cDNA clone 30728 5'. (from Genbank)
615	Breast	-0.018751	0.3954442	0 326992	RC_A 0.20111069.19.31	RC_AA4497	EST: zx07e10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
2	100010	2010.0	0.0004444	0.040004	0.201110034	מ מו	GIOTIE / 00002 0, HINNA SEQUETICE. (HOITI GETIDATIK)
616	616 Breast	-0.018825	0	0.326985	0.20098412 t	AA453136_a t	Phosphoribosyl pyrophosphate synthetase-associated protein 2
617	617 Breast	-0.018881	ļ.	0.326876	0.20090981 U51587 at	51587 at	Golgi complex autoantigen golgin-97 mRNA
618	618 Breast	-0.018927	0.3951604	0.326746	0.20089218 U00968_at	00968_at	SREBP-1 mRNA
619	619 Breast	-0.019054	0.3951426	0.326707	0.20084654 t	U48436_s_a t	FMR2 Fragile X mental retardation 2
620	620 Breast	-0.019157	0.3950504	0.326695	0.20075232 t	M22403_s_a t	PLATELET GLYCOPROTEIN IB ALPHA CHAIN PRECURSOR
67.1	Breast	-0 019218	0 3950452	0 326650	L(0.20067444.2	L08044_s_at-	Trofoil footor 2 (intratinal)
- -	ממסו	0.010610		0.040000			Helvii Idelvi o (ilitebiliai)
622	622 Breast	-0.019218	0.3950284	0.326521	0.20066702 L08044 s		at TFF3 Trefoil factor 3 (intestinal)
623	623 Breast	-0.019501	0.3950174	0.326357	0.20043099 2	L08096_s_at- 2	Tumor necrosis factor (ligand) superfamily, member 7

624 625 626 627 629 631 633 633 634 635	624 Breast 625 Breast 626 Breast 627 Breast 629 Breast 630 Breast 631 Breast 632 Breast 633 Breast 634 Breast 635 Breast 636 Breast 637 Breast 637 Breast 636 Breast	-0.019501 -0.019909 -0.020125 -0.020125 -0.0201032 -0.021183 -0.021451 -0.021451 -0.021451 -0.021455 -0.021453 -0.021835 -0.021835 -0.021935		0.326345 0.326315 0.326173 0.326162 0.325809 0.325747 0.325689 0.3252689 0.3252689 0.3252689 0.3252689 0.3252689	0.20038226 L08096 s g 0.20028324 t 0.20028324 t 0.20016424 t 0.19996712 t 0.19996712 t 0.199974118 U86214 at 0.19957174 N36040 at 0.19945112 t 0.19945112 t 0.1994512 t 0.1994563 t-2 0.19940563 t-2 0.19912635 U49928 at 0.19912635 U49928 at 0.1999728 X69878 at 0.1999728 X69878 at 0.1999728 X69878 at	0.20038226 L08096 s. at CD70 o.20034094 S49953 s. at N-cym AA367473 a Crysta C.20008324 t EST: EST: EST: EST: AA287706 a EST: Z C.20003535 Z20777 at Genba AA010324 a Zi09c0 o.19996712 t Clone 4 Clon	0.20038028[108096 s_ at CD70 CD70 antigen (CD27 ligand) 0.20038028[108096 s_ at CD70 CD70 antigen (CD27 ligand) 0.20028324 AA287706_a EST: zs53908.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 0.20016424 t AA287706_a EST: xs53908.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 0.20016424 t EST: H. sapiens putatively transcribed partial sequence. (from Genbank) 0.20016353 220777_at Genbank) AA010324_a Zi09c03.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA 0.19983742 t clone 430276 5', mRNA sequence. (from Genbank) 0.19985712 t clone 430276 5', mRNA sequence. (from Genbank) 0.19995714 N36040_at EST: zu38c01.r1 Soares voary tumor NbHOT Homo sapiens cDNA 0.1995714 N36040_at Genbank) 0.1995714 N36040_at Genbank) 0.1995714 N36040_at Genbank) 0.19945112 t RC_AA0191 EST: zes6N09.s1 Soares retina N2b4HR Homo sapiens cDNA clone 0.1994512 t RC_AA0191 EST: zes6N09.s1 Soares retina N2b4HR Homo sapiens cDNA clone 0.1997481 t 0.1997481 t 0.1997828_at TAK1 binding product (from Genbank) 0.1997883 (149928_at TAK1 binding product 1 (subtype EP1), 4ZkD 0.199783 x69878_at TEM4 Potassium voltage-gated channel, shaker-related subfamily, member 4 0.19980336 t
641 642 643	641 Breast 642 Breast 643 Breast 644 Breast	-0.022125 -0.02222 -0.022357 -0.022354	0.3935908 0.3934328 0.3934026	0.324752 0.32469 0.32469	0.1988587 D88795 at 0.19879825 W32012 at 0.19849059 T28246 at 0.10843247116787 at		EST: zb96c10.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320658 5', mRNA sequence. (from Genbank) Hepsin (transmembrane protease, serine 1)
044	Dreast	+7C7770-	0.393281 1	0.324482	0.19843242 L16782 at		Putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds

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Docket No.: 2825.2020-002	
Title: Genetic Markers for Tumors	
Inventors: Sridhar Ramaswamy, et al.	

645	645 Breast	-0.022697	0.3932196	0.324427	0.19837774 31	AA2533 at	EST: zr72g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668978 3', mRNA sequence. (from Genbank)
646	646 Breast	-0.022712		0.324427	0.19830844 63	AA2274 at	Homo sapiens mRNA for KIAA0859 protein, complete cds
647	647 Breast	-0.022738	0.3926503	0.324237	0.19822703	U52373_s_a t	Serine/threonine protein kinase
648	648 Breast	-0.02335		0.323959		U31120_rna 1 at	Interleukin-13 (IL-13) precursor gene
649	649 Breast	-0.02364			0.19808505 Y09267 at	Y09267 at	Flavin-containing monooxygenase 2
650	650 Breast	-0 02373	0.3924801		0.19806422	RC_AA5214 16 at	EST: aa68d12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826103.3; mRNA sequence. (from Genbank)
20 20	654 Broost	0.024440	1	373805	RC_AA4066 E	RC_AA4066	EST: zv15e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753742.3' mRNA sequence (from Genbank)
3 1	2000	21.1720.0	1			M95585_s_a	
652	652 Breast	-0.024281	0.024281 0.3923425	0.3237	0.1979998116464	16464 at	FISHER ATED PROTEIN PE-1
654	654 Breast	-0.024622	0.3920741		0.19775112 M13955	M13955 at	Mesothelial keratin K7 (type II) mRNA, 3' end
							ELAV-like neuronal protein 1 isoform Hel-N2 (Hel-N1) mRNA, partial
655	655 Breast	-0.024912	0.3920518	0.32347	0.19756006 U13706_at	U13706_at	cds
656	656 Breast	-0.024985	0.3918988	0.323403	X 0.1975012611	X60787_s_a	INTERLEUKIN ENHANCER-BINDING FACTOR
			1				Neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete
657	657 Breast	-0.025027	0.3918442	0.323208	0.19740452 L07615_at	L07615_at	spo
						AA461426_r	EST: zx63h02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
658	658 Breast	-0.025098	0.3917643	0.323025	0.19738203	at	clone 796179 5', mRNA sequence. (from Genbank)
629	659 Breast	-0.025314		0.322916	0.19723244 X06985_at	X06985_at	HMOX1 Heme oxygenase (decycling) 1
099	660 Breast	-0.025388	0.3917475	0.32281	0.19711089 U00944	U00944_at	Clone A9A2BRB6 (CAC)n/(GTG)n repeat-containing mRNA
200		0			700074070	X02176_s_a	
00 1	662 Breast	-0.025555	0.3915055	0.322569	0.197.10264 t	Ma7639 at	Transmamhrana racentor (ror2) mRNA
100	200			200		RC AA4501	EST: zx42e06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
663	663 Breast	-0.025776	0.3911917	0.322529	0.19695029 16	16_at	clone 789154 3', mRNA sequence. (from Genbank)
664	664 Breast	-0.025779	-0.025779 0.3911039	0.322486	0.19681126 X14675	X14675_at	Bcr-abl mRNA 5' fragment (clone 3c)
665	665 Breast	-0.025896	0.3909376	0.322439	0.196809 X72790	X72790_at	Endogenous retrovirus mRNA for ORF
0		000000	1000000		000007		Peroxisomal targeting signal import receptor (PXR1) gene, allele 5,
999	bbb Breast	-0.026019	-0.02b019 0.390/085		U.19662406 U.394U/	U354U/_at	partial cus
299	667 Breast	-0.026258		0.322342	0.19659062 U18914		19.8 kDa protein mRNA
899	668 Breast	-0.026348	0.3906833	0.322326	0.19647202 S58733	S58733_at	Pp52
699	669 Breast	-0.026473	0.390676	0.322237	0.19639546	U10690_f_at	0.19639546 U10690 f_at MAGE-5a antigen (MAGE5a) gene
l	İ						

			, e	Titl	e: Gen		2020-002 ters for Tu amaswamy	
no sapiens repetitive	5' end,	oryonic	01/E*0102	rosophila)-	ta .	sednence.	clone	A clone

AA203556_a 0.19615254_L02321_at 0.19605622_t 0.19605622_t 0.19599648_t 0.19599648_t 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_M16714_at 0.19569753_at 0.1957969_U79280_at 0.1957969_U79280_at 0.19573938_t 0.19573938_t 0.19573938_t 0.19573938_t 0.19573938_t 0.19573938_t 0.19573938_t 0.19573938_t 0.1957393903_at 0.19481182_44_s_at 0.19490126_D42039_at 0.19481182_44_s_at 0.19490126_D42039_at 0.194861151_t-2 D10537_s_a 0.19465151_t-2 D10537_s_a 0.19465151_t-2 D10537_s_a 0.19465136_D10537_s_a 0.19465136_D10537_s_a				-			EST: zx52a08.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
Breast -0.027101 0.3906609 0.322049 0.196299731 Breast -0.027137 0.3906453 0.321914 0.19615254 L02321_at Breast -0.027203 0.3904055 0.321765 0.196056221 A4332089_a Breast -0.027253 0.3903644 0.321747 0.19569763 M16714_at X13100_s_a Breast -0.027276 0.3902732 0.321387 0.19569753 M16714_at A13100_s_a Breast -0.027776 0.3901281 0.321271 0.19569763 M16714_at A122 Breast -0.027774 0.39011681 0.321271 0.19569763 M16714_at A236297_a Breast -0.027774 0.3901169 0.321271 0.19540407 M2054_at A236297_a Breast -0.028045 0.3899886 0.32144 0.1952969 U79289 U79289 A236297_a Breast -0.028417 0.3899881 0.320782 0.19513024 t AA386297_a Breast -0.02848 0.3897881 0.320782 0.19513024 t AA386390_a Breast -0.028601							a cDNA clone 446102 5' similar to contains element MSR1 repetitive
Breast -0.027137 0.3906453 0.321914 0.19615254 L02321_at Breast -0.027203 0.3904055 0.321765 0.19605622 t Breast -0.027257 0.3903644 0.321745 0.19509648 t Breast -0.027257 0.3903118 0.321465 0.1956978156 L10123 at Breast -0.027276 0.3902246 0.321387 0.19569783 M16714_at Breast -0.027776 0.3901581 0.321221 0.1956980 M16714_at Breast -0.027774 0.3901129 0.321221 0.1953946 Z46632_at Breast -0.027774 0.3999886 0.321221 0.1953946 L702054_at Breast -0.028045 0.3899886 0.320914 0.1951304 L702050_at Breast -0.028041 0.3899881 0.320914 0.1951309 L702080_at Breast -0.028604 0.389798 0.320773 0.19497311 t Breast -0.028606 0.389798 0.320697 0.194907311 t Breast -0.028867 0.389798 0.320697 0.194907311 t	670 Breast	-0.027101		0	0.19629973		element ;, mRNA sequence. (from Genbank)
Breast -0.027203 0.3904055 0.321766 0.19605622 t Breast -0.027253 0.3903644 0.321747 0.19599648 t Breast -0.027256 0.3903148 0.321747 0.19599648 t Breast -0.027276 0.3903718 0.321747 0.19599648 t Breast -0.027276 0.3902732 0.321845 0.19562389 M16714 at t Breast -0.027276 0.390129 0.321287 0.195639596 Breast -0.027774 0.3901129 0.321221 0.19539496 Breast -0.027774 0.3901016 0.321221 0.19539499 Breast -0.028045 0.3899886 0.320961 0.1951904 Breast -0.028045 0.3899886 0.320961 0.19513024 t Breast -0.028602 0.3899886 0.320773 0.19513024 t Breast -0.028602 0.3897899 0.320773 0.19513024 t Breast -0.028601 0.3897689 0.320773 0.194917311 t Breast -0.028804 0.3897747 0.320877 0.19490126 Breast -0.028804 0.3897747 0.320873 0.19490126 Breast -0.028804 0.3897747 0.320873 0.19480182 Breast -0.028804 0.3897749 0.320637 0.19481182 Breast -0.028804 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.19481182 Breast -0.028807 0.3897689 0.320637 0.1948182 Breast -0.028807 0.3894778 0.320637 0.1948182 Breast -0.028807 0.3894518 0.320637 0.19482365 Breast -0.028097 0.3894518 0.320037 0.19482365 Breast -0.028097 0.3894518 0.320007 0.19462365 Breast -0.028097 0.3894518 0.320007 0.19462365 Breast -0.028097 0.3894518 0.3200011 0.19462365 Breast -0.028007 0.3894518 0.3200011 0.19462365 Breast -0.028007 0.3894518 0.3	671 Breast	-0.027137	1	0	0.19615254	L02321_at	GSTM5 Glutathione S-transferase M5
Breast -0.027253	672 Breast	-0.027203	1	0		AA332089_a t	EST: EST36010 Embryo, 8 week I Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)
Breast -0.027257 0.3903118 0.321686 0.79578156 L10123 at at at at at at at at at at at at at	673 Breast	-0.027253	1			X13100_s_a t	MYH3 Myosin, heavy polypeptide 3, skeletal muscle, embryonic
Breast -0.027276 0.3902732 0.321445 0.19569753 M16714_at_at_at_at_at_at_at_at_at_at_at_at_at_	674 Breast	-0.027257		0	0.19578156	L10123	Surfactant protein A mRNA
Breast -0.027276 0.3902246 0.321387 0.19562389 M16714_at-2 Breast -0.02776 0.3901581 0.321271 0.19562389 M16714_at-2 Breast -0.02777 0.3901129 0.321221 0.19539496 Z46632_at Breast -0.027774 0.3901016 0.321221 0.19539496 Z46632_at Breast -0.028045 0.3899886 0.321221 0.19539496 Z46632_at Breast -0.028447 0.3899886 0.320961 0.1953969 U79280_at Breast -0.02848 0.3897989 0.320773 0.1957999 HT4464_at Breast -0.028666 0.3897787 0.320773 0.19497311 t AA393903_at Breast -0.028666 0.3897747 0.320597 0.19497311 t AA078906_a Breast -0.028867 0.3897699 0.320697 0.19481182 t4 s_at Breast -0.028867 0.38972027 0.19465151 t-2 D10537_sa Breast -0.028867 0.3894779 0.19	675 Breast	-0.027276	-	0	0.19569753	d I	HLA-E MHC class I antigen HLA-E
Breast -0.02756 0.3901581 0.321271 0.19548407 K02054 at Breast -0.0277 0.3901129 0.321269 0.19539496 246632 at Breast -0.028045 0.3899886 0.321221 0.1953938 t X95238 s a Breast -0.028045 0.3899886 0.320961 0.1957909 U79280 at AA386297 at Breast -0.028417 0.3899881 0.320782 0.19513024 t HG4194- Breast -0.02848 0.3897989 0.320773 0.19497311 t AA3893903 at Breast -0.028660 0.3897689 0.320777 0.19490126 D42039 at AA393903 at Breast -0.028867 0.3897689 0.320697 0.19480126 D42039 at AA078906 at Breast -0.028867 0.3897689 0.320549 0.19465151 t-2 D10537 s at Breast -0.028867 0.3897027 0.320207 0.19465151 t-2 D10537 s at Breast -0.028867 0.389526 0.320207 0.19454488 D88532 at -0.028867 0.3894518	676 Breast	-0.027276	0.3902246	0	0.19562389	M16714 at-2	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA CHAIN PRECURSOR
Breast -0.0277 0.3901129 0.321269 0.19539496 246632_at Breast -0.027774 0.3901016 0.321221 0.1953938 t X95238_s_a Breast -0.028045 0.3899886 0.320961 0.1953998 t 0.79280_at-2 Breast -0.028417 0.389981 0.320818 0.19513024 t 0.79280_at-2 Breast -0.02848 0.3899881 0.320782 0.19507909 HT4464_at 0.320773 Breast -0.02866 0.3897989 0.320773 0.19497311 t 0.40393903_at Breast -0.028661 0.3897689 0.320697 0.19490126 D42039_at 0.028861 Breast -0.028867 0.3897689 0.320697 0.19481182 44_s_at 0.058966_a Breast -0.028867 0.3897027 0.320237 0.19465151 t-2 0.10537_s_a Breast -0.028867 0.389526 0.320207 0.19465151 t-2 0.10537_s_a Breast -0.028867 0.389526 0.320207 0.194651179 t 0.053857_s_a Breast <td>677 Breast</td> <td>-0.02756</td> <td></td> <td>0.321271</td> <td>0.19548407</td> <td></td> <td>GRP Gastrin-releasing peptide</td>	677 Breast	-0.02756		0.321271	0.19548407		GRP Gastrin-releasing peptide
Breast -0.027774 0.3901016 0.321221 0.19533938 t X95238_s_a Breast -0.028045 0.3899886 0.320144 0.1951904 U79280_at-2 Breast -0.028417 0.389951 0.320818 0.1951904 U79280_at-2 Breast -0.028417 0.389951 0.320782 0.19513024 t HG4194-4 Breast -0.028502 0.3897747 0.320782 0.19497311 t HG4194-4 Breast -0.028566 0.3897747 0.320737 0.19490126 D42039_at AA393903_a Breast -0.028601 0.3897689 0.320737 0.19481182 44_s_at AA078906_a Breast -0.028867 0.3897697 0.19480126 D42039_at AA078906_a Breast -0.028867 0.3897747 0.320549 0.19476555 t Breast -0.028867 0.389789 0.320237 0.19465151 t-2 Breast -0.028867 0.389526 0.320207 0.1946518 B8532_at -0.028867 0.389526 0.320001 0.19452365 Z19702 219702 at<	678 Breast	-0.0277	ł.	0	0.19539496	Z46632 at	PDE4C Phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1)
Breast -0.028045 0.3899886 0.32114 0.19527969 U79280_at-2 Breast -0.028045 0.3899886 0.320961 0.19513024 AA386297_a Breast -0.028417 0.3899881 0.320782 0.19513024 theat HG4194-164130 Breast -0.028602 0.3897989 0.320773 0.19497311 theat AA393903_a Breast -0.028601 0.3897689 0.320737 0.19497311 theat AA393906_a Breast -0.028601 0.3897689 0.320697 0.19481182 44 sat AA078906_a Breast -0.028804 0.389769 0.320549 0.19481182 44 sat AA078906_a Breast -0.028867 0.389769 0.320549 0.19461182 44 sat AA078906_a Breast -0.028867 0.3897747 0.320549 0.19465151 4-2 D10537_sa Breast -0.028867 0.3897626 0.320207 0.19465161 4-2 D10537_sa Breast -0.028867 0.3894779 0.19454488 D88532 at D10537_sa Breast -	679 Breast	-0.027774	0.3901016	0	0.19533938	X95238_s_a t	H.sapiens mRNA for cysteine-rich secretory protein-1 delta
Breast -0.028045 0.3899886 0.320961 0.1951904 U79280_at-2 Breast -0.028417 0.389951 0.320818 0.19513024 t HG4194- Breast -0.02848 0.3897881 0.320782 0.19507909 HT4464_at HG4194- Breast -0.028502 0.3897747 0.320773 0.19497311 t AA393903_at Breast -0.028566 0.3897747 0.320697 0.19490126 D42039_at RC_AA2851 Breast -0.028601 0.3897689 0.320697 0.19481182 44_s_at AA078906_a Breast -0.028867 0.3897027 0.19461182 44_s_at D10537_s_a Breast -0.028867 0.3897027 0.320237 0.19465151 t-2 Breast -0.028867 0.389526 0.320237 0.19465151 t-2 Breast -0.028867 0.389526 0.320037 0.19461179 t Breast -0.028867 0.3894779 0.19454488 D88532 at	680 Breast	-0.028045	0.3899886		0.19527969	U79280_at	Clone 23575 mRNA, partial cds
-0.028417 0.389951 0.320818 0.19513024 t -0.02848 0.3899881 0.320782 0.19507909 HT4464_at -0.028502 0.3897989 0.320773 0.19497311 t -0.028601 0.3897689 0.320697 0.19490126 D42039_at -0.028804 0.3897689 0.320697 0.19481182 44_s_at -0.028867 0.3897027 0.320237 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19461179 t -0.028867 0.3894779 0.320001 0.19454488 D88532_at -0.028967 0.3894779 0.32001 0.19452365 Z19702_at	681 Breast	-0.028045	1	0	0.1951904	U79280 at-2	Human clone 23575 mRNA, partial cds
-0.028477 0.389951 0.320818 0.19513024 t -0.02848 0.3898881 0.320782 0.19507909 HT4464_at -0.028502 0.3897989 0.320773 0.19497311 t -0.028506 0.3897747 0.320777 0.19490126 D42039_at -0.028601 0.3897689 0.320697 0.19481182 44_s_at -0.028804 0.3897027 0.320549 0.19476555 t -0.028867 0.3897027 0.320237 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19465151 t-2 -0.028867 0.3894779 0.320037 0.19454488 D88532_at -0.028967 0.3894779 0.320011 0.19452365 Z19702_at				·		AA386297_a	AA386297_a EST: EST185039 Brain IV Homo sapiens cDNA, mRNA sequence.
-0.02848 0.389881 0.320782 0.19507909 HT4464_at -0.028502 0.3897947 0.320773 0.19497311 t -0.028601 0.3897689 0.320697 0.19490126 D42039_at -0.028804 0.389744 0.320549 0.19476555 t -0.028867 0.3897027 0.320237 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19465151 t-2 -0.028867 0.38954779 0.320037 0.19454488 D88532_at -0.028967 0.3894779 0.320011 0.19452365 Z19702_at	682 Breast	-0.028417		0	0.19513024	1	(from Genbank)
-0.028502 0.3897989 0.320773 0.19497311 t -0.028566 0.3897747 0.320773 0.19497311 t -0.028601 0.3897689 0.320697 0.19481182 44 s at -0.028804 0.389744 0.320549 0.19476555 t -0.028867 0.3897027 0.320237 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19461179 t -0.028867 0.3894779 0.320007 0.19454488 D88532 at -0.029097 0.3894518 0.320011 0.19452365 Z19702 at	683 Breast	-0.02848			0.19507909		Sodium/Hydrogen Exchanger 5
-0.028502 0.3897989 0.320773 0.194907311 t -0.028566 0.3897747 0.320737 0.19490126 D42039 at -0.028601 0.3897689 0.320697 0.19481182 44 s at -0.028804 0.389744 0.320549 0.19476555 t -0.028867 0.3897027 0.320237 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19461179 t -0.028867 0.3894779 0.32003 0.19454488 D88532 at -0.029097 0.3894518 0.320011 0.19452365 Z19702 at			1			AA393903 a	EST: zt85e04.r1 Soares testis NHT Homo sapiens cDNA clone
-0.028566 0.3897747 0.320737 0.19490126 D42039 at RC_AA2851 -0.028601 0.3897689 0.320697 0.19481182 44 s at AA078906 a AA078908 a AA	684 Breast	-0.028502		_	0.19497311	I	729150 5', mRNA sequence. (from Genbank)
-0.028601 0.3897689 0.320697 0.19481182 44 s at AA078906 a -0.028867 0.389744 0.320549 0.19476555 t AA078906 a -0.028867 0.3897027 0.320237 0.19465151 t-2 D10537 s a -0.028867 0.389526 0.320207 0.19461179 t -0.028964 0.3894779 0.32007 0.19454488 D88532 at -0.029097 0.3894518 0.320011 0.19452365 Z19702 at	685 Breast	-0.028566		0	0.19490126	D42039_at	KIAA0081 gene, partial cds
-0.028804 0.389744 0.320549 0.19476555 t	686 Breast	-0.028601			0.19481182	RC_AA2851 44 s at	EST: zs48h10.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700771 3'. mRNA sequence. (from Genbank)
-0.028867 0.3897027 0.320237 0.19465151 t-2 -0.028867 0.389526 0.320207 0.19461179 t -0.028964 0.3894779 0.320011 0.19452365 Z19702 at	687 Broset	N 028804			0.10476555	AA078906_a	
-0.028867 0.3894779 0.320207 0.19465151 1-2 -0.028867 0.389526 0.320207 0.19461179 t -0.029097 0.3894518 0.320011 0.19452365 Z19702 at			1		1000	0537 s	
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-0.028964 0.3894779 0.32003 0.19454488 D88532 at -0.029097 0.3894518 0.320011 0.19452365 Z19702 at	689 Breast	-0.028867		0	0.19461179	_s_/5c01C	MPZ Mvelin protein zero (Charcot-Marie-Tooth neuropathy 18)
-0.029097 0.3894518 0.320011 0.19452365 Z19702 at	690 Breast	-0.028964	1		0.19454488	Ł	P55pik
-0.029097 0.3894518 0.320011 0.19452365 Z19702_at							EST: H. sapiens putatively transcribed partial sequence; UK-HGMP sequence ID AAAAHXT: single read mRNA sequence (from
	691 Breast	-0.029097	0.3894518	0.320011	0.19452365	Z19702_at	Genbank)

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692 Breast	-0.029423		0.319976	M82967_s_ 0.19443801 t	Acrosomal vesicle protein 1
693 Breast	-0.0295	0.3893646	0.319864	0.19434194 Z29572 at	
694 Breast	-0.029501	0.3892904	0.319834	0.19424595 L40992_at	(clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds
695 Breast	-0.0296	0.3891564	0.319748	AA071106_f 0.19413926_at	EST: zm66e11.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 530636 5' similar to SW:PA10_YEAST P48363 PAC10 PROTEIN. [1] ;, mRNA sequence. (from Genbank)
696 Breast	-0.029649	0.389063	0.319717	0.19406885 R87549_at	t Ym89c04.r1 Homo sapiens cDNA clone 166086 5'. (from Genbank)
697 Breast	-0.029738	0.389023	0.319563	RC_AA4492 0.19401522 15 at	
698 Breast	-0.029969	0.3889602	0.319435	0.19390024 M11718	at COL5A2 Collagen, type V, alpha
699 Breast	-0.030033	0.3888889	0.319365	0.19380666 U87593_f	0.19380666 U87593 f at Endogenous retrovirus clone P1.8 polymerase mRNA, partial cds
700 Breast	-0.0301	1 1	0.31931	0,19370103 X51699 at	Bone gamma-carboxyglutamate (gla) protein (osteocalcin)
701 Breast	-0.030433	0.3888714	0.319301	0.1936362 X83127_at	
702 Breast	-0.030521	0.3887397	0.319211	0.19349878 N24988_at	
703 Breast	-0.030784	0.3885799	0.319186	HG3355- 0.1934782 HT3532 at	t Peroxisome Proliferator Activated Receptor (Gb:Z30972)
704 Breast	-0.03082	0.3885541	0.319117	RC_AA0211 0.19337611 57 at	1
705 Breast	-0.030839	0.3885389	0.318897	0.1933438[109609.5]	
706 Breast	-0.030947		0.318806	0.193263 hum alu at	_
707 Breast	-0.030947	0.3882127	0.318768	0.19315903 2	T .
708 Breast	-0.030952	0.3881313	0.318744	HG3111- 0.19305119 HT3287 at	İ
709 Breast	-0.031107	0.3880803	0.318708		w.
710 Breast	-0.031109	0.3880755	0.318662	X83492_s_a	-
711 Breast	-0.03202	0.3880634	0.318595	0.19276854 U39840 at	
712 Breast	-0.032318	0.3879453	0.318595	0.1927063 U72508	0.1927063 U72508 at-2 Human B7 mRNA, complete cds
713 Breast	-0.032318	0.387741	0.318436	0.19259281 U72508_at	B7 mRNA
					Proposition of the state of the

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

Trig Breast -0.032556 0.387623 0.318332 0.19242862 U37529 at gamma Hickorope Approximate Hickorope Approximate Hickorope Approximate Hickorope Approximate Hickorope Hickorope Approximate Hickorope Hickorope Approximate Hickorope Hickorope Approximate					TAC2 Tachykinin 2 (substance K. neurokinin A. neurokinin 2.	
Court Cour	714 Breast	.0 032536				neuromedin L, neurokinin alpha, neuropeptide K, neuropeptide
Coustries	ו ו הוכמפו	0.004000				gamilia)
-0.033031 0.3871545 0.318248 0.1923692 X53683 at RC_AA4238	715 Breast	-0.032688		$^{\circ}$	0.19241333 HT2698_at	Succinate Dehydrogenase, Flavoprotein Subunit
Course C	716 Breast	-0.033031			0.1923692 X53683 at	SCYA4 Small inducible cytokine A4 (homologous to mouse Mip-1b)
Colorada Colorada	747	744000	1		NOONOON 0	
-0.033679 0.3869321 0.318001 0.19199432 t 120.033614 0.3867262 0.31791 0.19187437 T83397 at -0.03365 0.3867241 0.317856 0.19185448 t AA126812_a 1.034379 0.3866734 0.317747 0.19171463 X03168 at -0.034379 0.3866734 0.317513 0.191585 L39060_at -0.034379 0.3866099 0.317747 0.19171463 X03168 at -0.03445 0.386594 0.317511 0.19149223 M61176_at -0.03445 0.3865145 0.31751 0.19130622 t_s_at -0.034781 0.3865183 0.316978 0.19114253 U63669_at -0.034781 0.3865183 0.316978 0.19114253 U63824_at -0.034781 0.386283 0.316978 0.19114253 U63824_at -0.034847 0.385284 0.316938 0.19094059 55_at -0.034781 0.3862173 0.316938 0.19094059 55_at -0.034847 0.38528423 0.316716 0.19084059 55_at -0.034894 0.3858423 0.316631 0.19084059 55_at -0.034994 0.3858423 0.316631 0.19084059 X04729_s_a	718 Breast	-0.033488	1		0.1921061 20 at	Glone 7 33433 31, mKNA sequence. (Ifom Genbank) Skelatal muscle alternate Stand of gene Kird 2 51 17D
-0.033579			Ī			טייטיטימן ווימסטיס מויטיומנס טייטיס אייטייטימן אייטיסייט מויטיומנס טייטיסייט
-0.033614 0.3867562 0.31791 0.19187437 T83397_at	719 Breast	-0.033579	1		8 60013	Lysy oxidase-like protein gene
C.0.03365 0.3867241 0.317856 0.19185448 t -0.034779 0.3866734 0.317856 0.19178328 L47125_s_at -0.034379 0.3866259 0.317747 0.19171463 X03168_at -0.034379 0.3866099 0.317515 0.191585 L39060_at -0.03445 0.386594 0.317515 0.19151199 L39060_at -0.034486 0.386584 0.317479 0.19149223 M61176_at -0.03479 0.386584 0.31751 0.19149223 M61776_at -0.034719 0.3865145 0.317479 0.19130622 1_s_at -0.034753 0.3865145 0.3176978 0.19119155 W04798_at -0.034781 0.3865173 0.316978 0.1911794 M32598_at -0.034781 0.3865183 0.316917 0.1911794 MA156670_r -0.034847 0.3859254 0.316716 0.19094059 55_at -0.034994 0.3857837 0.316716 0.19094059 55_at -0.035134 0.3856858 0.316376	720 Breast	-0.033614		0.31791	0.19187437 T83397 at	Homo sapiens peroxisomal phytanoyl-CoA alpha-hydroxylase (PAHX) mRNA, complete cds
-0.033779	721 Breast	-0.03365	1 1		AA126812_e 0.19185448 t	Homo sapiens mRNA for KIAA0690 protein, partial cds
-0.034154 0.3866259 0.317747 0.19171463 X03168 at -0.034379 0.3866137 0.317631 0.191585 L39060_atatatatatatatatatatatatatatatatatatat	722 Breast	-0.033779			တ	EEF1A1 Translation elongation factor 1-alpha-1
-0.034379	723 Breast	-0.034154			0.19171463 X03168 at	VTN Vitronectin (serum spreading factor, somatomedin B, complement S-protein)
1.0.034379 0.3866099 0.317515 0.19151199 1.39060_at-2-0.03445 0.3865914 0.317501 0.19149223 M61176_at -0.034486 0.386584 0.317479 0.19137911 1.000669_ma -0.034719 0.3865145 0.31721 0.19130622 1.5_at -0.034781 0.3862173 0.316978 0.19119155 W04798_at -0.034781 0.3862173 0.316917 0.19114253 U63824_at -0.034781 0.3861283 0.316817 0.19114253 U63824_at -0.034847 0.3859254 0.316798 0.19094059_55_at -0.034894 0.3858423 0.316716 0.19086787_at -0.035093 0.3857837 0.316631 0.19081274 t -0.035093 0.3856858 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.3857837 0.316376 0.19075832 X83412_at -0.035093 0.38508588 0.316376 0.19075832 X83412_at -0.035093 0.3850858 0.316376 0.19075832 X83412_at	724 Breast	-0.034379	1		0.191585 L39060 at	Transcription factor SL1 mRNA
-0.03495 0.3865914 0.317501 0.19149223 M61176_at U26446_s_a -0.034486 0.386584 0.317479 0.19137911 t 0.034719 0.3865145 0.31721 0.19130622 1_s_at -0.034739 0.3864797 0.317153 0.19119155 W04798_at -0.034781 0.3862583 0.316978 0.1911794 M32598_at -0.034781 0.3862173 0.316917 0.19114253 U63824_at -0.034781 0.3861283 0.316833 0.1910568 U63824_at -0.034847 0.3859254 0.316798 0.19094059_55_at -0.034894 0.3858423 0.316738 0.19086787_at -0.035093 0.3857837 0.316631 0.19081274 t -0.035093 0.3856858 0.3166376 0.190861274 t	725 Breast	-0.034379	, !		0.19151199 L39060_at-2	
-0.034486 0.386584 0.317479 0.19137911 t -0.034719 0.3865145 0.31721 0.19130622 1_s at -0.034739 0.3864797 0.317153 0.19119155 W04798 at -0.034781 0.3862583 0.316978 0.1911794 M32598 at -0.034781 0.3862173 0.316917 0.19114253 U63824 at -0.034781 0.3861283 0.316833 0.1910568 U63824 at -0.034847 0.3859254 0.316796 0.19094059 55 at -0.034994 0.3858423 0.316631 0.190986787 at -0.035093 0.3857837 0.316631 0.19081274 t -0.035134 0.3856858 0.316376 0.19075832 X83412_at	726 Breast	-0.03445			0.19149223 M61176_at	
-0.03496	100000	00.00			U26446_s_a	
-0.034719 0.3865145 0.31721 0.19130622 1_s_at	/2/ Breast	-0.034486				Protoporphyrinogen oxidase
-0.034739	728 Breast	-0.034719		0.31721	0.19130622 1 s at	Human 1 alpha,25-dihydroxyvitamin D3 24-hydroxylase (CYP24) dene, promoter region and partial CDS, (from Genbank)
-0.034763 0.3862583 0.316978 0.19119755 W04798 at -0.034781 0.3862583 0.316978 0.19114253 U63824 at -0.034781 0.3862173 0.316917 0.19114253 U63824 at -0.034847 0.3869254 0.316798 0.19094059 55 at AA156670 \text{PAAB50} -0.034994 0.3858423 0.316716 0.19086787 at X04729 s.a -0.035093 0.3857837 0.316631 0.19081274 t -0.035134 0.3855858 0.316376 0.19081274 t	7.00 Brooct	0627800	#04F8906 O			EST: za81b04.r1 Soares fetal lung NbHL19W Homo sapiens cDNA
-0.034781 0.3861283 0.316835 0.1910568 U63824 at-2 -0.034847 0.3859254 0.316798 0.19094059 55 at -0.034994 0.3858423 0.316716 0.19086787 at X04729 s.at -0.035093 0.3857837 0.316631 0.19081274 t -0.035134 0.3856858 0.316376 0.19081274 t	730 Breast	-0.034753	0.3862583			Glone 298927 5, mKNA sequence. (from Genbank)
-0.034781 0.3861283 0.316833 0.1910568 U63824 at-2 -0.034847 0.3859254 0.316798 0.19094059 55 at -0.034994 0.3858423 0.316716 0.19086787 at -0.035093 0.3857837 0.316631 0.19081274 t -0.035134 0.3856858 0.316376 0.19081274 t	731 Breast	-0.034781	0.3862173	0.316917	0.19114253 U63824 at	Transcription factor RTEF-1 (RTEF1) mRNA
-0.034847 0.3859254 0.316798 0.19094059 55 at AA156670_r -0.034994 0.3858423 0.316716 0.19086787 at X04729 s.a -0.035093 0.3857837 0.316631 0.19081274 t -0.035134 0.3856858 0.316376 0.19075832 X83412_at	732 Breast	-0.034781			0.1910568 U63824 at-2	
-0.034994 0.3858423 0.316716 0.19086787 at X04729 s a -0.035093 0.3857837 0.316631 0.19081274 t -0.035134 0.3856858 0.316376 0.19075832 X83412 at	733 Breast	-0.034847	L		0.19094059 55 at	Homo sapiens sperm flagellar protein Repro-SA-1 mRNA, complete cds
-0.035093 0.3857837 0.316631 0.19081274 t -0.035134 0.3856858 0.316376 0.19075832 X83412_at	734 Breast	-0.034994				Homo sapiens agrin precursor mRNA, partial cds
-0.035134 0.3856858 0.316376 0.19075832 X83412_at	735 Breast	-0.035093	1			Plasminoden activator inhibitor tyne 1 N-ferminus
	736 Breast	-0.035134			0.19075832 X83412_at	B1 mRNA for mucin

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737 Breast	-0.035134	-0.035134 0.3856494	0.316271		83412 at-2	0.19066155 X83412_at-2 H.sapiens_B1 mRNA for mucin
					HG944-	
/38 Breast	-0.0354	1 0.3856175			T944_s_at	Dopamine Receptor D4
739 Breast	-0.035602	-0.035602 0.3855714	0.316193	0.19035721 U92074	92074_at	RAD51 (S. cerevisiae)-like 1
					HG371-	
740 Breast	-0.03629	0.3855714	0.346147	0 19032341 at	H 20388_S	Mirely 1 Enithalia Alt Calina o
741 Breact	-0.036315		\perp		7	Mercill 1, Epinielial, Air. Oplice 9
740 0	21.0000.0-		1			Metallothionein I-B gene
742 Breast	-0.03644	- 1		0.19018021 U25801_at		Tax1 binding protein mRNA, partial cds
743 Breast	-0.036725					Inward rectifier K channel
744 Breast	-0.036862	0.3848574	0.315766			ATP binding cassette transporter (ABCR) mRNA
***						EST: zq39h04.s1 Stratagene hNT neuron (#937233) Homo sapiens
						cDNA clone 632119 3' similar to contains Alu repetitive
					_AA1668	element;contains element MSR1 repetitive element ;, mRNA
745 Breast	-0.036925	0,3848563	0.31576	0.1899569	3_at	sequence. (from Genbank)
2,0	00000			₹	4283662_a	AA283662_a EST: zt16h03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
740 Breast	-0.037002	0.3846765	0.315584	0.18993308 t		IMAGE:713333 5', mRNA sequence. (from Genbank)
747 Breast	-0.037156	0.384391	0.315584	0,18985245 t	4444115_a	AA444115_a EST: zv51b08.r1 Soares testis NHT Homo sapiens cDNA clone
7.0	10000			R	484	
748 Breast	-0.03/231	0.3843007	0.315368	0.18972932 80_s_at		Flavin containing monooxygenase 5
749 Breast	-0.037298	0.3841811	0.315365	HG2157 0.18967877 HT2227	_ at	Mucin 4. Tracheobronchial
/50 Breast	-0.037299	0.3841666	0.315357	0.18952338 UZ7699_at		SODIUM- AND CHLORIDE-DEPENDENT BETAINE TRANSPORTER
751 Breest	0.037248	0 2020064	2,00	,	3101	EST: af19g10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
750 Breest	-0.001340		0.515548			clone 1032162 3', mRNA sequence. (from Genbank)
752 Dreast	-0.03/41	0.3839824	0.315344		at	Clone 23907 mRNA sequence
77.4 BI East	-0.037521	- 1	0.315335	0.18934816 Y10205	at	CD88 protein
754 Breast	-0.03//05	- 1	0.315279	0.18925376 M94893		TSPY Testis specific protein, Y-linked
/55 Breast	-0.037743	0.3838683	0.315149	0.18915528 Y10260_at		EYA1A gene
756 Breast	-0.037829	0.3837707	0.315115	0 18907477 NA5402 at		EST: yw97f08.r1 Homo sapiens cDNA clone 260199 5'. (from
				DG CALLES	1	COT. COSE ON 14 MOI OOM COSE 11.
757 Breast	-0.037857	0.383661	0.315012	0.18900041 17_at	A3031	EST: adoppus:s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825785 3', mRNA sequence. (from Genbank)
758 Breast	-0.037981	0.3836543	0.314924	AA 0.18894482 t	1043894_a	AA043894_a EST: zk57b05.r1 Soares pregnant uterus NbHPU Homo sapiens
759 Breast	-0.038016	-0.038016 0.3835911	0.314865	O 18880864 H25082	7	EST: yl56g01.r1 Homo sapiens cDNA clone 162288 5'. (from
W-7-7-10-10-10-10-10-10-10-10-10-10-10-10-10-		1100000	00011000	0.10003004116	ซี.	Genbarik)

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Inventors: Sridhar Ramaswamy, et al.

760 Breast	-0.038383	0.3834648	0.314852	HG3231- 0.18882492 HT3408	HG3231- HT3408 at	Protease Receptor-1, Effector Cell
761 Breast	-0.038459	0.3833663	0.314788	RC_A 0.18878222 46_at	RC_AA4170 46_at	Fatty-acid-Coenzyme A ligase, very long-chain 1
762 Breast	-0.038896	0.3832846	0.314589	0.18866111 J05582_s_	J05582_s_at	at MUC1 Mucin 1, transmembrane
763 Breast	-0.039355	0.3829456	0,31455	0.18860418	AA504384_a	AA504384_a IMAGE:825218 5' similar to contains element MIR repetitive element ;; mRNA sequence. (from Genbank)
764 Breast	-0.039476	0.3829375	0.31439	0.18851428 D61596	D61596 at	Human fetal brain cDNA 5'-end GEN-421F03, mRNA sequence. (from Genbank)
765 Breast	-0.039592	0.3829375	0.314274	0.18847165 N73185	N73185 at	EST: yv46a09.r1 Homo sapiens cDNA clone 245752 5'. (from Genbank)
766 Breact	992050	0.3820346	0.344072	0 48826270		PSG11 gene (pregnancy-specific beta-1-glycoprotein 11 C-A domain) extracted from Human pregnancy-specific beta-1-glycoprotein alternatively spliced C-R, C-S, C-B, and C-A domains (PSG11) gene,
767 Breast	-0.039783		0.314272	0.18828952 52 at	RC_AA4305 52 at	Proline-rich Gla (G-carboxalufamic acid) nolynentide 2
768 Breast	-0.039802	0.3828232	0.314235	0.18826889 (U32674_s_a t	Orohan receptor GPR9 (GPR9) gene nartial cds
769 Breast	-0.04008	0.382802	0.314233	0.1881376 U35459	U35459_at	Bomapin mRNA
770 Breast	-0.040125	0.3824697	0.314123	0.18804514 W87936	W87936 at	EST: zh68d10.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417235 5' similar to gb:M74525 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (HUMAN);contains Alu repetitive element: mRNA sequence (from Genhank)
771 Breast	-0.040346	0.3824697	0.314053	0.18796603		Duchenne Muscular Dystrophy Protein (Dmd)
772 Breast	-0.0406	0.382423	0.313974	0.18780902 M11058 at		3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASF
773 Breast	-0.040858	0.3822903	0.313893	RC 0.187753 54		EST: zu65a10.s1 Soares testis NHT Homo sapiens cDNA clone 742842 3', mRNA sequence. (from Genbank)
774 Breast	-0.041114	0.3822249	0.313862	0.1877031 Z70218	တ	at MN1 protein (clone ICRFp50710498)
775 Breast	-0.041126	0.3821041	0.313813	0.18766877	AA004333_a	AA004333_a EST: zh91a01.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens t cDNA clone 428616 5', mRNA sequence. (from Genbank)
776 Breast	-0.041236	-0.041236 0.3820344	0.313651	0.18754639 W01059	ja,	EST: za55e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 296488 5', mRNA sequence. (from Genbank)

777 Breast	-0.041472	0.3010730	0.0	0.101 +023 2221 00 - 41	1	
	-0.041654	0.3818504	0.313586	0.18743448 W19984_at		EST: zb38d11.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305877 5', mRNA sequence. (from Genbank)
i _	-0.041679	0.3817395	0.3135	0.18733877 t	AA362598_a t	EST; EST72534 Ovary II Homo sapiens cDNA 5' end, mKNA sequence. (from Genbank)
	-0.041703		0.313489	0.18728574 M21494	at.	CKM Creatine kinase, muscle
1	-0.041738	ł	0.313473	0.18724519 X52003	jat j	TFF1 Trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in)
	-0.04187	0.3816702	0.313414	RC_A 0.18713742 17_at	A0106	EST: zi09f12.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 430319 3', mRNA sequence. (from Genbank)
	-0.041888	0.3816606	0.313414	0.18708766	J73394_f_at	0.18708766 U73394_f_at H.sapiens mRNA for NK receptor, clone 12.11C
	-0.04192	0.381577	0.31335	D870 0.1870719 2_at	087002_cds	D87002_cds POM121-like 1 gene extracted from Human (lambda) DNA for 2_at immunoglobin light chain
	-0.042124	0.3815632	0.313284	0.18691987 t	AB000115_a t	mRNA
	-0.042367	ļ	0.313261	0.18682547 Y09321_at	709321_at	TAFII105 mRNA, partial
	-0.042618	0.3813474	0.313211	RC_A 0.18681543 19_at	RC_AA4366 19_at	EST: zw55d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773959 3', mRNA sequence. (from Genbank)
	-0.042849	0.3813261	0.313104	0.18677084 M37763	M37763_at	Neurotrophin-3 (NT-3) gene
	-0.043119		0.312946	0.18675461 U09877	J09877_at	Helicase-like protein (HLP) mRNA
	-0.043255	0.3812952	0.312914	0.1867369 L14269_	_14269_at	SLC18A2 Solute carrier family 18 (vesicular monoamine), member 2
	-0.0433	0.3812754	0.312909	0.18663359 W28035	W28035_at	EST: 41a8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
		i			AA018852_a	
	-0.043619	0.3811475	0.312854	0.18641348 t		362868 5', mRNA sequence. (from Genbank)
	-0.043679	0.3810659	0.312835	0.18639849 U26209_at	J26209_at	Solute callier raining to (socialing depointed according a member 2
	-0.043703	0.3810654	0.312828	AFF. 0.18635501 5_at	AFFX-LysX- 5_at	AFFX-LysX-5_at (endogenous control)
	-0.043703	0.3808901	0.31271	AFFX- 0.18621843 5 at-2	AFFX-LysX- 5 at-2	AFFX-LysX-5_at (miscellaneous control - 11k chips)
	-0.043819	0.3807985	0.312639	0.18615448 N28643	N28643_at	Melastatin 1
	-0.043947	0.3807322	0.312404	0.18608798 HT4163	HG3893- HT4163 at	Phosphoglucomutase 1, Alt. Splice
	-0.043956		0.312303			MLN137 mRNA
	-0.044317	0.3805767	0.312237	0.18601997 D87012	D87012_at	Immunoglobulin lambda gene locus DNA, clone:61D6

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Analinomotein All	MUNITUDAL OF THE TAIL OF THE PROPERTY OF THE P	Myelin associated glycoproteil	HOK-2 mRNA for zinc finger protein	Selenium-binding protein (hSBP) mRNA	Zm70c03.r1 Stratagene neuroepithelium (#937231) Homo sapiens	cDNA clone 530980 5', mRNA sequence. (from Genbank)	Core-binding factor, runt domain, alpha subunit 2; translocated to, 2		CCAAT/enhancer binding protein (C/EBP), epsilon	ORF2: function unknown from Human Tigger1 transposable element,	complete consensus sequence./ntype=DNA /annot≃CDS	M81780_cds SMPD1 gene (acid sphingomyelinase) extracted from Homo sapiens	acid optimigatings (arm 21) gard, and a	FMR2 Fragile X mental refardation 2	Protein disulfide isomerase-related protein (PDIR)	EDN2 Endothelin 2	PTGER3 Prostaglandin E receptor 3 (subtype EP3) (alternative	products}	EST: zv26h12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	754823 5' similar to contains Alu repetitive element;, mRNA	sequence. (from Genbank)		Synuclein, gamma (breast cancer-specific protein 1)	Mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-	0.18463843 D17716_at-2 glucosaminyltransferase	N-acetylglucosaminyltransferase V	Axonemal dynein heavy chain (partial, ID hdhc3)	EST: similar to none, mRNA sequence. (from Genbank)	Excision repair cross-complementing rodent repair deficiency,	0.18430896 L04791_s_at complementation group 6	RC_AA6217 EST: af54f07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 1035493 3', mRNA sequence. (from Genbank)	EST: ae37h03.s1 Gessler Wilms tumor Homo sapiens cDNA clone	898037 3', mRNA sequence. (from Genbank)	MaTu MN mRNA for p54/58N protein	No description for gene: P-Select at
398_rna		at	at at	ä	45 a		ਲ	ma	1_s_at	U49973_xpt	2 at	M81780_cds	000	A93403_S_B	D49490 at	M65199 at	a	1		AA422123_i	-at	AF010126_a			D17716_at-2	D17716_at	Z83802_at	D82286_at		L04791_s_at	RC_AA6217	18_at	RC_AA5989	51_at	X66839_at	0.183937 P-Select_at
X048	0.100001.90	0.18585421 X98405 at	0.18581752 X82125	0,18564828 U29091		0.18558545	0.18545094 W26635		0.18541189		0.18533006 2 at	M81	0.10321202	0.1851911	0.18512306 D49490 at	0.18500948 M65199 at		0.18489403 t			0.18474871		0.18473122 t		0.18463843	0.18455261 D17716_at	0.18446992	0.18439811 D82286	The state of the s	0.18430896		0.1842122 18_at		0.18408595 51	0.18405467 X66839	0.183937
2020	0.312191	0.312105	0.312079	0.311941		0.311941	0.311858		0.311818		0.311811	0.0440	0.011003	0.344772	0.311642	0.31164		0.311621			0.311497		0.311447		0.311387	0.311354	0.311285	0.311238		0.311175		0.311125		0.311086	0.310965	0.310964
7	0.3805085	0.3805693	-0.044589 0.3804854	0,3804589	- Company of the Comp	0.3804506	0.3803745		0.3802944	A. A	0.3802944	2000000	0.3002003	0.38021	0.3801895	0.380162		0.3801511			0.3800442		0.3800312		0.3800042	0.379957	0.3798629	0.3796748	1	0.3796173		0.379601		0.3795269	ł	0.3794064
	- 1	-0.044387	-0.044589	-0.045062		-0.045064	-0 045145		-0.045175		-0.045283	0.047.047	-0.045517	-0.045327	-0.045598	-0.045622		-0.045629			-0.045709	The state of the s	-0.045846		-0.045977	-0.045977	-0.046085	-0.046102		-0.046132		-0.046141		-0.046276	-0.046374	-0.046503
	800 Breast	801 Breast	802 Breast	803 Breast		804 Breast	805 Breast		806 Breast		807 Breast		808 Breast	120018	810 Breast	811 Breast		812 Breast			813 Breast		814 Breast		815 Breast	816 Breast	817 Breast	818 Breast		819 Breast		820 Breast		821 Breast	822 Breast	823 Breast

Docket No.: 2825.2020-002

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

					The state of the s	DMA gene extracted from H.sapiens DMA, DMB, HLA-Z1, IPP2,
					X87344_cds	
824	824 Breast	-0.046598	0.3793238	0.310916	0.18382798 10_r_at	genes
825	825 Breast	-0.046808	-0.046808 0.3792819	0.31084	0.18379238 L41147_at	serotonin receptor mRNA
826	826 Breast	-0.047033	0.3790966	0.310591	0.18376642 U12140_at	Tyrosine kinase receptor p145TRK-B (TRK-B) mRNA
827	827 Breast	-0.04711	0.3790465	0.310565	0.18370172 M99063_at	KERATIN, TYPE II CYTOSKELETAL 2 ORAL
1				1000	X91653_s_a	
828	828 Breast	-0.047221	0.3788799	0.310537	0.163547031	Up) / (Chartenant Elbrahlant (#037949) Home conjune CDNA
000	920 Broset	7077700	0.3788275	0 340703	AA099995	AA0999995_a (2m65e06,f1 stratagene librobiast (#357212) notifio saprens curva t
020	830 Breact	-0.047494		0.310455	0.18347153 M31651 at	SHRG Sex hormone-binding alobulin
3	בו כמפר	1000		2		OB17-228 nene extracted from Human olfactory receptor gene cluster
					U58675 cds	
831	831 Breast	-0.047503	0.3785127	0.310432	0.1834047 1_at	
					A LANK A LANK AND A LANK AND A LANK AND A LANK A LA	EST: yi82b05.r1 Homo sapiens cDNA clone 145713 5'. (from
832	832 Breast	-0.047893	0.3785102	0.310279	0.18335998 R78309_at	Genbank)
					BC 040019	EST: zh83a05 s1 Soares fetal liver snleen 1NFI S S1 Homo sapiens
833	833 Breast	-0.048011	0.3785049	0.310219	0.18329163 08 at	
					AA249437 a	
834	834 Breast	-0.048012	0.3783343	0.310149	0.18323077 t	
					HG4272-	
835	835 Breast	-0.048071	0,3783139	0.310091	0.183159 HT4542_at	Hepatocyte Growth Factor Receptor
836	836 Breast	-0.048148	0.378209	0.30999	0.18310912 H47161_at	Acyl-Coenzyme A dehydrogenase, short/branched chain
837	837 Breast	-0.048182	0.3781759	0.309966	0.1830362 U34044_at	Selenium donor protein (selD) mRNA
						EST: yu11a03.r1 Homo sapiens cDNA clone 233452 5'. (from
838	838 Breast	-0.048856	0.3781345	0.309846	0.18286031 H78886_at	Genbank)
839	839 Breast	-0.048856	0.3780817	0.3098	M91463_rna 0.1828543_1_at-2	Solute carrier family 2 (facilitated olucose transporter), member 4
			ì			+
840	840 Breast	-0.048856	0.3779767	0.309789	0,18269047 1_at	Glucose transporter (GLUT4) gene
					RC_AA4777	
841	Breast	-0.048877	0.377887	0.309704	0.18265112 39_at	clone 739860 3', mRNA sequence. (from Genbank)
842	Breast	-0.048953	0.377817	0.309605	AA251078_ 0.18256605 t	a EST: zs01b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683903 5; mRNA sequence, (from Genbank)
						PTGER3 Prostaglandin E receptor 3 (subtype EP3) {alternative
843	843 Breast	-0.0491	0.3777879	0.309457	0.18247831 X83863_at	products}
844	844 Breast	-0.049134	0.3777756	0.309446	0.18239106 U70136_at	THPO Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)
		W1401-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1				

-LS S1 Homo sapiens ISSUE FACTOR (from Genbank)	growth factor)	syltransterase, myelolu-		CO1 mRNA seguence			locus .	Homo sapieris curva nbank)	Express Homo saplens			202722 5' similar to	ank)	sapiens cDNA clone			ma-1 subunit) extracted	31-q32	oHPU Homo sapieris	Oction in the second in the se		NFLS S1 Homo sapiens rom Genbank)	imed sublibrary Homo		The state of the s
EST: zi03a02.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429674 3' similar to gb:J02931 TISSUE FACTOR PRECURSOR (HUMAN);, mRNA sequence. (from Genbank)	FGF7 Fibroblast growth factor 7 (keratinocyte growth factor)	FUT4 Fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myelolu-	specific)	ESP1/CKP2	EST: Human placenta culvA 3 -eriu GLN-55505 t, fili va cospositori (from Genbank)	0 18202047 Z49825 s at HEPATOCYTE NUCLEAR FACTOR 4	Human V beta T-cell receptor (TCRBV) gene locus	EST; zw31c06.r1 Soares ovary tumor NbHOT Homo sapieris curva clone 770890 5', mRNA sequence. (from Genbank)	AA094735_a EST: cp1422.seq.F Fetal heart, Lambda ZAP Express Horno sapiens to cDNA 5', mRNA sequence. (from Genbank)	Control of the Contro	Transcription factor TBX5 mRNA	Lunatic fringe (Drosophila) nomorog	EST: yddog 10.11 Huffid Saprens Com Conic 20.2 contains L1 repetitive element;. (from Genbank)	AA479990 a EST: zv18a05,r1 Soares NhHMPu S1 Homo sapiens cDNA clone	753968 5', mRNA sequence. (from Genbank)	BRAIN NEURON CYTOPLASMIC PROTEIN	Lymphoma proprotein convertase (LFC) Illinae	AC002076 c WUGSC:GS345D13.2 gene (G-protein gamma-1 subarmy common ds2_at from Human BAC clone GS345D13 from 7q31-q32	EST: zk48g01.r1 Soares pregnant uterus NbHPU Homo sapiens	CDINA CIONE 486096 5, IIIKINA SEQUELICE. (ILOIT CETIBELIN)	ZING FINGER PROTEIN 33	EST; zh92b04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 428719 3', mRNA sequence. (from Genbank)	EST: 54f5 Human retina cDNA randomly primed sublibrary Homo	sapiens conA, mina sequence. (non co	at Paraoxonase 3
	at		at	म		749825 s at H	U03115_cds 10_at H	AA434506_a E t	AA094735_a E	J80987 s a				AA479990 a E	t 7	at	U33849 at 1	AC002076_c \ ds2_at	AA043160_a		at	A0046		ä	0.18084833 T57140 s at
RC 0.1823877 41	0.18227758 M60828		0.18225089 M58597	0.1822192 D42123	0.18214276 C17139 at	0 18202047	0.1819276 10 at	0.18181373t	0.181731631		0,181710631	0,18159907 U94354 at	0.18153572 H53555 at		0.1814945 t	0.1814329	0.1813518 U33849	AC0020 0.18123417 ds2_at		0.18114	0.18112722 L35269	RC_A 0.18098173 37_at		0.1808933 WZ8988	
0.30937	0.309295		0.309253	0.309077	0.308997	0 30800	0.308935	0 308833	0.308774		0.308741	0.308637	0.308632	1	0.308521	0.308514	0.308414	0.308362		٥	0.308195	0.308156		0.308058	0.30799
0.377745	0.3777053	200	0.3774585	0.3774023	0 3773/01	0.2773456	0.3772548	0.3771061	0.3771682	10:0	0.3770363	0.3769881	0 3787901	0.00	0.3766713	0.3764956	0.3764089	0.3763587			0.3762389	0.3762241	1	0.3762117	0.3760914
0.040408	-0.049166		-0.049375	-0.049551	1	,					-0.05043	-0.050445 0.3769881	0.050541	-0.000.0-	-0.050779		-0.050916	-0.051229			-0.051305	-0.051386		-0.051656	-0.051685
í	845 Breast	846 Breast	847 Breast	848 Breast	C	049 Diedal	850 Breast	60 I Diedal	85Z Breast	803 Diedsi	854 Breast	855 Breast	1000	820 516981	857 Breast	858 Breast	859 Breast	860 Breast		861 Breast	862 Breast	ogs Breset	2000	864 Breast	865 Breast
	845	846	847	848		04)		8 8	ζ <u>γ</u>	ά2,	\$2£	85	i	82	85	85	85	88	3	98	86	98	5	8	8

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

-0.051809 0.3760473 0.307774 0.18071191 M57730 at CAO51809 0.3760147 0.307765 0.18063948 95 at RC_AA0339 0.052036 0.3758713 0.307725 0.18063948 185 at RC_D51215 0.052563 0.375773 0.30766 0.18028252 D50495 at -0.052563 0.375773 0.30766 0.18028252 D50495 at -0.052517 0.375494 0.307265 0.18028252 D50495 at -0.053207 0.375494 0.307265 0.18028252 D50495 at -0.053207 0.375428 0.307448 0.18028252 D50495 at -0.053207 0.375428 0.307448 0.18028258 X74837 at -0.053401 0.375428 0.307144 0.17994717 X53961 at -0.053401 0.375428 0.307001 0.17989717 X53961 at -0.053401 0.375428 0.307001 0.17989718 H74478 at -0.05398 0.375009 0.307001 0.179895919 J03801 f at -0.05398 0.374812 0.306897 0.17947209 D70830 at -0.05398 0.3748727 0.306897 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05418 0.374820 0.306807 0.17947209 D70830 at -0.05482 0.374823 0.306802 0.17940383 0.17940383 0.1794038 0.374623 0.306842 0.17940389 0.1794038 0.374623 0.306842 0.17940389 0.1794038 0.374623 0.306802 0.17940389 0.1794038 0.374623 0.306842 0.17940389 0.1794038 0.374623 0.306842 0.17940389 0.1794038 0.374623 0.306842 0.1794038 0.1	866 Breast	ş	-0.051717	0.3760565	0.307867	0.18077622 D79603)79603 at	EST: Human aorta cDNA 5'-end GEN-286H04, mRNA sequence. (from Genbank)
Course C	867 Brea	ıst	-0.051809	1	0.307774	0.18071191 N	A57730_at	EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1 PRECURSOR
O.052036 O.3759982 O.307725 O.18054827 f at m14159 cds -0.052444 O.3758713 O.307713 O.180486132 at m14159 cds -0.052613 O.3756713 O.30766 O.18028252 D50495 at -0.052619 O.3756714 O.307577 O.18028252 D50495 at -0.052717 O.3755494 O.307448 O.18028252 D50495 at -0.052307 O.3755494 O.307498 O.18028252 D50495 at -0.053207 O.3755494 O.307262 O.18018182 D7. at -0.053207 O.3755498 O.307262 O.18018182 D14539 at -0.053207 O.3755498 O.307169 O.18006826 X74837 at -0.053207 O.3755423 O.307001 O.17994717 X53961 at -0.053461 O.3752009 O.307001 O.17987238 HT4448 at -0.053545 O.375207 O.306893 O.1797704 19 at -0.053661 O.3750678 O.306807 O.17967913 H81241 at -0.053999 O.3748842 O.306867 O.17967913 H81241 at -0.053999 O.3748842 O.306867 O.17967913 D86425 at -0.054421 O.374623 O.306743 O.17957899 D70830 at -0.054421 O.374623 O.306688 O.1791847 HT180 at -0.054652 O.3745989 O.306688 O.17914847 HT180 at -0.054652 O.3746000000000000000000000000000000000000	868 Brea	ast	-0.051955	,	0.307765	0.18063948	3C_AA0339	EST: zi05f09.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429929 3', mRNA sequence. (from Genbank)
0.052444 0.3758713 0.3077713 0.18048613 2 at	869 Brea	ıst	-0.052036		0.307725		3C_D51215 f_at	STATHMIN
-0.052563 0.375773 0.30766 0.18032736 W28545 at -0.052619 0.375601 0.307577 0.18028252 D50495 at -0.052617 0.3755494 0.307448 0.18020238 M88279 at -0.052717 0.3755494 0.307448 0.18020238 M88279 at -0.053207 0.3754799 0.307262 0.18010736 D14539 at -0.053207 0.375428 0.307159 0.18005826 X74837 at -0.053207 0.375428 0.307169 0.18005826 X74837 at -0.053401 0.375428 0.307169 0.1799728 H74448 at -0.053461 0.375428 0.307001 0.17987238 H74448 at -0.05346 0.375428 0.306998 0.1797704 19 at RC_AA2428 -0.05361 0.3750678 0.306999 0.1797704 19 at -0.05361 0.3750678 0.306999 0.17967913 H81241 at -0.05399 0.3748797 0.30687 0.17967913 H81241 at -0.05399 0.3748797 0.306807 0.1794739 D70830 at -0.05418 0.3748206 0.306807 0.17940383 0.1 at -0.054421 0.374820 0.306807 0.17940383 0.1 at -0.054421 0.374829 0.306743 0.306807 0.17940383 0.1 HG180-0.054421 0.3745989 0.306743 0.306808 0.17940389 1 HG180-0.054421 0.3745989 0.306688 0.17914847 H7180 at HG180-0.054652 0.3745989 0.306688 0.17914847 H7180 at -0.054652 0.374598 0.306688 0.17914847 H7180 at -0.054652 0.374598 0.306680 0.17914847 H7180 at -0.054652 0.37459 0.30640 0	870 Brea	ast	-0.052444	L		0.18048613	A14159_cds	T-cell receptor beta-chain J2.1 gene extracted from Human T-cell receptor germline beta-chain D2.1 and J2.1 to J2.7 genes
-0.052019 0.375601 0.307577 0.18028252 D50495 at -0.052717 0.3755494 0.307448 0.18020238 M88279 at -0.053207 0.3755499 0.307262 0.18010736 D14539 at -0.053207 0.3754799 0.307262 0.18010736 D14539 at -0.053207 0.375428 0.307159 0.18005826 X74837 at -0.053401 0.3754231 0.307144 0.17994717 X53961 at -0.053461 0.3754231 0.307001 0.17987238 HT4448 at -0.05345 0.3752009 0.307001 0.17985919 J03801 f at -0.053545 0.3751927 0.306998 0.1797704 19 at -0.053938 0.3749172 0.306999 0.17967913 H81241 at -0.053999 0.3748842 0.306867 0.17957013 H81241 at -0.053999 0.3748797 0.306807 0.17956713 D86425 at -0.05418 0.3748797 0.306807 0.17956313 D86425 at -0.05418 0.3748797 0.306807 0.1795639 D70830 at -0.05418 0.3748797 0.306807 0.1795639 M19159 at -0.05418 0.3748797 0.306807 0.1795639 D70832 at -0.05418 0.374623 0.306743 0.1795689 2 at -0.054652 0.3745989 0.306743 0.1794847 HT180 at -0.054652 0.3745989 0.306848 0.17914847 HT180 at -0.054652 0.3745989 0.306848 0.17914847 HT180 at -0.054652 0.3745989 0.306688 0.17914847 HT180 at -0.054652 0.3745989 0.306688 0.17914847 HT180 at -0.054652 0.3745989 0.306688 0.17914847 HT180 at -0.054652 0.3745989 0.306688 0.17914847 HT180 at -0.054652 0.3745989 0.306688 0.17914847 HT180 at -0.054652 0.3745989 0.306688 0.17914847 HT180 at -0.054652 0.3745989 0.306688 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3066888 0.17914847 HT180 at -0.054652 0.3745989 0.3745989 0.374599 0.374599 0.374599 0.374599 0.374599 0.374599 0.374599 0.374	871 Brea	ıst	-0.052563		0.30766	0.18032736		EST: 48c7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
-0.052717 0.3755494 0.307448 0.18020238 M88279_at -0.053207 0.3755472 0.307386 0.18018182_57_r_at -0.053207 0.37554799 0.307262 0.18010736_D14539_at -0.053207 0.3755428 0.307763 0.18005826_X774837_at -0.053401 0.3755428 0.307744 0.17994717_X53961_at -0.053461 0.37554231 0.307083 0.17997777 X53961_at -0.0535 0.3752099 0.307001 0.17987238 H74448_at -0.053561 0.3752099 0.307001 0.17985919_J03801_f_at -0.053561 0.37550578 0.306999 0.1797704_19_at -0.053938 0.3749172 0.306897 0.17969985_H71067_r_at -0.053939 0.3748797 0.306867 0.17967913_H81241_at -0.05399 0.3748797 0.306807 0.17967913_D86425_at -0.05418 0.3748797 0.306807 0.17940383 0.1_at -0.054421 0.374623 0.306743 0.17935634_M19159_at -0.054421 0.374623 0.306743 0.17925899_2_at -0.054652 0.3745989 0.306688 0.17914847_HT180_at -0.054652 0.3745989 0.306688 0.17914847_HT180_at -0.054652 0.3745989 0.3066888 0.17914847_HT180_at -0.054657 0.3745989 0.306688 0.17914847_HT180_at -0.054657 0.3745989 0.306688 0.17914847_HT180_at -0.054657 0.3745989 0.306688 0.17914847_HT180_at -0.054657 0.3745989 0.3066888 0.17914847_HT180_at -0.054657 0.3745989 0.3066888 0.17914847_HT180_at -0.054657 0.3745989 0.306743 0.17914847_HT180_at -0.054657 0.3745989 0.306743 0.17914847_HT180_at -0.054657 0.3745989 0.3066888 0.17914847_HT180_at -0.054657 0.3745989 0.37	872 Brea	ast	-0.052619		0.307577	0.18028252)50495_at	Transcription elongation factor S-II, hS-II-T1
-0.05291 0.3755172 0.307386 0.18018182 57 r at -0.053207 0.3754799 0.307262 0.18018182 57 r at -0.053207 0.375448 0.307159 0.18005826 X74837 at -0.053401 0.375428 0.307144 0.17994717 X53961 at -0.053461 0.3754231 0.307083 0.17987238 H74448 at -0.05356 0.3752009 0.307001 0.17987238 H74448 at -0.05361 0.3751927 0.306998 0.1797704 19_at -0.053661 0.3751927 0.306998 0.1797704 19_at -0.053681 0.3748172 0.306867 0.17967913 H81241 at -0.053938 0.3748172 0.306867 0.17967913 H81241 at -0.053999 0.3748797 0.306807 0.17967913 H81241 at -0.05418 0.3748797 0.306807 0.17940383 0.1 -0.054421 0.374623 0.306743 0.17925899 2 at -0.054652 0.3745989 <td< td=""><td>873 Brea</td><td>ast</td><td>-0.052717</td><td>0.3755494</td><td>0.307448</td><td>0.18020238</td><td>/188279_at</td><td>FKBP4 FK506-binding protein 4 (59kD)</td></td<>	873 Brea	ast	-0.052717	0.3755494	0.307448	0.18020238	/188279_at	FKBP4 FK506-binding protein 4 (59kD)
-0.05291 0.3755172 0.307386 0.18018182 57 r at -0.053207 0.3754799 0.307262 0.18010736 D14539 at -0.053207 0.375428 0.307159 0.18005826 X74837 at -0.053401 0.375428 0.307144 0.17994717 X53961 at -0.053461 0.3754231 0.307083 0.17987238 H74448 at -0.05356 0.3752009 0.307001 0.17985919 J03801 f at RC_AA2428 -0.053561 0.3751927 0.306998 0.1797704 19_at HG1067-0.053938 0.3749172 0.306919 0.17967913 H81241 at -0.053999 0.3748797 0.306867 0.17956713 D86425 at -0.05418 0.3748797 0.306802 0.17947209 D70830 at RC_AA4436 -0.05448 0.374623 0.306743 0.17940383 0.1 at -0.054652 0.3745999 0.306688 0.17944838 0.1794789 0.374623 0.306743 0.17925899 2 at HG180-0.054652 0.3745989 0.306743 0.17925899 2 at HG180-0.054652 0.3745989 0.306743 0.17925899 2 at HG180-0.054652 0.3745989 0.306688 0.17914847 HT180_at						Lie	3C_AA0373	EST: zc03c04.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321222 3' similar to contains Alu repetitive element,
-0.053207 0.375448 0.307159 0.18010730 D14539 at -0.053401 0.375428 0.307159 0.1805826 X74837 at -0.053401 0.375428 0.307169 0.180905826 X74837 at -0.053461 0.3754231 0.307083 0.17987238 HT4448 at -0.053545 0.3751927 0.306998 0.1798731 H610670.053938 0.3751927 0.306999 0.17969985 HT1067 r at -0.053999 0.3748797 0.306807 0.17967913 H81241 at -0.054418 0.3748797 0.306807 0.17947209 D70830 at -0.054421 0.374623 0.306743 0.17940383 0.1 at -0.054421 0.374623 0.306743 0.17940383 0.1 at -0.054652 0.3745989 0.3066898 0.17944847 HT180_at -0.054652 0.3745989 0.3066898 0.17914847 HT180_at	874 Bree	ast	-0.05291	0.3755172	0.307386	0.18018182		mRNA sequence. (from Genbank)
-0.053401 0.375428 0.307144 0.17994717 X53961_at	0/0 Bree	1SI	-0.053207	0.3754799	0.307262	0.18010/361	и	Human mKNA for L.1G19. (from Genbank)
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HG4178- -0.053461 0.3754231 0.307083 0.17987238 HT4448 at -0.053545 0.3752009 0.307001 0.17985919 J03801 f at RC_AA2428 -0.053645 0.3751927 0.306998 0.1797704 19_at HG1067- -0.053938 0.3749172 0.306819 0.17969985 HT1067_r at HG1067- -0.053999 0.3748842 0.306867 0.17967913 H81241_at -0.053999 0.3748797 0.306807 0.17967913 H81241_at RC_AA4436 -0.05418 0.3748206 0.306807 0.17940383 0.1_at RC_AA4436 -0.054421 0.374623 0.306743 0.17925899 2_at HG180-at -0.054652 0.3745989 0.306688 0.17914847 HT180_at HG180-at -0.054652 0.3745989 0.306688 0.17914847 HT180_at -0.054652 0.306898 0.306688 0.3745989 0.306698 0.3745989 0.306698 0.3745989 0.306698 0.3745989 0.306698 0.3745989 0.306698 0.3745989 0.3745989 0.306698 0.3745989 0.3745989 0.306698 0.3745989 0.3745989 0.306698 0.3745989 0.374598 0.3745989 0	877 Brea	ıst	-0.053401	0.375428	0.307144	0.17994717)	- 11	LTF Lactotransferrin
-0.0535 0.3752009 0.307001 0.17985919 J03801 f at RC_AA2428	878 Brea	ast	-0.053461		0.307083	0.17987238	1G4178- 1T4448 at	Af-17
Colorada Colorada	879 Brea	ıst	-0.0535	1	0.307001	0.17985919	103801 f at	LYZ Lysozyme
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-0.053938 0.3749172 0.30687 0.17967913 H81241_at -0.053999 0.3748842 0.306867 0.17956713 D86425_at -0.05418 0.3748797 0.306807 0.17947209 D70830_at RC_AA4436 RC_AA4436 -0.054343 0.3748206 0.306802 0.17940383 0.1 at -0.054421 0.374623 0.306767 0.17935634 M19159_at -0.054652 0.3745989 0.306688 0.17914847 HG180-at	881 Brea	ast	-0.053661			0.17969985	اً د	Mucin (Gb:M22406)
-0.054959 0.3748842 0.306867 0.17956713 D86425 at -0.05418 0.3748797 0.306807 0.17947209 D70830 at RC_AA4436 0.05418 0.3748206 0.306802 0.17940383 01 at -0.054343 0.374623 0.306743 0.17925899 2 at HG180-0.054652 0.3745989 0.306688 0.17914847 HT180_at	882 Brea	ts:	-0.053938		0.30687	0.47967943	1812/11 at	EST: yu73c07.r1 Homo sapiens cDNA clone 239436 5' similar to
-0.05418 0.3748797 0.306807 0.17947209 D70830_at RC_AA4436 -0.05418 0.3748206 0.306802 0.17940383 01_at RC_AA4436 -0.054343 0.3747226 0.306767 0.17935634 M19159_at L78833_cds -0.054421 0.374623 0.306743 0.17925899_2_at HG180-	883 Brea	ıst	-0.053999	1	0.306867	0.17956713)86425 at	Osteoblast mRNA for osteonidoden
-0.05418 0.3748206 0.306802 0.17940383 0.1 at CAA4436 0.3747226 0.306767 0.17940383 0.1 at CAA4436 0.054421 0.374623 0.306743 0.17925899 2 at CAA652 0.3745989 0.306688 0.17914847 HT180 at CAA652 0.3745989 0.306688 0.17914847 HT180 at CAA652 0.3745989 0.306688 0.17914847 HT180 at	884 Brea	ıst	-0.05418	1	0.306807	0.179472091	770830 at	Doc2 beta
-0.054343 0.3747226 0.306767 0.17935634 M19159 at L78833_cds -0.054421 0.374623 0.306743 0.17925899 2_at HG180-0.054652 0.3745989 0.306688 0.17914847 HT180_at	885 Brea	ast	-0.05418		0.	0.17940383	3C_AA4436	Ribosomal protein S6 kinase, 90kD, polynentide 4
-0.054421 0.374623 0.306743 0.17925899 2 at HG180- -0.054652 0.3745989 0.306688 0.17914847 HT180_at	886 Brea	st	-0.054343		0.306767	0.17935634	M19159 at	ALPP Alkaline phosphatase, placental (Regan isozyme)
-0.054652 0.3745989 0.306688 0.17914847 HT180 at	887 Brea	ast	-0.054421	0.374623		0.17925899	. 78833_cds	Rho7 gene extracted from Human BRCA1, Rho7 and vatl genes, and ipf35 gene, partial cds
	888 Brea	ast	-0.054652	1	0.306688		4G180- 4T180 at	Ahnak-A Nucleoprotein Ahnak-A

Docket No.:	2825.2020-002
Title: Genet	ic Markers for Tumors
Inventors: Sri	dhar Ramaswamy, et al.

889	889 Breast	-0.054693	0.3745869	0.306619	0.1790261 X06268	X06268_at	COL2A1 Collagen, type II, alpha 1 (primary osteoarthritis, spondyloepiphyseal dysplasia, congenital)
890	890 Breast	-0.054745	0.3745835	0.306541	HG3104- 0.17898135 HT3280_	HG3104- HT3280_at	Serine Protease Met1
891	891 Breast	-0.05484	0.3745231	0.306418	0.1789223	M55998_s_a t	Alpha-1 collagen type I gene, 3' end
892	892 Breast	-0.054841	0.3745231	0.306286	0.17885049 D86968_at	D86968_at	KIAA0213 gene, partial cds
893	893 Breast	-0.055135	0.3743204	0.306183	0.17877047 X81333	X81333_at	PPH beta subunit protein
			1	A VANDORAL MANAGEMENT AND THE PARTY AND THE		RC_AA2436	EST: zs16c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
894	894 Breast	-0.055178	- 1	0.306167	0.17868887 17_at	17_at	IMAGE:685358 3', mRNA sequence. (from Genbank)
895	895 Breast	-0.055237	0.3742955	0.306089	0.17864491 L02867	L02867_at	62 kDa paraneoplastic antigen mRNA, 3' end
				and the first control of the control		L10955_cds	Carbonic anhydrase IV gene extracted from Human carbonic
968	896 Breast	-0.055254	0.3742814	0.306064	0.17860605 1_s_at	1_s_at	anhydrase IV gene, promoter region and
897	897 Breast	-0.055465	0.374211	0.305976	0.17845528 M20218	M20218_at	F11 Coagulation factor XI (plasma thromboplastin antecedent)
868	898 Breast	-0.055468	0.3740773	0.30588	0.17838494 M28210	M28210_at	GTP-binding protein (RAB3A) mRNA
899	899 Breast	-0.05553	0.374075	0.305778	HG732- 0.17836434 HT732 at	HG732- HT732 at	Senim Amyloid A1
						RC AA2434	
006	900 Breast	-0.055584	0.3739264	0.305723	0.17826432 42 at	42_at	Homo sapiens clone 192 Rer1 mRNA, complete cds
901	901 Breast	-0.055911	0.3738658	0.305512	0.1781995 X75535_at	X75535_at	33 KD HOUSEKEEPING PROTEIN
902	902 Breast	-0.05631	0.3737828	0.305512	0.17817293 L34060	L34060_at	Cadherin-8 mRNA
903	903 Breast	-0.056686	0.3735604	0.305508	0.17813462 L27584 s	L27584 s at	at CAB3b mRNA for calcium channel beta3 subunit
							Human Xp22 BAC CT-285l15 (from CalTech/Research Genetics),
							PAC RPCI1-27C22 (from Roswell Park Cancer Center), and Cosmid
						U79549_ma	U35B5 (from Lawrence Livermore), complete sequence. (from
904	904 Breast	-0.0568	0.3734772	0.305397	0.17806292 1_s_at	1_s_at	Genbank)
905	905 Breast	-0.056874	0.3734614	0.305338	0.17801876	AA401605_a t	Homo sapiens BAC clone RG060N22 from 7g21
906	906 Breast	-0.056927	0.3734582	0.305299	0.17792776 D21205		Estrogen responsive finger protein
	ı					U21051_rna	
907	907 Breast	-0.057185	0.3732237	0.305228	0.17791052	1_at	G protein-coupled receptor (GPR4) gene
908	908 Breast	-0.057302	0.3731872	0.305169	0.17789173 U02019 at	U02019 at	Heterogeneous nuclear ribonucleoprotein D (hnRNP D), partial cds, clone cDx4
909	909 Breast	-0.057316	0.3731569	0.304987	0.17780292 L20433_at	L20433_at	Octamer binding transcription factor 1 (OTF1) mRNA
910	910 Breast	-0.057436	0.3730936	0.304807	0.17773566	L09190_rna1 at	Trichohvalin (TRHY) gene
3		0011100		1017000	CHACLE	HG3405-	
911	911 Breast	909/90.0-	0.3729651	0.304797	0.17764536 H13586_at	H13586_at	Zinc Finger Protein Hzf3 (Gb:X60153)

						AnM2 mRNA for GS2374 (unknown product specific to adinose
912	Breast	-0.057529	0.3728566	0.304769	0.1775865 D45370_at	tissue)
913	Breast	-0.057863	0.3728035	0.304581	RC_AA1578 0.1775261 14_at	EST: zo35h03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588917 3', mRNA sequence. (from Genbank)
914	Breast	-0.057876	0.3727866	0.304545	HG2479- 0.17743216 HT2575_at	Helix-Loop-Helix Protein Sef2-1d
915	Breast	-0.057903	0.3727756	0.304495	0.17735155 T23709 at	Seq545 Homo sapiens cDNA clone HY6cDNA2-4 5'. (from Genbank)
916	916 Breast	-0.057974	0.3727756	0.304477	0.17730957 U53506_at	Type II iodothyronine deiodinase mRNA
917	Breast	-0.058242	0.3727748	0.304462	0.17720616 X05246 at	Testis-specific PGK-2 gene for phosphoglycerate kinase (ATP:3-nhospho-D-alycerate 1-nhosphotransferase FC 2 7 2 3)
918	918 Breast	-0.058318	1	0.304454	0.17715988 L22569 at	CTSB Cathepsin B
919	Breast	-0.058393	0.3724536	0.304373	0.17705312 S73288_at	Small proline-rich protein SPRK [human, odontogenic keratocysts, mRNA Partial, 317 nt]
920	Breast	-0.058404	0.3724106	0.304293	0.17701097 274616_s_a	at COL1A2 Collagen, type I, alpha-2
921	Breast	-0.058513	0.372294	0.304228	0.17692845 W26666_at	EST: 11a12 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
922	922 Breast	-0.058533	0.372294	0.304204	AA258463_a	N-ethylmaleimide-sensitive factor attachment protein, gamma
923	923 Breast	-0.058547	0.3722833	0.304159	0.17683078 M77836_at	PYCR1 Pyrroline-5-carboxylate reductase 1
924	924 Breast	-0.058582	0.3722216	0.304096	RC_AA1645 0.17665292 89_at	
925	925 Breast	-0.058613	0.3721394	0.304029	0.17661144 N48927 at	EST: yy75e09.r1 Homo sapiens cDNA clone 279400 5'. (from Genbank)
926	926 Breast	-0.058835		0.303903	0.17659022 J03060_at	GBA Glucosidase, beta; acid (includes glucosylceramidase)
927	927 Breast	-0.059035		0.303854	0.17651705 X13238_at	COX6C Cytochrome c oxidase subunit VIc
928	928 Breast	-0.059042	0.3719516	0.303847	0.17647325 D37965_at	PDGF receptor beta-like tumor suppressor (PRLTS)
929	929 Breast	-0.059211	0.3719358	0.303798	RC_AA4304 0.17635514 66 at	EST: zw23d05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 7701213' mRNA sequence (from Genhank)
930	930 Breast	-0.059753	0.3718463	0.303788	0.17629062 D31764 at	KIAA0064 gene
931	931 Breast	-0.059829		0.303701	. 0.17626233 Y08564_at	GalNAc-T4 gene
932	932 Breast	-0.059846		0.303597	0.1761759 D50645_at	SDF2
933	933 Breast	-0.059907	0.3715959	0.303532	0.1760991 Y10256_at	Serine/threonine protein kinase, NIK
934	934 Breast	-0.059971	0.3715022	0.303524	AA476894_a	Neuronal PAS domain profein 2
935	935 Breast	-0.060106	1	0.303492	0.17597793 U25771 at	ARF4L ADP-ribosylation factor 4-like
936	936 Breast	-0.06016	0.3714579	0.303449	HG3477- 0.17594817 HT3670_at	Cd4 Antigen
				-		

April, Jung, Jung, Hann Hann, Jang, Jung,
937	Breast	-0.060673	0.3713124	0.303449	0.17588738 t	1191072_a	AA191072_a EST: zq43c11.r1 Stratagene hNT neuron (#937233) Homo sapiens t
			1 .		X	X12662_rna	Arginase gene exon 1 and flanking regions (EC 3.5.3.1) (and joined
938	938 Breast	-0.060823		0.303367	0.17581081		CDS)
939	939 Breast	-0.060912	0.3712269	0.303222	0.17572095 L48211	8211_at	Angiotensin II receptor gene
			1		RC	AA4439	EST: zv44b09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
940	940 Breast	-0.060921	0.3710788	0.303183	0.1756554193	äţ	clone 756473 3', mKNA sequence, (from Genbank)
941	941 Breast	-0.060959	-0.060959 0.3710275	0.303071	0.1755605 M93311		GIF
942	942 Breast	-0.060983	0.3709529	0.302986	0.17546663 X69090_at	39090_at	Skeletal muscle 190kD protein
943	943 Breast	-0.061105	0.3709426	0.302914	0.17536747 S74445	74445_at	Cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt]
	-				R	RC_AA4959	EST: zw06a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
944	944 Breast	-0.061163	0.3709199	0.302914	0.17531127 52_at	اعز	768470 3', mRNA sequence. (from Genbank)
945	945 Breast	-0.06129	0.3707676	0.302878	0.17528987 U55258	55258_at	HBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene
946	946 Breast	-0.061732	0.3707493	0.302854	0.17517972 U18288	18288_at	Clone CIITA-10 MHC class II transactivator CIITA mRNA
947	947 Breast	-0.061797	0.3707097	0.302781	0.17510882 M37190	37190_at	Ras inhibitor mRNA, 3' end
948	948 Breast	-0.061829	0.370707	0.302686	0.17505069 M81830	81830_at	Somatostatin receptor isoform 2 (SSTR2) gene
0	-	00000	1		007400		(Jacob One of Classes) 17 (1070) 12 (Jacob One of Classes)
949	949 Breast	-0.061922	0.3706661	0.302646	0.17495133 H05559 at	\neg	EST: yr/3c08.rr Homo sapiens culvA clone 43873 3. (Irorn Geribalik)
050	050 Breast	-0 061038	03705680	0.30257	AA 0 17487931 t	AA090632_a	EST: y1095.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
3	2000	200.0	- 1	0.505.0		VEEV CroV	
951	951 Breast	-0.062256	0.3705308	0.302568	0.17481978 3 st-2	st-2	AFFX-CreX-3 st (miscellaneous control - 11k chips)
					AF	AFFX-CreX-	
952	952 Breast	-0.062256	0.3704386	0.302537	0.17477928 3_st	st	AFFX-CreX-3_st (endogenous control)
			•				
953	953 Breast	-0.06229	0.3703011	0.302469	0.17471492 X58399	58399_at	L2-9 transcript of unrearranged immunoglobulin V(H)5 pseudogene
954	954 Breast	-0.062453		0.302447	0.17470723 D38535_at	38535_at	PK-120
952	955 Breast	-0.062493	0.3701396	0.302427	0.17463356 M18731	18731_at	GALT Galactose-1-phosphate uridyltransferase
					R	RC_AA4339	EST: zw52h02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
926	956 Breast	-0.062691	0.3701046	0.302365	0.17455885 50	at	clone 773715 3', mRNA sequence. (from Genbank)
							Dystrophin, dystrophin {Purkinje promoter, alternatively spliced}
957	957 Breast	-0.062832	0.3700884	0.302321	0.17443383 \$81419	31419_at	[human, cortical brain and adult heart, mRNA Partial, 377 nt]
958	958 Breast	-0.062943	0.370081	0.302229	0.17437036 M34344	34344 at	ITGA2B Integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41B)
959	959 Breast	-0.063046	0.370081	0.302219	0.17435224 t	AA209290_a t	cDNA clone 648384 5' similar to contains element MER22 repetitive element;, mRNA sequence. (from Genbank)
090	060 Breast	-0.063085	0.3700262	0.302186	HG67-0 17429526 HT67	HG67- HT67 f at	Zinc Einnar Drofein (Gh-X61870)
200	Dicasi	-0.00000	ı		0.1174.004.0111	-	(2010) (2010) (2010)

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961	Breast	-0.063111	0.3699893	0.30215	RC 0.17419226 78_	RC_AA4420 78_at	RC_AA4420 EST: zw63c01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 78_at clone 774720 3', mRNA sequence. (from Genbank)
962	962 Breast	-0.063122	0.3697913	0.302081	0.17412324 R19997	R19997_at	Homo sapiens exportin t mRNA, complete cds
0		0	000000000000000000000000000000000000000	L C	0,000	AA338308_a	
963	963 Breast	-0.063124	0.3696035	0.30205	0.17409343		Homo sapiens mKNA for KIAAU524 protein, partial cds
964	964 Breast	-0.063188	0.3693799	0.301999	0.17401792 D14686_at		AMT Glycine cleavage system protein T (aminomethyltransferase)
965	965 Breast	-0.063234		0.301975	0.1740153 X72879	_at	14A2AK DNA sequence
996	966 Breast	-0.063301	0.3692876	0.301924	0.1739759 X00237	X00237_at	F variable segment 5' to antithrombin III gene (AT III)
790	067 Breast	10.00 PESS30	0.3602851	0.3017/19	RC 0 17383315 76	RC_AA3982	EST: zt60c07.s1 Soares testis NHT Homo sapiens cDNA clone
968	968 Breast	-0.063366	•	0.301673	0.17379622 S82185	S82185 at	Fscharichia coli unknown mRNA
090	060 Breast	-0.063421	- 1	0.301672	0 17370985 1 187972	1187972 at	NADA-isocitrate dehydrogenase mRNA nartial cds
970	970 Breast	-0.063576	1	0.301593	0.17365451 1101157 at	U01157 at	GI P1R Glicagon-like neutide 1 recentor
971	971 Breast	-0.063648		0.30154	0.17359863	AA280253_a	Himan activated n21cdcd2Hs kinase (ack) mRNA complete cds
5				2	200		יים ויים ויים ויים לאחול (ממי) אין אין אין אין אין אין אין אין אין אין
972	972 Breast	-0.06373	0.3689103	0.301485	0.17348851	U79295_at-2	0.17348851 U79295_at-2 Human clone 23961 mRNA sequence
973	973 Breast	-0.06373	0.3688502	0.301454	0.17340961 U79295	,at	Clone 23961 mRNA sequence
974	974 Breast	-0.063895	0.3687235	0.301433	0.1733959 X58401	jt,	CLL-12 transcript of unrearranged immunoglobulin V(H)5 gene
975	975 Breast	-0.063945	0.3686968	0.301324	0.17334343 M60315_at		BONE MORPHOGENETIC PROTEIN 6 PRECURSOR
976	976 Breast	-0.064086	0.368655	0.301296	0.17332555	M20778_s_a t	Homo sapien, alpha-3 (VI) collagen
			1			U20816_s_a	
977	977 Breast	-0.064148	0.3686425	0.301285	0.17321171	+	Nuclear factor kappa-B2 (NF-KB2) gene, partial cds
						RC AA0013	EST: zh83d11.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
978	978 Breast	-0.064266	0.3684953	0.301243	0.1730964 59_at		cDNA clone 427893 3', mRNA sequence. (from Genbank)
979	979 Breast	-0.064439	0.3684856	0.301199	0.17302833 L04569	ä	Calcium channel L-type alpha 1 subunit (CACNL1A1) mRNA
980	980 Breast	-0.064448	0.368409	0.301142	0.17300284	0.17300284 X16282_at-2	Human mRNA for zinc finger protein (clone 647)
981	981 Breast	-0.064448	0.3684041	0.301017	0.17287046 X16282		Zinc finger protein (clone 647)
982	982 Breast	-0.064584	0.3683977	0.300911	0.17282745	M87313_s_a t	DM Dystrophia myotonica (includes dystrophia myotonia protein kinase)
983	983 Breast	-0.06461	0.3682191	0.300874	0.17275523 M86933	M86933_at	AMELY Amelogenin (chromosome Y encoded)
(AA399432_a	EST: zt60b01.r1 Soares testis NHT Hómo sapiens cDNA clone AA399432_a 726697 5' similar to TR:G541730 G541730 IGD B-CELL RECEPTOR-
984	Breast	-0.064813	0.3681234	0.300776	0.17264907		ASSOCIATED PROTEIN;, mRNA sequence. (from Genbank)
686	985 Breast	-0.06488	0.3681157	0.300766	0.1725389 L33477	at	(clone 8B1) Br-cadherin mRNA

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FIG. 2T2

٠		,		-	N. 1944, Marie 34		ABO blond group (transferase A, alpha 1-3-N-
-							acetylgalactosaminytransferase; transferase B, alpha 1-3-
986 Breast	sast	-0.064963 0.3680508	0.3680508	0.300642	0.17245314 U1	15197_at-2	0.17245314 U15197 at-2 galactosyntransiel ase) ABO ABO blood group (transferase A, alpha 1-3-N-1-1-2-1-2-1-1-1-1-1-1-1-1-1-1-1-1-1-1
1	-	0.084963	0 084963 0 3680224	0.300602	0.17244586 U15197_at		acetylgalactosallinyn ar siccesor galactosyltransferase)
98/ Breast	east	-0.001000	0.065004 0.3680146	0,300552	0.17225446 U66036_at		Sulfotransferase mixing
900 Dreast	gast	-0.065035	-0.065035 0.3679706	0.300537	0,17221446 S74720_at		UAX-1
2000	1000	0.085074	0.367948	0.300302	0,17218089	U51333_s_a t	HK3 Hexokinase 3 (white cell)
.990 Breast	east	+ /00000-	1			U51333 s a	
991 Breast	east	-0.065074	0.36794	0.300291	0.17210503 t-2 AA	2 A285229 a	1-2 Hexokinase 3 (white cell) AA285229 a PMY0709 KG1-a Lambda Zap Express cDNA library Homo sapiens
992 Breast	-east	-0.065317	0.3679378	1	0.17209774 t	***************************************	cDNA 5', mRNA sequence. (from Genbank)
993 Breast	reast	-0.06542	-0.06542 0.3679375	0.300191	0.17203608 X	197267 F at	0.17203608 X97261 alimetalloullollollollollollollollollollollollo
	-	0.085506	0.085506.0.3678798	0.3001	0.17197551	7.5 at	Interferon, beta 1, fibroblast
994 Breast	reasi	20,000,0-	20.00.0			HG4185-	
995 Breast	reast	-0.065569	0.3677944	0.300096	0.17185599	4T4455 at	HT4455 at Estrogen Sulfotransferase, Ste
006 Breast	reast	-0.065598	-0.065598 0.3677728	0.300071	0.17183031	7 12 12 12 12 12 12 12 12 12 12 12 12 12	sapiens cDNA 5', mRNA sequence. (from Genbank)
997 Breast	reast	-0.065611	0.367685	0.300059	0.17176764 U50315_at	U50315_at	EST: EST06762 Homo sapiens cDNA clone HIBBL42 5' end. (from
998 B	998 Breast	-0.065632	-0.065632 0.3676511	0.299907	0.17155029 T08870_at	T08870_at	Genbank) Yn50b11.r1 Homo sapiens cDNA clone 171837 5' similar to contains
999 E	999 Breast	-0.06568	-0.065684 0.3675023	ĺ		H19258 at	PTR5 repetitive element ;. (from Genbank)
1000 Braset	Transt	-0.06568	0.065685 0.3674599	0.299835	5 0.1/1495/8 Ubsobs at	D00000 at	

			The state of the s	RC AA4320	RC AA4320 EST: zw89d03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
1 CNS	1.5821122	.5821122 0.5227835 0.466243	0.466243	0.36578274	clone 784133 3', mRNA sequence, (from Genbank)
2 CNS	1.3601404	1.3601404 0.4887298 0.	0.435394	0.3433382 D54949 at	0.3433382 D54949 at Calmodulin 1 (phosphorylase kinase, delta)
	-			RC AA0097	RC AA0097 EST: ze82q01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
3 CNS	1.3382851	1.3382851 0.471399	0.420481	0.33068585	clone 365520 3', mRNA sequence. (from Genbank)
				AA093923 a	
4 CNS	1.3208506	1.3208506 0.4620444	0.411019	0.411019 0.321907221	Tissue inhibitor of metalloproteinase 2
(RC_AA2623	RC_AA2623 EST: zr71g09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
5 CNS	1.3130109	1.3130109 0.4570996		0.402494 0.31520054 40 at	668896 3', mRNA sequence. (from Genbank)
					And the state of t
				RC_AA2335	RC_AA2335 EST: zr30h08,s1 Stratagene NT2 neuronal precursor 937230 Homo
e CNS	1.2842487	1.2842487 0.4508557	0	.398151 0.31018427 41 at	sapiens cDNA clone 664959 3', mRNA sequence. (from Genbank)

FIG. 3A

				Her than the street of the street	માં મામ મામ મામ મામ મામ મામ મામ મામ મામ
7 CNS	1.2712225	0.4456711	0.392711	RC_AA3386 0.30596718 46 f at	Homo sapiens mRNA for APCL protein, complete cds
0140	1 0205614	700000	000000	RC_AA494	EST: zx05d05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
O CINO	110000771	0.4420221	0.308300	0.3021363441 81	CIONE (800// 3, MIRINA Sequence. (110/11 Genibanik)
9 CNS	1,236307	0.4378117	0.385896	0.29888466 U04811_at-2 Trophinin	Trophinin
10 CNS	1.236307	0.4335288	0.383609	0.2957457 U04811 at	Trophinin mRNA
Parketine dates de la constante de la constant				AA046593_a	EST: zk62g01.r1 Soares pregnant uterus NbHPU Homo sapiens
11 CNS	1.2355561	0.4291814	0.380423	0.29338214 [cDNA clone 487440 5', mRNA sequence. (from Genbank)
	!			AA464334_s	EST: zx78f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
12 CNS	1.2335474	1	0.3783	0.29120103 at	clone 809881 5', mRNA sequence. (from Genbank)
13 CNS	1,2186718	0.4267445	0.375897	0.28868046 T08879_at	Cathepsin F
					EST: ym59h02.r1 Homo sapiens cDNA clone 52919 5'. (from
14 CNS	1.2162564	0.4235237	0.37428	0.28660512 H29161_at	Genbank)
				AB002357_a	
15 CNS	1.2048391		0.37261	0.28457886 t	Kinesin family protein 3B
16 CNS	1.199385	0.4192172	0.370695	0.28270283 R10931_at	Discs, large (Drosophila) homolog 5
					EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence.
17 CNS	1.1938953	0.417314	0.369058	0.2810516 D31289_at	(from Genbank)
				U12597_s_a	
18 CNS	1.1865215	0.4153346	0.367431	0.27924994 t	TNF receptor-associated factor 2
(1				EST: HUMGS0007992, Human Gene Signature, 3'-directed cDNA
19 CNS	1.1835281	0.4138258	0.366073	0.27753633 C01257_at	sequence, mRNA sequence, (from Genbank)
				RC_AA4602	
20 CNS	1.1815939	0.4126025	0.364142	0.27608213 70_at	Midline 1 (Opitz/BBB syndrome)
					EST: yi50c01.r1 Homo sapiens cDNA clone 142656 5'. (from
Z1 CNS	1.1729355	- 1	0.363086	0.2747583 R70976_at	Genbank)
ZZ CNS	1.159/135	0.4084373	0.361936	0.27326974 N98707 at	Kinesin family member 5C
0.40	000000000000000000000000000000000000000			RC_AA4901	EST: ab06e01.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
Z3 CNS	1.1538289	0.4080156	0.360021	0.2719937 82_at	clone 840024 3', mRNA sequence. (from Genbank)
0140	L				AA393961_a EST: zt78b10.r1 Soares testis NHT Homo sapiens cDNA clone
24 CNS	1.150455	1	0.359134	0.27068698 t	728443 5', mRNA sequence. (from Genbank)
25 CNS	1.1500549	- 1	0.357859	0.26955417 T09191_at	Homo sapiens Luman mRNA, complete cds
Z6 CNS	1.1481502	0.4050371	0.356555	0.26827115 H59008_at	Homo sapiens mRNA for NIK, partial cds
				DC AA3092	EST: zł60a06.s1 Soares testis NHT Homo sapiens cDNA clone
27 CNS	1.1449691	0.4050371	0.355957	0.26732045 55 at	mRNA sequence, (from Genbank)
				RC_AA2565	EST: zr86f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
28 CNS	1.1443744	0.4035838	0.35473	0.26626778 56 f at	682593 3', mRNA sequence. (from Genbank)

				il. Serrff Teacil 41" threat teath .	That's First, Sinst and Savett Real Shab
0.00	7 7 707504		0000	40700700	EST: yu17c10.r1 Homo sapiens cDNA clone 234066 5'. (from
28 CN2	1,143/384	0.4022301	0.33389	0.26530507 FI56988 at	Genbank)
				RC_AA4118	
30 CNS	1.1396248		0.35304	0.2642311 19_at	Homo sapiens mRNA for KIAA0898 protein, partial cds
31 CNS	1.139285	0.3999776	0.352451	0.2632767 L44416_at	Human DEAD-box protein p72 (P72) mRNA, complete cds
32 CNS	1.1370252	0.3990943	0.351405	RC_AA4521 0.26244372 13 at	EST: zx15b11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 786525 3', mRNA sequence, (from Genbank)
				RC_AA1133	The state of the s
33 CNS	1.1369255	0.3988254	0.350446	0.261485 63_at	Homo sapiens mRNA for KIAA0810 protein, partial cds
CNO	1 1051005			RC_AA2580	Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity,
34 CINS	1.1351825	0.3984377	0.349938	0.260667422_at	collagenase inhibitor)
35 CNS	1.134893	0.3973183	0.349227	AA310328_a 0.25975117 t	EST: EST181171 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)
				AA481723_a	
36 CNS	1.1326729	0.3964586	0.348202	0.25880587 t	Deleted in oral cancer-1
37 CNS	1 1260254	0.39439	0.34761	RC_AA4800	RC_AA4800 EST: zv41a04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
38 CNS	1,125968	0		0.25702432 H12112 at	Vm16a10 r1 Homo sanians cDNA clone 47042 5" (from Genhank)
				AB002368 a	The supplied supplied to the state of the supplied to the supp
39 CNS	1.1251478	0.3936734	0.345778	0.2562541 t	Human mRNA for KIAA0370 gene, partial cds
-				AA401052_a	
40 CNS	1.1242508	!	0	0.25542974 t	clone 741453 5', mRNA sequence. (from Genbank)
41 CNS	1.1216179	0.3927719	0.344282	0.2546986 Y09836 at	3'UTR of unknown protein
				RC_AA4169	EST: zt94g03.s1 Soares testis NHT Homo sapiens cDNA clone
42 CNS	1.1213297	0.3917421	0.343594	0.25389153 70_at	730036 3', mRNA sequence. (from Genbank)
A D C N I O	7000		0	RC_AA3996	
45 CNS	1.1188872	0.3906457	0.342703	0.25319153 63_s_at	729222 3', mRNA sequence. (from Genbank)
AAICNIO	77000277		0	RC_AA2847	EST: zt21h07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
2	100011.	0.030227	0.342333	0.25241002 67 at	clone 713821 3, mRNA sequence. (from Genbank)
45 CNS	1.116263	0.3897033	0.341336	0.05163070 5/1 s. at	Homoronica Management of the state of the st
		1		DC A4630	EST: 306f03 of Source Candidate Protein MRNA, complete cds
46 CNS	1.116161	0.3896734	0.340667	0.2509302 78 at	clone 810653 31, mRNA sequence, (from Genbank)
				W01587 s	EST: za80f11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA
47 CNS	1.1098641	0.3879441	0.340058	0.2504129 at	clone 298893 5', mRNA sequence. (from Genbank)
				RC_AA3981	
48 CNS	1.1091572	0.3878151	0.339252	0.24985288 67_at	Glutathione S-transferase A4
0				RC_AA2868	RC_AA2868 EST: zs58b06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
49 CNS	1.1086977	0.3875319	0.338474	0.24928012 62_at	IMAGE:701651 3', mRNA sequence. (from Genbank)

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	HNK-1 sulfotransferase	Lysosomar statogrycoprotein Small inducible cytokine A5 (RANTES)	AA425719_a EST: zv47f04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	EST: aa13e06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	orace of the sequence (non delibalik)	Human mRNA for KIAA0325 gene, partial cds. (from Genbank)	EST: H. sapiens partial cDNA sequence; clone c-1fh06, mRNA sequence. (from Genbank)	Phosphatidylinosital-4-phosphata 5. Linasa two 11 bota	Homo sapiens clone 23565 unknown mRNA partial cds	Homo sapiens mRNA for APCI protein complete cdc	Homo sapiens mRNA for KIAA0515 protein partial ods	ליים יים יים יים יים יים יים יים יים יים	Homo sapiens clone 23965 mRNA sequence	EST: za95c12.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 300310 5', mRNA sequence (from Genhank)	EST: zw11a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	Homo sapiens ornithine decarboxylase antizyme 2 (OAZ2) mRNA,	Complete cds	EST: zv90a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	767032 3, mRNA sequence. (from Genbank) EST: vz88005 r1 Soaree multiple enferocic subtutiven uses	cDNA clone 290097 5' similar to contains element MER11 repetitive	element ;, mRNA sequence. (from Genbank)	EST: yq19g03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 274349 5'. mRNA sequence (from Canhank)	EST: 46c8 Human retina cDNA randomly primed sublibrary Homo	Heterogeneous nuclear ribonucleonrotein D-like	EST: zv57c03.s1 Soares testis NHT Homo sapiens cDNA clone 757732 3', mRNA sequence. (from Genbank)
RC_AA6213	25 at	0.2474161 N76496 at		RC_AA4562 89_at	اِسَّ ا	ţ	Z43594 at	RC_AA6002 46 at	D31483 at	RC_D59321 f at	A4811	A4356			AA4265	1	, d	244			at .	149 <i>42</i> 2_s_a	ţ	at	A4366
	0.2487205 25 at	0.2474161	0.24681646	0.24623369 89		0.24563473 t	0.24498488 Z43594	RC_A 0.24429488 46 at	0.24380438 D31483 at	0.24319646	RC_A 0.2426396943 at		0.24220833 33_at	0.24175566 W07195 at	0.2411023 18	7 24086080 W. COORD	0.24000082 W266 IT	RC A	0.40303031		0.2390876 N90328	0.23850404 t	0.2380899 W28390	0.23774487 D81925	RC_A 0.23728606 55_at
00000	0.338023	0.337093	0.336166	0.335525	1001000	0.334967	0.334556	0.333862	0.333433	0.333183	0.332454	7	0.332056	0.331863	0.331076	0.330858	0.330074	0.329968	200	0.0000	0.023124	0.328476	0.328069	0.327955	0.327613
7022000			0.3853312	0.3852245	7020000	0.3039727	0.383254	0.3831663	0.3822998	0.3822985	0.382079	0.2044040	0.30 14940	0.3805644	0.3804849	0.380351	0.3795781	0.37861		0.3785376	0.500.00	0.3784324	0.3776164	0.3776164	0.3772638
4 4070407	1.107.0427	1.0997258	1.099367	1.0993154	4 00E0007	1.0332221	1.0949132	1.093505	1.0932192	1.091907	1.0909321	1 0858	0000.1	1.0843205	1.082367	1.0819024	_L	1.0803376		1 080035	i	1.0787363	1.077306	1.0749671	1.0745177
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Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors

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72 CNS	1.0732971	0.3765062	0.327109	RC_AA490	RC_AA4902 EST: aa44c08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 61 s. at 823790.31 mRNA sequence (from Genbank)
73 CNS	1.072461	0.3761596	0.326687	0.23644234 t	
74 CNS	1.07 7345	0.3758686	0.326149	0.23610336 85_at	6 EST: zu49g09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741376 3', mRNA sequence. (from Genbank)
75 CNS	1.0696682	1.0696682 0.3757239	0.326105	RC_AA2934 0.2357275 36 s at	
76 CNS	1.0683788	0.3756529	0.325567	RC_AA0853 0.23501241 99_at	
77 CNS	1.06823	0.3749681	0.325105	0.23457171 at	AA311931_s Ras-related C3 botulinum toxin substrate 3 (rho family, small GTP at binding protein Rac3)
78 CNS	1.0663271	0.3745332	0.32472	0.2343164 W81301_at	
79 CNS	1.0657293	0.3743767	0.32441	0.23398116 D31550_at	
80 CNS	1.0650709	0.3742216	0.323926	0.23355766 W26376 at	Homo sapiens ornithine decarboxylase antizyme 2 (OAZ2) mRNA, complete cds
81 CNS	1.0650405	0.3739961	0.323725	AA455208_a 0.23311743 t	
82 CNS	1.0640874	0.3729959	0.323476	AA136360_a 0.23270209 t	
83 CNS	1.0633168	0.3728446	0.323225	RC_AA0593 0.2322415 86_at	3
84 CNS	1.0599332	0.3725329	0.322862	AA431268 0.23183836 t	Ø,
85 CNS 86 CNS	1.0580418	0.3719045	0.322629	0.23140343 Y12711_at- 0.230991 Y12711_at	0.23140343 Y12711 at-2 H.sapiens mRNA for putative progesterone binding protein
87 CNS	1.0576942	0.3712107	0.321699		
88 CNS	1.057471	0.3711056	0.321566	0.23041363 T99604 at	Ye65g07.r1 Homo sapiens cDNA clone 122652 5' similar to SP:NECD MOUSE P25233 - (from Genhank)
89 CNS	1.0572321	0.3704442	0.321222	0.23000205 41_at	Homo sapi
90 CNS	1.056566	0.3702271	0.320691	0.22964175 N77151 at	Homo sapiens mRNA for KIAA0799 protein, partial cds
91 CNS	1.0474865	1.0474865 0.3702271	0.32043	RC_AA447 0.22916757 17_at	AA4476 EST: zw97a02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA at clone 784874 3', mRNA sequence. (from Genbank)

Docket No.. 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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. 92	92 CNS	1.0471169	39 0.3700851	51 0.320289	9 0.22893718		AA284647 a EST: zt23g10,r1 Soares ovary tumor NbHOT Homo sapiens cDNA
93	93 CNS	1.0466598	98 0.3699072	2 0.319766		RC AA2522	EST: 2764905.51 Soares NhHMPu S1 Homo sapiens cDNA clone
94	94 CNS	1.046282	0.3688252	0.319169		0.22830428 W26406	EST: 30d2 Human retina cDNA randomly primed sublibrary Homo
95	95 CNS	1.0460862	1	1		RC_AA4851	sapiens cDNA, mRNA sequence, (from Genbank)
			1	v.513049	0.2279134 15_at	15_at	KIAA0793 gene product
96	96 CNS	1.0454617	7 0.3685715	5 0.318571	RC A	RC_AA1358	EST: zn93h05.s1 Stratagene lung carcinoma 937218 Homo saniene
97	97 CNS	1.0453646	5 0.3685074			, d	cDNA clone 565785 3', mRNA sequence. (from Genbank)
86	98 CNS	1.0453646		1	0	Y09616 at-2	0.22/1155/Y09616_at-2_Intestinal carboxylesterase; liver carboxylesterase-2
) 66	99 CNS	1.045011	0.3683571			AA095791_a	Carboxylesterase (hCE-2) mRNA EST: 15920.seq.F Fetal heart, Lambda ZAP Express Homo sonioso
100 CNS	SNS	1.0439073	1		0.22500112	VA455403_a	cDNA 5', mRNA sequence. (from Genbank) EST: aa03d07.r1 Soares NhHMPu S1 Homo saniens cDNA close
					0.44.093043		812173 5', mRNA sequence, (from Genbank)
101 CNS	SNS	1.0416962	0.3681786	0.316998	RC_A 0.22572534 55_at	A1268	EST: zn88f12.s1 Stratagene lung carcinoma 937218 Homo sapiens
102 CNS	SNS	1.0412948	0.3677616	0.316626	0.22547990	07107	Control 303233 3, MKNA sequence. (from Genbank)
				1	0.447339	540/19 s at (U.22041339 S4U/19 s at GFAP Glial fibrillary acidic protein
							ruman DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Vices
103 CNS	NS	1.0408907	0.3673216	0.316375	0.22521017 N77574 ; of		Isolog of a Rat gene) and a novel alternatively spliced gene. Contains
104 CNS	NS	1.04008	0 388800	0.00		ਰ -¦	a putative CpG island, ESTs and GSSs
				0.316224	0.22484718 U46116		at-2 Protein tyrosine phosphatase, recentor type gamma, 1
105 CNS	NS	1.04008	0.3668033	0.316088	0.22457357 U46116 at		PTPRG Protein tyrosine phosphatase, receptor type, gamma
106 CNS	NS	1.039616	0.3668033	0.315721	RC_A 0.22427085 33_at	A4257	EST: 247a10.s1 Soares ovary tumor NbHOT Homo sabiens cDNA
107 CNS	S	1.039451	0.3667739	0.31546	0.223893051	0200_a	AA410200 a EST: 2v32d11r1 Soares ovary tumor NbHOT Home sanions CONA
108 CNS	4S	1.0361865	0.3664435	0.315048	0.22452246	5	Gone 755349 5', mRNA sequence. (from Genbank)
109 CNS	St	1.033165 0 3658772	0.3658772	270770	R. R.	RC AA4636	RC_AA4636
			7	0.3 14934	0.2231686 29 at		Homo sapiens mRNA for KIAA0721 protein, partial cds

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

FIG. 3F

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110 CNS	1.0315324	0.3657871	0.314699	0.2229604	376756 s at	4R-MAP2=microtubule-associated protein 2 4R isoform [human, 0.2229604 S76756 s at brain mRNA Partial 1012 ntl
111 CNS	1.0313895	1.0313895 0.3645982	0.314543	0.2227114 W27023	V27023 at	Homo sapiens mRNA for KIAA0886 protein, complete ods
110 CNS	4 0204070		•		VA046674_a	AA046674_a EST: zf12d12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
217	1.000101	0.3045953	0.314168	0.22235774 t		clone 376727 5', mRNA sequence. (from Genbank)
113 CNS	1.029867	0.3645953	0.314026	0.22210413	AA405775_s at	EST: zu57c10.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
114 CNS	1.028171		0		10746 at	H. sapiens mRNA for protein containing MBD 1
7 0 0 0 0	0.1000			Œ	A2071	EST: zq81b03.s1 Stratagene hNT neuron (#937233) Homo sapiens
0 CNO	1.02/2/13	0.3645103	0.313343	0.22148871 03 at		cDNA clone 647981 3', mRNA sequence. (from Genbank)
116 CNS	1.0268342	0.364446	0.313005	0.2211354 t	C14203_s_a t	EST: Human fetal brain cDNA 5'-end GEN-037E11, mRNA sequence. (from Genbank)
117 CNS	1.0265732	0.3642832	0.312996	RC_A 0.22094995 83 at	(C_AA1890 3 at	RC_AA1890 EST: zq45b09.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632633 3' mRNA sentience (from Cenhank)
118 CNS	1.0264816	0.3642044	0.312879	0.22065304 31_at	A2348	EST: zs38b04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687439 3', mRNA sequence. (from Genbank)
119 CNS	1.0247778	0.3639924	0.312635	W 0 22034481 at	26436_s_	Missoft thurst of the state of
120 CNS	1.0243666	1 1	0.312468	0.22003654 D86981	at	KIAA0228 gene, partial cds
121 CNS	1.0243666	0.3626002	0.311862	0.21983251	86981 at_2	0.21983251 D86981 at-2 Hirman mbnia for Viaacoo and in the state of th
122 CNS	1.0219347	0.3622816	0.311694	0.21958862 D80897	80897 at	Homo saniens clone 24736 mDNA securiors
123 CNS	1.0215923	0.3622252	0.311444	0.21930876 N77277 at		EST: yv43a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens
124 CNS	1.0211011	0.3621407	0.31142	0.21915452 X		H Sapiens mRNA for 7VG homologing
125 CNS	1.0211011	0.3619148	0.311078	0.21886241 X99802 at		ZYG homologue
126 CNS	1.0209804	0.3615916	0.310755	0.21862793 M	62302 at-2	0.21862793 Me23.02 at 2 (from Control)
127 CNS	1.0209804	0.3613792	0.310566	0.21845424 M62302 at	62302 at	Growth/differentiation factor 4 (GDE-1) mDNA
128 CNS	1.0205418	0.361154	0.310433	0.21814896 t	A130156_a	AA130156_a EST: zl35d12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA t
129 CNS	1.0176283	0.3607447	0.310396	A. 0.21796905 t	AA393666_a	Mannose-6-phosphate recentor (cation denondant)
130 CNS	1.0173213	0.3604674	0.310363	RC_A 0.21763197 53_at	A4275	EST: zw22e04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770046 3', mRNA sequence. (from Genhank)
131 CNS	1.0170012	0.3600439	0.310338	RC_A 0.21742667 80_at	A5986	KIAA0618 gene product

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132 CNS	1.0154105	0.3599196	0.309925	RC_A 0.21723431 55_at	RC_AA4598 55_at	AA4598 EST: zx51g08.s1 Soares testis NHT Homo sapiens cDNA clone at 795806 3', mRNA sequence. (from Genbank)
133 CNS	1.0151407	0.3599196	0.309806	0.2168594	AA480828_a t	EST: zx87d05.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810729 5' similar to TR:G1262329 G1262329 RETICULOCALBIN PRECURSOR. ;contains Alu repetitive element;, mRNA sequence. (from Genbank)
134 CNS	1.0147551	0.3596523	0.309613	0.21663097	AA252381_a t	KH-type splicing regulatory protein
135 CNS	1.0146048	1.0146048 0.3595384	0.309218	RC_A 0.2165199 25 at	RC_AA4372 25 at	EST: zv54b11.s1 Soares testis NHT Homo sapiens cDNA clone 757437 3', mRNA sequence. (from Genhank)
136 CNS	1.0141691		0.308927	0.21612594 N49353	N49353 at	EST: yy23h12.r1 Homo sapiens cDNA clone 272135 5'. (from Genbank)
137 CNS	1.0136988	0.3587981	0.308914	0.21589483 U58856 at	U58856_at	Endocytic receptor (macrophage mannose receptor family)
138 CNS	1.0132961	0.3587409	0.308868	0.215676861	AB002360_a t	Human mRNA for KIAA0362 gene, partial cds
139 CNS	1.012922	0.3584979	0.308692	RC_A 0.21550402 14_at	A0072	EST: 13cDNA52-3.seq Soares infant brain 1NIB Homo sapiens cDNA clone HY18-117,159,251 3', mRNA sequence. (from Genbank)
140 CNS	1.0-2517	0.3581604	0.308384	0.21535349	AA058759_a t	Homo sapiens mRNA for KIAA0461 nerotein nartial cds
141 CNS	1.0120515	0.3578871	0.308102	0.2150522	AA040512_a t	Homo sapiens KIAA0431 mRNA nartial cds
142 CNS	1.0117236	0.3576369	0.307855	0.21491116 65 at	A4528	Deferoes not montide
143 CNS	1.0104562	0.3573959	0.307447	0.21471475 71 at	A4355	EST: zt73g10.s1 Soares testis NHT Homo sapiens cDNA clone 728034 3', mRNA sequence (from Genhank)
144 CNS	1.0101736	0.357391	0.307317	RC_A 0.21445861 43_at	A5996	EST: ag10b05.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1069905 3', mRNA sequence, (from Genhank)
145 CNS	1.009497	0.3573434	0.307087	0.21425956 98 at	A4794	EST: zv21d10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754291 3', mRNA sentence (from Genhank)
146 CNS	1.0094161	0.3567238	0.306915	RC 0.21403474 47	_AA4851 at	EST: aa40h06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:8157713' mRNA serijance (from Conbunk)
147 CNS	1.0084629	0.3566788	0.306705	0.213902971	VA096178_a	EST: 18434.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
148 CNS	1.0050942	0.3563182	0.306324	0.21358328 H46787	at	Aconitase 2 milochondrial
149 CNS	1.0044037	0.3562298	0.306123	0.21333948 t	AA095885_a	EST: I6748.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', mRNA sequence. (from Genbank)
150 CNS	1.0027878	0.3559859	0.306029	RC_A 0.21311955 17_at	२८_AA0266 । 17_at	RC_AA0266 EST: ze93c06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA 17_at clone 366538 3', mRNA sequence. (from Genbank)

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151 CNS	1.0027362	0.3559338	0.305807	RC_A 0.2128191 68 at	A4599 E	RC_AA4599 EST: zx66c12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 68 at clone 796438 3' mRNA sequence (from Canbark)
152 CNS	1.001813	1		0.21255636 at	6526_s E	AA496526_s EST: zv36h01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA at clone 755761.5' mRNA semiance (from Genbank)
153 CNS	1.0015508	0.3557579			AB002308_a	KIAA0310 gene product
154 CNS	1.0015498	0.3556455	0.305414		RC_AA4029 E	EST: zu55a06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741874 3', mRNA sequence. (from Genbank)
155 CNS	1.0014266	1.0014266 0.3552023	0.305358	RC_A 0.21205635 99_at	A4313	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA, complete cds
156 CNS	1.0001297	0.3551805	0.305155	0.21181707 H14744 at		EST: ym24è06.r1 Homo sapiens cDNA clone 48792 5'. (from Genbank)
157 CNS	0.9978548	0.3544163	0.304786	0.2116652 C01747 at		EST: HUMGS0003679, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence
158 CNS	0.9975388	0.3540663	0.304638	RC_A 0.21140084 35 at	A2591	EST: zs30d01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686689 3' mRNA sequence. (from Genbank)
159 CNS	0.9969791	0.3540631	0.304243	AA092 0.21119729 t	2968_a E	AA092968_a EST: m0992.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)
160 CNS	0.9959125	0.3539636	0.304213	RC_A 0.21102984 32_at	RC_AA4286 E 32_at 7.	EST: zw69a09.s1 Soares testis NHT Homo sapiens cDNA clone 781432 3', mRNA sequence. (from Genbank)
161 CNS	0.9954314	0.3539217	0.303825	0.21094486 D31091	ät	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)
162 CNS	0.9949913		0.303576	0.21063513 64 at	 	Homo sapiens clone 23714 mRNA sequence
163 CNS	0.9945802	0.3538354	0.303531	0.21045855 H08068 at		Homo sapiens clone 23967 unknown mRNA, nartial cds
164 CNS	0.9939117	0.3537598	0.303407	RC_A/ 0.21030046 37_at	Ţ	EST: zx98h04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 811831 3', mRNA sequence. (from Genbank)
165 CNS	0.9938311	0.3531174	0.303171	H83527_s_a 0.21001343 t		KIAA0618 gene product
166 CNS	0.9918591	0.3530565	0.303078	AA203 0.20985585 t	AA203628_a t	Insulin-like growth factor binding protein 6
167 CNS	0.9918453	0.3530507	0.302795	RC_AA4066		EST: zv15b10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753691 3' similar to gb:X02067 H.saplens mRNA for 7SL RNA pseudogene (HUMAN);contains Alu repetitive element;, mRNA
168 CNS	0.9899077		0.302619	AA032 0.20951113 t	AA032048 a E	EST: zk15c03.r1 Soares pregnant uterus NbHPU Homo sapiens
169 CNS	0.9897113 0.3528417	0.3528417	0.302469	0.20928946 35 s at	372	EST: zv54c11.s1 Soares testis NHT Homo sapiens cDNA clone 757460 3', mRNA sequence. (from Genhank)

						. 1017 1017 1017 1017 1017 1017.
170 CNS	0.9876819	0.3527185	0.302273	RC_A 0.20902368 72_at	AA4432 at	RC_AA4432 EST: zw87e10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 72 at clone 783978 3' mRNA sequence (from Genhank)
171 CNS	0.9876165	0.3526356	0.302148	0.20874907 t	AA094107_a t	EST: cl1862.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', mRNA sequence, (from Genhank)
172 CNS	0.9864547	0.352388	0.301841	RC_A 0.20860974 61 at	RC_AA2521 61 at	EST: zr64c03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668164 3', mRNA sequence, (from Genhank)
173 CNS	0.9853885	0.3522965	0.301695	0.20842624 31 f at	AA5988 at	EST: ae40f06.s1 Gessler Wilms tumor Homo sapiens cDNA clone 898307 3', mRNA sequence (from Ganbank)
174 CNS	0.984585	0.3521034	0.301486	RC_A 0.20828773 07_at	RC_AA4355 07_at	Homo sapiens mRNA for KIAA0731 protein nartial cds
175 CNS	0.984182	0.3519741	0.301375	0.20801869 t	AA479995_a t	Discs. large (Drosonhila) homolog 5
176 CNS	0.9826071	0.3519678	0.301088	AA27 0.20789962 t	AA279561_a t	EST: zs92a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
177 CNS	0.9821494	0.351353	0.300896	0.20768821 t	AA248802_a t	EST: j4151.seq.F Human fetal heart, Lambda ZAP Express Homo
178 CNS	0.9818472	0.3512219	0.30076	0.20754325 92_at	A4798	EST: zw44b02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 772875 31, mRNA sequence. (from Genbank)
179 CNS	0.9817755		0.300619	RC_A 0.2073333391_at	A1338	EST: zn86b06.s1 Stratagene lung carcinoma 937218 Homo sapiens
180 CNS 181 CNS	0.981034	0.3509861	0.300501	0.20723455 U95822 at		Human putative transmembrane GTPase mRNA, partial cds
		1000000	0.500290	0.20/05643 C01394 at	7	H.sapiens gene from PAC 42616, similar to syntaxin 7
182 CNS	0.9802766	0.3508498	0.300095	0.20678534 32 at		Glutathione peroxidase 3 (plasma)
183 CNS	0.9787967	0.3507122	0.299869	0.20646276 H51057	.च	EST: yp84f11.r1 Homo sapiens cDNA clone 194157 5'. (from Genbank)
184 CNS	0.9780007	0.3506287	0.299772	0.2062332 78_at	RC_AA4881 78_at	EST: ad08c04.s1 Soares NbHFB Homo sapiens cDNA clone 877638 3', mRNA sequence. (from Genbank)
185 CNS 186 CNS	0.9763234	0.3503568	0.299606	RC_A 0.20606102 37_at	VA0704	Human smoothened mRNA, complete cds
187 CNS	0.9759226	0.3500681	0.299352	0.20581107 D49958 at RC_AA149	8	Fetus brain mRNA for membrane glycoprotein M6 EST: zl48d11.s1 Soares pregnant uterus NbHPU Homo sapiens
188 CNS	0.9755471	0.3500381	0.298731	0.20557974 06 at	A4781	CDINA clone 505173 3', mRNA sequence. (from Genbank) EST: zt89d01.s1 Soares testis NHT Homo sapiens cDNA clone 729505 3', mRNA sequence, (from Conhant)
189 CNS	0.9751933	0.3499295	0.298574	0.20536038 22_at	A2558	EST: zr84g09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682432 3', mRNA sequence (from Genhank)
190 CNS	0.9742862 0.3497171	0.3497171	0.298399	0.20532204 t	3917_a E	AA453917_a EST: zx32f02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA totone 788187 5', mRNA sequence. (from Genbank)

				H. steel, daring the steel, and		
191 CNS	0.9736393	0.3495999	0.298081	0,20513378 t	AA194766_a	Homo sapiens mRNA for KIAA0850 protein, complete cds
192 CNS	0.9729598		0.297923	0.20495585 W75980 at		KIAA0214 gene product
193 CNS	0.9700761	0.349426	0.297858	RC_A 0.20476721 18_at	A5987	EST: ae49e04.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950238 3', mRNA sequence. (from Genbank)
194 CNS	0.9689111	0.3490906	0.297712	AFFX- HSAC07/X0 0.20461504 0351_5_at-2 No info for gene	AFFX- HSAC07/X0 0351_5_at-2	No info for gene
195 CNS	0.9689111	0.3490325	0.297574	AFFX- HSAC07/X 0.20446858 0351_5_at	AFFX- HSAC07/X0 0351_5_at	AFFX-HSAC07/X00351_5_at (endogenous control)
196 CNS	0.9686173	0.3487854	0.297364	RC_A 0.20433103 78_at	A2583	EST: zr6za09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667960 3', mRNA sequence. (from Genbank)
197 CNS	0.968174	1 0.3483558	0.297352	0.20413762 R37560_at		Myotubularin related protein 4
198 CNS	0.9678751	0.3482869	0.297182	RC_AA. 0.20401448 49_f_at	2325	EST: zr24c06.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664330 3', mRNA sequence. (from Genbank)
199 CNS	0.966854	0.9668545 0.3482148	0.29691	0.20380266 t	AA371121_a t	EST82873 Prostate gland I Homo sapiens cDNA 5' end, mRNA sequence, (from Genbank)
					,	EST: zt59e10.s1 Soares testis NHT Homo sapiens cDNA clone
ONO	0.0663124	0 3/8/166	0.296769	RC 0 20354801 21	RC_AA3982	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II RETA CHAIN: mRNA sequence (from Genbank)
2000	1.00000	1	201	AF	AF006012_a	Homo sapiens dishevelled 2 (DVL2) mRNA, complete cds. (from
201 CNS	0.9657993	3 0.3481166	0.29672	0.2033493 t	l	Genbank)
202 CNS	0.9657444	4 0.3479804	0.296447	0.20317283 07	RC_AA6203 07_at	EST: af05g12.s1 Soares testis NHT Homo sapiens cDNA clone 1030822 3', mRNA sequence. (from Genbank)
203 CNS	0.9655124	4 0.347499	0.296332	RC_A 0.20302619 23 at	A4644	EST: zx78g08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809918 3', mRNA sequence. (from Genbank)
204 CNS	0.9654415		0.296199	0.20292503 R67297	7297 at	EST: yh08d12.r2 Homo sapiens cDNA clone 42704 5'. (from Genbank)
205 CNS	0.9654146	6 0.3472382	0.296072	0,20278879 t	C00808 s a	EST: HUMGS0003083, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)
206 CNS	0.9651779	9 0.3466997	0.295929	0.20262823 06_s_at	RC_AA2845 06_s_at	EST: zt20f02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713691 3', mRNA sequence. (from Genbank)
207 CNS	0.9650673	3 0.3463053	0.295638	RC_A 0.20250314 54_at	RC_AA4253 54_at	EST: zw46e02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773114 3', mRNA sequence. (from Genbank)
208 CNS	0.9637535	5 0.3461667	0.29544	RC_A 0.20228057 81_at	RC_AA4304 81_at	EST: zw23e02.s1 Soares ovary tumor NbHOT Homo sapiens cUNA clone 770138 3', mRNA sequence. (from Genbank)

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209 CNS	0.9636452		0.295341	0.2019788 t	AA092716_a t	HLA-B associated transcript-3
210 CNS	0.963081	0.3461072	0.295329	0.20185208 D82603	at,	EST: similar to F26F4.1, mRNA sequence. (from Genbank)
(RC	A3499	Homo sapiens brain expressed ring finger protein mRNA, complete
211 CNS	0.9624962	0.3459891	0.295164	0.2017906 15_at		spo
212 CNS	0.962081	0.3458137	0.295137	0.20153604 W28214 at		EST: 45f7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
213 CNS	0.962053	0.3457714	0.294782	0.201415751	AA496423_a E	EST: zv37d02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
				RC	RC AA4608 E	EST: zx64h08.s1 Soares total fetus Nb2HF8 9w Homo saniens cDNA
214 CNS	0.9610634	0.3456965	0.294619	0.20122379 49 at		clone 796287 3', mRNA sequence. (from Genbank)
215 CNS	0.960719	0.3456629	0.294597	RC_A 0.20109265 29_at	A2335	EST: zr30g05.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664952 3', mRNA sequence. (from Genbank)
216 CNS	0.9597902	0.345295	0.294418	0.2009026 H58970_at		EST: yr40b03.r1 Horno sapiens cDNA clone 207725 5' similar to contains Alu repetitive element;, (from Genbank)
217 CNS	0.9591184	0.3451828	0.294213	0.2008066 73 at	A1672	KIAA0468 gene product
218 CNS	0.9584609	0.3451705	0.294118	RC_A 0.20062812 31 at	A2054	EST: zq66a10.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 646554 31 mRNA seguence (from Genhank)
219 CNS	0.958143	0.345123	0.293841	0.20043863 t	3572_a	V-ral simian leukemia viral oncodene homolog A (ras related)
220 CNS	0.957246	0.3451031	0.293708	0.20033564 t	AA278412_a E t	EST: zs81h03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703925 5: mRNA sequence. (from Genhank)
221 CNS	0.9560762	0.3450495	0.293603	0.20015222 69_s_at	344	EST: zr74h07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669181 3', mRNA sequence. (from Genbank)
222 CNS	0.9552402	0.3450189	0.293351	RC_A 0.19985208 48_at	764	EST: zx02f06,s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785315 3', mRNA sequence, (from Genbank)
223 CNS	0.9550276	0.3448438	0.293246	0.1998251 C01139	ä	EST: HUMGS0007818, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)
224 CNS	0.9548962	0.344729	0.293192	0.19957082 t	AA401850_a t	Homo sapiens clone 23856 unknown mRNA, partial cds
225 CNS	0.9546772	0.3445809	0.29308	RC_A 0.19940169 41_at	A0820	EST: zn21c01.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 548064 3', mRNA sequence. (from Genbank)
226 CNS	0.9545261	0.3445375	0.292985	RC_A 0.19928686 46_at	A4639	Pigment epithelium-derived factor
227 CNS	0.9541986	0.9541986 0.3443775	0.292878	0.19915034 T68246	,ज	EST: yc40f01.r1 Homo sapiens cDNA clone 83161 5' similar to contains PTR5 repetitive element;, (from Genbank)
					The state of the s	

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228	228 CNS	0.9539833	3 0.3441235	5 0.292525	0.19897382	RC_AA2915 51 at	Human ets domain protein ERE mRNA complete ods
229	229 CNS	0.9537966	6 0.3440925	5 0.292477	RC_A 0.19883154 59 at	A5998	
230	230 CNS	0.9537156	6 0.3440479	9 0.292464	0.1986734 t	AA298180_a t	EST: EST113862 Bone VII Homo sapiens cDNA 5' end, mRNA sequence. (from Genhank)
231	CNS	0.9517934	4 0,3439757	0.292362	0.19844995	RC_AA4875 10 at	EST: aa95c11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 839060 31 mRNA sequence (from Genhank)
232	232 CNS	0.9498384	4 0.3438279	0.292062	0.19834965	RC_AA4240 25 at	Sperm surface profein
233	CNS	0.9498376	6 0.3436411	0.291944	0.19825117	A255918_a	AA255918_a Homo sapiens mRNA for putative vacuolar proton ATPase membrane tector associated protein M8-9
234	234 CNS	0.9495384	4 0.3433476	0.291763	0.1981267 20 at	RC_AA6217 20 at	Glufathione neroxidace 3 (nlacma)
235	235 CNS	0.9486534	4 0.3430688	0.291685	0.19803612 18 at	A4872	EST: ab19g10.s1 Stratagene lung (#937210) Homo sapiens cDNA
236	236 CNS	0.9483126	5 0.3430532	0.291409	0.197919761	5463_a	Tronomizein 4
237 CNS	CNS	0.9479108	9 0.342795	L	0.19784653	4091278_a	AA091278_a EST: cchn2404.seq.F Fetal heart, Lambda ZAP Express Homo
238 CNS	CNS	0.9479089	0	0.291289			Sapiens Culty 3, mKNA sequence, (from Genbank)
239 CNS	CNS	0.9476763	3 0.3424581		0.19745554	A4252	EST: zw48c01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
240 CNS	CNS	0.9469206	5 0.3422883		0.19736661 W81268 at	1	Eukarvotic translation initiation factor 2 cultural 2 / 2000
241 CNS	SNS	0.9465747	0.3420135	0.290734	RC_A		EST: zn20d05.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547977 3', mRNA sequence. (from
242 CNS	SNS	0.9459087			0.1970026 10	RC_AA4799	EST: zw44c09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
243 CNS	SNS	0.9442487	0.3417354	0.290365	0.19690289 77 at	AA4321	EST: zw71112.s1 Soares testis NHT Homo sapiens cDNA clone 781679.3' mRNA certionce (from Contact)
244 C	CNS	0.9438028	0.3414481	0.290133	RC_AA6208 0.19674788 99 at		Homo sapiens clone 24684 mRNA company
245 CNS	SNS	0.9437864	0.3414093	0.289991	0.19663103 t	3602_a	EST: aa12f12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
246 CNS	SNS	0.9431379	0.3413717	0.289945	0.19639803 00_at	A3982	Homo sapiens mRNA for KIAA0875 protein, partial cds
247 CNS	SNS	0.9421586	0.9421586 0.3412744	0.289842	RC_A 0.19626512 37_at		RC_AA6085 EST: ae53c08.s1 Stratagene lung carcinoma 937218 Homo sapiens 37_at cDNA clone 950606 3', mRNA sequence. (from Genbank)

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

FIG. 3M

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248 CNS	0.9420937	0.3411845	0.289833	0.19611757	AA436315_a EST: zv22e11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t 754412 5', mRNA sequence. (from Genbank)
249 CNS	0.9417201	0.3410694	0.289742	RC_AA1507 0.19601606 76_at	Homo sapiens clone 24405 mRNA sequence
250 CNS	0.9415796	0.3408538	0.28967	RC_AA4545 0.19587982 81_at	Homo sapiens mRNA for KIAA0602 protein, partial cds
7 7 7 N N N N N N N N N N N N N N N N N	0 0 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	1,7070kg 0	777	RC_AA4552	
252 CNS	0.9404758		0.289226	0.1955017430 r at	Sequence. (from Genbank) EST: zw24e10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770250.31 mRNA sequence (from Ganbank)
253 CNS	0.9404371	0.3404388	0.289111	RC_AA0453 0.19542396 42 at	EST: zk59g01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 487152 3. mRNA seruence (from Genhank)
254 CNS	0.9396198	0.3403753	0.289044	RC_AA2281 0.19523694 16 at	Homo saniens mRNA for KIAA0551 profain partial ada
255 CNS	0.9383699	0.3402981	0.288912	0.19516522 MIP1-B at	No info for gene
256 CNS	0.9378721	0.3402134	0.288737	AA488230_a	
257 CNS	0.9373376	0.3399583	0.288536	0.19486225 t	AA427783_a EST: zw49b02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA to clone 773355 5' mRNA sequence (from Ganbank)
258 CNS	0.9370789	0.3398952	0.288328	0.19476531 40 at	
259 CNS	0.9357977	0.3397292	0.28827	RC_AA4584 0.19459064 54_at	
260 CNS	0.9340786	0.3394536	0.288203	0.19435151 t	PFKM Phosphofructokinase, muscle
261 CNS	0.9334054	0.3394105	0.288132	0.19425146 W72943_at	EST: zd54f12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344495 5', mRNA sequence. (from Genbank)
262 CNS	0.9333692	0.3391886	0.287951	RC_AA0578 0.19410947 42_at	RC_AA0578 EST: zl95e03.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 512380 3. mRNA sequence (from Garbank)
263 CNS	0.9329568	0.3388807	0.287827	RC_AA1211 0.19397263 21_at	EST: zl88c03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511684.31 mRNA sequence (from Genhank)
264 CNS	0.9326395	0.338879	0.287653	0.19390693 53_at	EST: 13cDNA40-3.seq Soares Infant brain 1NIB Homo sapiens cDNA clone HY18-44 3', mRNA sequence. (from Genbank)
265 CNS	0.9322209	0.3388363	0.287586	AA405937_a 0.19379193 t	AA405937_a EST: zu66a10.r1 Soares testis NHT Homo sapiens cDNA clone t 742938 5', mRNA sequence, (from Genbank)
266 CNS	0.9318144	0.9318144 0.3385669	0.287567	RC_AA0355 0.19363035 42_at	

		With the same of t					
267	CNS	0.9313584	0.3385087	0.287174	RC_A 0.1935239 28_at	C_AA2243 3_at	RC_AA2243 EST: zr12f02.s1 Stratagene hNT neuron (#937233) Homo sapiens 28_at cDNA clone 648603 3', mRNA sequence, (from Genbank)
268	268 CNS	0.9310966	0.3383984	0.28691	Av 0.19343401 t	A056361_a	AA056361_a clone 359947 5' similar to contains element PTR5 repetitive element; mRNA sequence. (from Genbank)
269 CNS	CNS	0.9305229	0.3383817	0.286848	0.19328254 Du	85815 at-2	0.19328254 D85815 at-2 Homo saniens DNA for rhoHD1 complete add
270	CNS	0.9305229	0.9305229 0.3382067	0.286778	0.1930946 D85815 at	85815 at	DNA for rhoHP1
271 CNS	CNS	0.9304102	0.9304102 0.3382044	0.286756	0.19302273 49	C_AA4361	RC_AA4361 EST: zv22b03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754349 3', mRNA sequence, (from Genhank)
272 CNS	SNS	0.9293105	0.3381902	0,286566	0.19289578 93		Homo sapiens mRNA for KIAA0544 profein partial cds
273 CNS	SNS	0.9287321	0.3381902	0.286395	RC 0.19279495 41	AA4177 at	EST: zv01c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746226 3: mRNA sequence (from Genhank)
274 CNS	SNC	0.9287133	0.3379416	0.286327	0.19269516 t	4464918_a	AA464918_a clone 838821 5' similar to contains Alu repetitive element;, mRNA
275 CNS	SNS	0.9286905	0.3378868	0.286307		AA384184_s l	AA384184_s EST; EST97722 Thyroid Homo sapiens cDNA 5' end, mRNA at
276 CNS	SNS	0.9286417	0.3378617	0.286265		A4790	EST: zu36b09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740057 3', mRNA sequence, (from Genbank)
277 CNS	SNS	0.9286303	0.9286303 0.3376463	0.286237	RC_A 0.19237445 32_at	A5987	EST: ae49g02.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950258 3, mRNA seguence (from Contact)
278 CNS	SNS	0.9284996	0.3375374	0.286153	0.19229238 96	A2113	EST: zq88d01.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 649057 3' similar to TR:G257387 G257387 HTS1;,
279 CNS	SNS	0.9275916	0.3375039	0.286033	0.19206153 48 at	A4211	Solute carrier family 5 (sodium/glucose cotransporter), member 2
280 CNS	SN:	0.927029	0.3373744	0.285955	RC_A 0.19195415 46_at	A1715	EST: zp22d10.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610195 3', mRNA sequence, (from Genhank)
281 CNS	NS	0.9268475	0.3372175	0.285828	0.19180332 H05871	Ţ,	ST: v173f05 r1 Home conjugate to the state of the state o
282 CNS	:NS	0.9262156	0.3372084	0.285681	0.191698981	26_a	EST: zv72a04.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759150 5' mRNA serulence (from Genhant)
283 CNS	NS	0.9258798		0.285609	0.19150257 59_at	894	EST: ae31b11.s1 Gessler Wilms tumor Homo sapiens cDNA clone 897405 3', mRNA sequence. (from Genbank)
204 CN3	NN	0.9252191	0.3365977	0.285513	0.19140908 N24994	ä	KIAA0710 gene product

285 CNS	0.9250717	0.3364383	0.285466	0.19124807 20 at	Cone 714038 31 mRNA segrence (from Genhank)
286 CNS	0.9248542	0.3363085	0.285314	0.19117658 55 s at	
287 CNS	0.9247506	0.3362466	0.28505	0.1910659 C15772_at	
288 CNS	0.9243805	0.3362401	0.28487	RC_AA4240 0.19081888 33 at	+
289 CNS	0.9239809	0.336111	0.284727	0.19068578 65 at	
290 CNS	0.9230045	0.3360803	0.284606	RC_AA0289 0.19058996 42_at	+
.291 CNS	0.9224028	0.3359724	0.284461	0.19051273 S76992 at	at-2 Vav 2 oncordene
292 CNS	0.9224028	0.3359576	0.28424	0.19035532 S76992 at	VAV2 Vav 2 oncodene
293 CNS	0.9222903	0.3357034	0.284199	0.1902372 R12974 at	1
294 CNS	0.9221217	0.3351448	0.284069	0.1900884 R67290 at	Homo sapiens clone 24607 mRNA secritario
295 CNS	0.9212725	0.3350744	0.283978	AA151569_s 0.1899677_at	
296 CNS	0.9202628	0.334947	0.283856	0.18994865 99 at	
297 CNS	0.9199286	0.3348722	0.283763	0.18974149 44 s_at	+
298 CNS	0.9197363	0.3348287	0.283562	0.18965021 19_at	
299 CNS	0.9194799	0.3348156	0.283511	0.18949175 43_s_at	
300 CNS	0.9193137	0.334677	0.283378	0 18939152 T08287 at	EST: EST06178 Homo sapiens cDNA clone HIBBB85 5' end. (from
301 CNS	0.9188231	0.3346414	0.283279	0.18928197 N56625 at	Cellibrity)
302 CNS	0.9178692	0.3345639	0.283251	RC_AA4033 0.18915163 05_at	
303 CNS	0.9177618 0.3343968	0.3343968	0.283042	0.18900076 76 s at	

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Docket No.:	2825.2020-002
Title: Genetic	Markers for Tumors
Inventors: Srid	har Ramaswamy, et al.
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304 CNS	0.9171396	0.3343027	0.282852	RC_A 0.18889138 82_at	3C_AA6100	RC_AA6100 EST: af08g08.s1 Soares testis NHT Homo sapiens cDNA clone 82 at 1031102 3' mRNA sequence (from Genhank)
305 CNS	0.9167273	0.334239	0.282845	0.18869998 50 at	RC_AA2369 50 at	EST: zs43f01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
306 CNS	0.9167028	0.3341688	0		M25667 at	GAP43 Growth associated profein 43
307 CNS	0.9165799	0.3341104	0.28262	RC_A 0.1884490136 =+	RC_AA4103	EST: zv16d12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
308 CNS	0.9148403		0		200771 at	ATPase type IV, phospholibid-transporting (P-type) (putative)
309 CNS	0.9146573	0.3340074	0.282468	0.18816735	AA476564_s	EST: zx02f07,r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785317 5' similar to TR:G553813 G553813 DNA-BINDING
310 CNS	0.9145317	,	0.282425	0.18808039)42991_s	EST: zk56a01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486792 5' mRNA seguence (from Carbank)
311 CNS	0.9137443	0.3335142	0.282071	RC 0.18799073 68	AA4789 at	EST: zv18e04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754014 3', mRNA sequence. (from Genbank)
312 CNS	0.9131467	0.3335136	0.282054	RC 0.1878114 65	AA2354 at	EST: zt31b07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 723925 3', mRNA sequence. (from Genbank)
313 CNS	0.9129232	0.3333525	0.281906	0.18771234 \$74039	S	at Homo sapiens creatine franshorter mRNA complete cdc
314 CNS	0.9121473	0.3333097	0.281872	0.18753573 W68255 at		EST: zd33f12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342479.51 mRNA sequence (from Genhand)
315 CNS	0.9120022	0.3331609	0.281775	0.18745464 12 at		EST: aa07d06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 812555 3' mRNA sequence (from Genhank)
316 CNS	0.9119647	0.3329263	0.281751	0.1873864 09 at	A4298	EST: zw64a12.s1 Soares testis NHT Homo sapiens cDNA clone 780958 3' mRNA seriience (from Genbank)
317 CNS	0.9115763	0.3328778	0.281611	0.18718566 06	_AA6208 at	EST: af95c05.s1 Soares testis NHT Homo sapiens cDNA clone 1055528 3' mRNA sequence (from Genhank)
SISICNS	0.9114778	0.3326972	0.281528	0.18717408 R56383 at		CDC23 (cell division cycle 23, yeast, homolog)
319 CNS	0.9113318	0.3326895	0.281254	0.18709591	RC_AA5996 79 s at	Homo sabiens clone 23584 mRNA contrance
320 CNS	0.9113081	0.3326083	0.281196	0.18692344 W27301	at	EST: 27b5 Human retina cDNA randomly primed sublibrary Homo sabiens cDNA, mRNA secuence, from Garbarky
321 CNS	0.9112123	0.3324861	0.281118	0.18681057 17	379	EST: zs55b10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone MAGE:701371 31 mRNA sertience (from Centers)
322 CNS	0.9109531	0.3322273	0.28104	0.18673289 t	7_s_a	EST; similar to none. mRNA segrence. (from Genhank)
323 CNS	0.9108422	0.3319761	0.280885	0.18652676 47_at	A6214	Af36h03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1033781 3', mRNA sequence
324 CNS	0.9107899	0.3319129	0.280718	0.18647857 C	14228 f at (0.18647857 C14228 f_at (from Genbank)

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325 (325 CNS	0.910032	2 0.3318965	0.280575		0.18641502 Z82022 at	Dolichyl-phosphate N-acetylglucosaminephosphotransferase 2 (GICNAC-1-P transferase)
326 CNS	CNS	0.9097309	9 0.331785	0.280535		RC_AA4220 47_at	EST: zv28e08.s1 Soares ovary fumor NbHOT Homo sapiens cDNA clone 754982 3', mRNA sequence. (from Genbank)
327 CNS	CNS	0.9096921	0.3317281	0.280476		RC_AA4049 88_at	Homo sabiens mRNA for KIAA0674 profein partial cds
328 CNS	CNS	0.9092219	9 0.3317064	0,28033	RC_A 0.18590525 80_at	RC_AA4482 80_at	EST: zw83h05.s1 Soares testis NHT Homo sapiens cDNA clone 782841 3', mRNA sequence. (from Genbank)
329 CNS	SNS	0.9089643	0.331525	0.280272	0.18578438	AA477214_a t	AA477214_a clone 7393515' similar to contains Alu repetitive element;, mRNA
330 CNS	SNS	0.908928	0.3314865		0.18565504	AA232738_a t	Sarcodivcan. epsilon
331 CNS	SNS	0.9086279	0.3314186	0.279951	0.185556 t	AA461215_a t	AA461215_a EST: zx61a09.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA to clone 795928 5', mRNA sequence (from Genhank)
332 CNS	SNS	0.9083716	0.3312341	0.279915	0.18536836	2531	EST: zr52g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667058 3' mRNA sequence (from Conbont)
333 CNS	SNS	0.9080692	0.3311848	0.279744	0.18529294 00 at	2530	EST: 2752h04.51 Soares NhHMPu S1 Homo sapiens cDNA clone
334 CNS	SNS	0.9076743	0.3311738	0	0.18512663	A4560	EST: aa17c01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
335 CNS	SNS	0.9074756	0.3310127	0.279582	0.1850877128 at	A2580	EST: zs76a05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
336 CNS	SNS	0.9070862	0.9070862 0.3309577	0.279347	0.1850575 94 at	A4651	EST: aa33g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
337 CNS	SN:	0.9070412	0.3308105	0.279284	0.18494342	A378597_a	EST: EST91316 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA seminance (from Goobset)
338 CNS	SN:	0.906994	0.3307675	0.279115	0.18485843 15 at	1C_AA4366 5 at	EST: zw55c09.s1 Soares total fetus Nb2HF8 9w Homo saplens cDNA clone 773968 3' mRNA sequence #com Contact.
339 CNS	NS NS	0.9067808	0.3306317	0.279067	0.18477507 t	302_a	KIAA0304 cene product
340 CNS	NS	0.9065295	0.3304749	0.279055	0.1845846	RC_AA4537 95 at	EST: aa19708.s1 Soares NhHMPu S1 Horno sapiens cDNA clone 813735.31 mRNA sequence (from Conhact)
341 CNS	NS	0.9058477	0.3304187	0.278969	RC_A 0.18450525 62_at	A4439	EST: zv51f04.s1 Soares testis NHT Homo sapiens cDNA clone 757183 3', mRNA sequence (from Genhank)
342 CNS	NS	0.904971	0.330216	0.278722	U55312 0.1843542 1_s_at	rna	G protein-coupled receptor 19
343 CNS	NS	0.9045503	0.3300984	0.278706	0.18422922 t	AA460511_a	AA460511_a EST: zx51h09.r1 Soares testis NHT Homo sapiens cDNA clone t
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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. the street was the tends of the street stree

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. RC_AA4339 EST: zw52c04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: zw94e05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA AA236286_a 666892 5' similar to SW:GCN5_YEAST Q03330 TRANSCRIPTIONAL RC_AA4772 | EST: zu39a12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488 RC_AA3994 EST: zt53a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA RC_AA2561 EST: zr79c08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zr68a03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA4970 EST: aa42c03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 0.18368259 88 at 781933 3', mRNA sequence (from Genbank) Yu53g07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA EST: zu81a08.s1 Soares testis NHT Homo sapiens cDNA clone AA258972_a EST: zs34d01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone N79674_s_a | EST: yz81h05.r1 Homo sapiens cDNA clone 289497 5'. (from ACTIVATOR GCN5. [1];, mRNA sequence. (from Genbank) Homo sapiens mRNA for KIAA0869 protein, partial cds Homo sapiens mRNA for KIAA0829 protein, partial cds IMAGE:687073 5', mRNA sequence. (from Genbank) clone 740350 3', mRNA sequence. (from Genbank) clone 773670 3', mRNA sequence. (from Genbank) clone 784640 3', mRNA sequence. (from Genbank) clone 726026 3', mRNA sequence. (from Genbank) Upstream regulatory element binding protein 1 681902 3', mRNA sequence. (from Genbank) 744374 3', mRNA sequence. (from Genbank) 781933 3', mRNA sequence. (from Genbank) 668524 3', mRNA sequence. (from Genbank) 823588 3', mRNA sequence. (from Genbank) clone IMAGE:229884 5', mRNA sequence 0.1830403 J03544 s_at Phosphorylase, glycogen; brain Putative Ac-like transposon Genbank) 0.18345508 07 at | Cr 0.18323226 79 s at RC AA4433 E 0.1831334 21 at c AB002310_a AA089559 a AA166776_a RC AA6211 H01766 s a RC_AA4301 0.18219829 H67964 at 0.18358363|71 at 0.18400048 63 at 0.18339877 42_at 0.18271835 45 at 0.18260302 88_at 0.1823823 50 at 0.18374318 0.18285912 t 0.1839001 0.18408261 0.1825605 0.18235160.1821126 0.278538 0.278551 0.278296 0.27839 0.278196 0.278156 0.277892 0.277728 0.277928 0.27766 0.277515 0.277487 0,277332 0.277036 0.276939 0.277227 0.276899 0.276747 0.276611 0.3300789 0.9023477 | 0.3295342 0.32992 0.9026005 0.3296566 0.3299009 0.329793 0.3296487 0.9019314 0.3292249 0.9027182 0.3298551 0.3292249 0.9009711 | 0.3291293 0.3291293 0,3289509 0.8968484 | 0.3285141 0.328941 0.8993013 0.3289307 0.328855 0.8979144 | 0.3287333 0.8975303 | 0.3285351

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0.8949432 0 0.8945633 0 0.8944442 0	0.3284345				cepiers on the seducine. (II of II delibally)
	7.70	0.276376	0.18196289 20_at	RC_AA4493 20_at	EST: zx06e03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785692 3', mRNA sequence. (from Genbank)
					Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1
	0.3282835	0.276316	0.18192057	AA214730_a t	AA214730_a (Hematological and Neurological expressed sequence 1) downstream to a putative CoG island. Contains ESTs and GSSs.
	0.3282348	0.276249	RC 0.18180585 67	RC_AA4566 67_at	EST: aa01f07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 812005 3. mRNA segrence (from Genhank)
	0.3281789	0.276193	0.18170495 24 at	RC_AA6216 24 at	Homo sapiens clone 24515 mRNA segmence
_	0.3280276	0.276176	RC_A 0.18155804 51 at	RC_AA1582 51 at	Human growth factor-regulated tyrogical kinds and harden
0.8938357 0	0.3278598	0.276056	0.18141976	RC_AA1950 31 at	EST: zr35f08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665415.3" mRNA sequence (from Corbons)
i	0.3277756	0.275925	RC_D59847 0.18128863 at	RC_D59847 at	EST: Human fetal brain cDNA 3'-end GEN-070G07, mRNA sequence.
0.8932131 0	0.3276595	0.275889	0.1811862 D82346_at		HNSPC
0.8927829 0.	0.3274034	0.275694	0.18107748	4A059401_a	AA059401_a EST: z!96c05.r1 Stratagene comeal stroma (#937222) Homo sapiens t
0.8924663 0.	0.3272977	0.275688	0.1809682 W28255 at		EST: 44b8 Human retina cDNA randomly primed sublibrary Homo
642 0.	0.8917642 0.3272079	0.275685	0.18079548 7	1	EST: 2v83d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 760243.3° mRNA sequence (from Conhact)
0.8915897 0.	0.3271901	0.275632	RC_AA4262 0.18075244 20_at		Homo sapiens mRNA for KIAA0523 protein martial sets
0.8912345 0.	3271645	0.275514	0.18056597	A6087	EST: af04b05.s1 Soares testis NHT Homo sapiens cDNA clone 1030641 3' similar to contains element TAR1 repetitive element;
0.8905333 0.3		0.275492	0.18052281 ₀		EST: 2749g05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
0.8904765 0.3		0.275312	0.18042365		Doublecortex: lissencenbalv X-linked (doublecortex)
0.8900428 0.3		0.275277	R 0,1802816	A4599	Bradvkinin recentor R2
0.8896193 0.3		0.275069	0.18015333 t	3304_a	GTP-RINDING NI ICI EAD ODOTEIN DAN
		0.3271645 0.3268903 0.3268522 0.3267535	0.3268903 0.3268903 0.3268522 0.3267535 0.3267422	0.3271645 0.275514 0.1805659 0.3268903 0.275492 0.18052281 0.3268522 0.275312 0.18042365 0.3267535 0.275277 0.1802816 0.3267422 0.275069 0.18015333	0.3271645 0.275514 0.1805659 72 at 0.3268903 0.275492 0.18052281 0.9 at 0.3268522 0.275312 0.18042365 30 at 0.3267535 0.275277 0.1802816 16 at 0.3267422 0.275069 0.18015333 4A436304 at

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0.3264561 0.3263621 0.3263038 0.3262521	0.274652	RC_AA2 0.17998132 60_at	279	EST: zr56d10:s1 Soares NhHMPu S1 Homo sapiens cDNA clone
0.3263621 0.3263038 0.3262521		000		00/4113, mKNA sequence, (from Genbank)
0.3263038	0.274565	AB00 0.17989685 1	322_a	Human mRNA for KIAA0324 gene nartial cde (from Conhomb)
0.3262521	0.274444	RC_A 0.17983982 85_at	A3484	KIAA0438 gene product
0.3260302	0.274436	RC_A 0.17962293.46 at	A5987	EST: ae49h07.s1 Stratagene lung carcinoma 937218 Homo sapiens
	0.274367	0.17955106 75 s		EST: zs96e10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711498 3' mRNA sequence (from Genhank)
0.325856	0.274356	0.17944467 14 s at	+	EST: zs94c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705126.31 mRNA sequence (from Genhank)
0.3258103	0.274279	RC_A 0.17926483 47_at	A2591	EST: zs30f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686713 3', mRNA sequence (from Genhank)
0.3254135	0.27424	H093	34 s a	EST: yl95a06.r1 Homo sapiens cDNA clone 45792 5' similar to SP:A42792 A42792 SUCCINATE DEHYDROGENASE;. (from Genbank)
0.3253922	0.274204	0.17909473 46 s	260	EST: ze86a02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 365834 31 mRNA sequence (from Conhock)
0.3251919	0.274136	RC F 0.1789898 41 at	981	EST: zf58g11.s1 Soares testis NHT Homo sapiens cDNA clone 726596 31 mRNA sequence (from Contract)
0.3249258	0.27395	0.17885493 W587		protein 2
0.3248851	0.273847	RC A 0.17878127 09_at	A4253 EST: zw46c clone 77308	EST: zw46c01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773088 3', mRNA seguence. (from Genhank)
0.3246657	0.273404	AA090	1687_a EST: y1297 cDNA 5', m	AA090687_a EST: y1297.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)
0.3246276	0.273296	0.17858195 R8822	at	Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin))
0.3243329	0.273236	0.17844316 R8057	!	EST: yi92f11.r1 Homo sapiens cDNA clone 146733 5'. (from Genbank)
0.3242738	0.273236	RC A 0.17834364 06 at	2	EST: zo55d01.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 590785 31 mRNA sections of from Control 1
0.3241518	0.273015	RC_A 0.17825201 82_at		Homo sapiens clone 23770 mRNA secilience
0.3240429	0.272988	RC_A 0.17815068 39_at	44609 EST: zx61d clone 79594	RC_AA4609 EST: zx61d03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 39_at clone 795941 3', mRNA sequence, (from Genbank)
		0.27 0.27 0.27 0.27 0.27 0.27 0.27 0.27	0.27424 0.17920062 0.274204 0.17909473 0.274136 0.1789898 0.273847 0.17885493 0.273296 0.17868166 0.273296 0.17844316 0.273236 0.17844316 0.273236 0.17834364 0.273236 0.17825201	H09364_s_a

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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RC_AA2349 EST: zr50c05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 95_at 666824 3', mRNA sequence. (from Genbank)		AA363338_a Ubiquitin protein ligase E3A (human papilloma virus E6-associated topologia. Angelman syndrome)		KIAA0652 gene product	RC_AA4433 EST: zw94g05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 34_at clone 784664 3', mRNA sequence. (from Genbank)	AA044715_a cDNA clone 488708 5' similar to PIR:B54857 B54857 transcription factor NE-AT 90K chain human and a constant of the chain human and a constant of the chain human and a constant of the chain human and a constant of the chain human and a constant of the chain human and a constant of the chain human and a constant of the chain human and a constant of the chain human and a constant of the constant of the chain human and a constant of the chain human and a constant of the constant of	RC_AA3985 EST: 2t73g07.s1 Soares testis NHT Homo sapiens cDNA clone	SCG10	EST: za54c04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 296358 51 mBNA sociones (from Control of the Control o						IMAGE:825083 3', mRNA sequence. (from Genbank) EST: vo18b06 r1 Homo canione CDNA close 175050 r1:::::				0.17617007 U06863 at-2 (from Genhank)	Follistatin-related protein precursor mRNA
RC_AA2349 95_at	RC_AA4532 89_at	AA363338_a t	AA094441_a t	RC_AA4022 68_at	RC_AA4433 34_at	AA044715_a t	RC_AA3985	S82024 at	W03178 at	RC_AA4253	0.17683512 45 at		A399200_a	A4892		at	_AA2562 at	A455331_a	J06863 at-2	J06863_at
RC 0.17804533 95	RC_A 0.1779011 89_at	0.17786632 t	0.1776822 t	RC_A 0.17756717 68 at	RC_A 0.1775123 34_at	β 0.17746037 t	RC_A 0.17724355 72 at	0.17714423 \$82024	0.17701282 W03178 at	0.17695235 02 at	0.17683512	0.17675941	A 0.17672397 t	0 47666955	V. 17 000 333 45 at	0.17653482 H46831	0.17636923 08	0.176198151	0.17617007	0.17601943 U06863
0.27289	0.272841	0.272721	0.27271	0.272652	0.272648	0.272591	0.272553	0.272441	0.272346	0.272159	0.272097	0.272077	0.271953	0.271833	0.51	0.271693	0.271669	0.271527	0.271518	0.271384
0.3238381	0.3238223	0.3237092	0.3235939	0.3234656	0.3233967	0.3233528	0.3233399	0.3231237	0.3230982	0.322961	0.3229579	0.322877	0.3228021	0.3226229		0.3224933	0.3224571	0.3224205	0.3221654	0.3221408
0.8842527	0.8831623	0.8831182	0.8823555	0.8822184	0.8816973	0.8815104	0.8812974	0.8811587	0.8811452	0.8810003	0.8803201	0.880312	0.880078	0.8795734		0.8790923	0.8790079	0.8786764		0.8783413 (

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Docket No.: 2825.2020-002	
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Inventors: Sridhar Ramaswamy, et	al.

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420 CNS	0.8781272	2 0.3220042	0.271285	0.17584619	C_AA3791	RC_AA3791 EST: EST91932 Skin tumor I Homo sapiens cDNA 3' end, mRNA 26's at sequence (from Genhank)
421 CNS	0.8774802	0.3219739	0.271118	0.17579037	H21148_s_a	
422 CNS	0.8764464	0.8764464 0.3219698	0		82477 at	EST: similar to none, mRNA sertience, (from Genhank)
423 CNS	0.8764378	3 0.3218825	0.270816	0.17568316	RC_AA2627 10_s at	Homo sapiens mRNA for KIAA0627 protein partial cds
424 CNS	0.8760315	0.3218065	0.270742	R(0.175538 25		EST: zu65b07.s1 Soares testis NHT Homo sapiens cDNA clone 742837 31 mRNA sequence (from Genhank)
425 CNS	0.8759868	0.3217611	0.270706	RC_AA4477 0.17553158 69 at	A4477	EST: aa20e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 813816 31 mRNA sequence (from Genhank)
426 CNS	0.8757927	0.3216643	0.270654	AA 0.17547399 t	AA482453_a t	EST: zv05b12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 752735 5', mRNA sequence. (from Genbank)
427 CNS	0.8753265	0.321655	0.2705	0.1753202 W26883	26883_at	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA, complete cds
						EST: zl83d11.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511221 3' similar to contains Alu repetitive element contains
428 CNS	0.8752369	0.8752369 0.3216257	0.270446	RC_A 0.17522325 80_at	A0864	element MER22 repetitive element;, mRNA sequence. (from Genbank)
429 CNS	0.8751909	0.3216005	0.270426	0.17513151 46 f at	44361 at	EST: zv2za12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754366 3' mRNA sequence (from Conhomb)
430 CNS	0.8749581	0.3215883	0.270391	0.1749306 t	36_а	Procellanen-liveine 2 avadutarato E discussos
431 CNS	0.8749492	0.3211414	0.270369	RC_A 0.17488083 67_at	A2136	EST: zr93e10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683274 3' mRNA sequence (from Goobsel)
432 CNS	0.873919	0.3210794	0.27031	0.17477958 at	412_s	Homo canions mDNA containing (2001)
433 CNS	0.8736669	0.3209994	0.270221	0.17474262 65 at	A5211	EST: aa73d12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
434 CNS	0.8734883	0.3208085	0.270152	0.17464387 t	4023_a	Homo saniens evnortin t mDNA complete del
435 CNS	0.873412	0.3205961	0.270125	0.1745725 at	D59420	Homo sapiens mRNA for KIAAAAA
436 CNS	0.8730769	0.3204384	0.270095		A2322	EST: zr75g08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669278 3', mRNA sequence (from Genhank)
437 CNS	0.8726217	0.3202697	0.269996	0.17429751 T87560_at	30 at	EST: yd83b10.r1 Homo sapiens cDNA clone 114811 5'. (from Genbank)
438 CNS	0.8723564	0.8723564 0.3201354	0.269974	AB(0.17421918 t	AB002348_a t	Human mRNA for KIAA0350 gene, partial cds

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A30 CNS		0 8722791	0.3200499	0.269941	0.1741314 t		Homo sapiens mRNA for KIAA0465 protein, partial cds
440 CNO		0 8722293		0.269872	RC_A 0.1740282 72_at		EST: af12b02.s1 Soares testis NPT Horito Sapreus Corty, Control 1031403 3', mRNA sequence. (from Genbank)
4440		0.01.5550	- 1	0.269846	0.1738497	0.1738497 90 at 7	EST: zv14c07.s1 Soares NhHMPu S1 Homo sapielis CDIA Society 753612 3', mRNA sequence. (from Genbank)
250		0.0	ŧ		1 701000710		EST: csg4860.seq.F Human fetal heart, Lambda ZAP Express rioning regions cDNA 5' mRNA sequence. (from Genbank)
442 CNS	SNS	0.8718835	0.3199524	0.269722	0.17383437	RC AA0403 E	EST: z/05h02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
443 CNS	SN:	0.8715387	0.3198913	0.26968	0.17376097 94	94 at	94 at clone 376083 3', mRNA sequence. (from Genbank)
444 CNS	SNS	0.8714629	0.319816	0.269605	0.17367683	AA126592_a	clone 502232 5', mRNA sequence. (from Genbank)
	9	0.074.00034	0.9406943	0.280508	0 17358626	m	C-ferminal binding protein 1
445 CNS	SNS	0.01 12021		0.269379	0.17352396 D82284 at		Homo sapiens mRNA for KIAA0733 protein, partial cds
7 0440	CNIS	0.0100020	200			Ø.	EST: zr37g05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
447 CNS	SNS	0.8704747	0.319455	0.269258	0.17337993 t		665624 5, mKNA sequence. (Hour denibation)
ONJ 877	SMC	0 8700701	0.3192615	0.269095	0.17325737	AA092.765_a t	cDNA 5', mRNA sequence. (from Genbank)
ONO OFF	SNO	0.8606305		0.269074	0.17315294 R78991 at		Lactate dehydrogenase B
1844	CINO	0.000000	2400044	0.088068	RC_A	~	Homo sapiens mRNA for KIAA0874 protein, partial cds
450 CNS	CNG	0.00937.10		0.5003.0	0.000	AA48522 a	
AE4 CNS	SNS.	0 8694489	0.3191114	0.268946	0.172932091	1	Human smoothened mRNA, complete cds
45.	28.0	2000					EST: ze55e09.s1 Soares retina N2b4HR Homo sapiens cDNA clone
					1010001	A0189	362920 3' similar to contains Alu repetitive element;, mKNA
452	452 CNS	0.8693954	4 0.3189533	0.268897	0.1728852776 at	10 at	sequence: (non censeur)
453	453 CNS	0.8690352	2 0.3188826	0.268884	0.172847231	1	Mannose-6-phosphate receptor (cation dependent)
			1			AA465434_a	
454	454 CNS	0.8682405	5 0.3188277	0.268773	0.17268021	17	FST: FST76547 Homo sapiens cDNA 5' end similar to None. (from
455	455 CNS	0.8680446	6 0.3186049	0.26873		0.17261161 T34896_s_at	Genbank)
710	4EG ONIO	0 8670040		0.268597	0 1725334 †	AA093862_a	AA093862_a EST; c1256.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)
2	250					AA430011_a	
457	457 CNS	0.8677273	3 0.3185546	0.268574	0,172453	31	Radixin
458	458 CMS	0.8673101	0.3183403	0,268467	0.17236339 24	RC_AA1348 9 24_at	
200	2						

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459 CNS	0.8672912	2 0.3182977	0.268361	0.17233655	AA195457_a t	AA195457_a EST: zr36a12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t 665470 5', mRNA sequence. (from Genbank)
460 CNS	0.8672099	9 0.3182463	0.268304	0.17225803 W40410	W40410_at	EST: zb74f10.r1 Soares fetal lung NbHL19W Horno sapiens cDNA clone 309355 5', mRNA sequence, (from Genbank)
461 CNS	0.8672053	3 0.3180966	0,268213	0.17225154 H78550	H78550_at	EST: yu13g03.r1 Homo sapiens cDNA clone 233716 5'. (from Genbank)
462 CNS	0.8671424	4 0.3179736	0.268052	0.17211534	R20031_at	EST: yg31g03.r1 Homo sapiens cDNA clone 20078 5'. (from Genbank)
463 CNS	0.8671183	3 0.3178086	0.267951	RC_A 0.17198934 63_at	RC_AA6091 63_at	Small inducible cytokine A5 (RANTES)
464 CNS	0.8668292	2 0.3178054	0.267817	RC_AA2 0.17185512 85_s_at	RC_AA2155 85_s_at	RC_AA2155 Homo sapiens clone 486790 diphosphoinositol polyphosphate 85_s at phosphohydrolase mRNA, complete cds
465 CNS	0.8666653	3 0.3176784	0.267752		0.1717201 W26395 at	EST: 29h10 Human retina cDNA randomly primed sublibrary Homosapiens cDNA mRNA sequence (from Carbank)
466 CNS	0.8665986	0.3175967	0.267715	0.17170309 95 s at	202	EST: af04h10.s1 Soares testis NHT Homo sapiens cDNA clone
467 CNS	0.866149	0.3175961	0.267637	0.17159374 C02016 at		KIAA0447 cana product
468 CNS	0.8657075	0.3174503	0.267563	0.17151907 41 at	3C_AA0708	RC_AA0708 Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA
469 CNS	0.8656745	0.3173472	0.267298	0.17143741 D78012 at		CRMP1 Collansin response mediator mateix 4
470 CNS	0.8653678	0.3172293	0.267277	0.17127916	S	H canions m DMA for O Albo
471 CNS	0.865122	03171641	70200	1	95021_a	Codpicing in MARIO GARZZ protein
472 CNS	0.8644858	- 1	0.20121	0.171215271		Glioblastoma amplified sequence
473 CNS	0.8644858	1	0.267079	0.17109527 X82207 at	C	BETA-CENTRACTIN
474 CNS	0.8644258	0.3169101	0.267004	0.170946121	28 a	EST: zl34c12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA
475 CNS	0.8637341	0.3168535	0.266916	0.1708864 t	A504549_a	AA504549_a EST: aa60c12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
476 CNS	0.8630804	0.3167527	0.266839	A 0.17077659 t	AA278829_a	Homo sapiens mRNA for KIAA0871 protein completed.
477 CNS	0.862962	0.862962 0.3167299	0.26682	0.170759841t	A488103_a	EST: ad07a08.r1 Soares NbHFB Homo sapiens cDNA clone 877526 5' similar to SW:YAH8_YEAST P39707 HYPOTHETICAL 31.3 KD AA488103_a PROTEIN IN RFA1-ADE1 INTERGENIC REGION.;, mRNA
478 CNS	0.8629395	0.31663	0.266738	0.17063084 28 at	A4536	EST: zx48c06.s1 Soares testis NHT Homo sapiens cDNA clone
						octoo o, minary sequence. (nom Genbank)

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479 CNS	0.8628446	6 0.3165369	0.26682	0.47058223 WE2620	00000	EST: zc49f01.r1 Soares senescent fibroblasts NbHSF Homo sapiens
				0.11030323	W52638 at	cUNA clone 325657 5', mRNA sequence. (from Genbank)
480 CNS	0.8624148	8 0.3164192	0.266576		at	CONE 756086 3', mRNA segrence (from Genhank)
481 CNS	0.8614368	8 0.316418	0.266474	0.17044353 67 at	_AA4358	EST: zt80f08.s1 Soares testis NHT Homo sapiens cDNA clone
180 CNG	0 06400	ŀ		RC	RC_AA4522	EST: zx15f06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
102 010	0.001293	3 0.3163188	0.266444	0.17031217 45 s at	s at	clone 786563 3', mRNA sequence. (from Genbank)
483 CNS	0.8607888	3 0.3160881	0.266116	0.1702379 03 at	RC_AA4341 03_at	EST: zw24a08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770198 3' mRNA segretaria (from Conhant)
484 CNS	0.8607813	3 0.3160742	0.266069	RC_AA4 0.17015016102 s. at	RC_AA4503	Dorogiomal biogenetic for the companies of the control of the cont
	A CONTRACTOR OF THE PARTY OF TH			20 CI 20 CI	AA1502	eroxisorital diogenesis ractor 14
485 CNS	0.8607601	0.3160489	0.265969	0.17005959 05_at	05_at	Ubiquitous Kruppel-like transcription factor
486 CNS	0.8603923	0.3160449	0.265911	0.16994965 04 at	A4781	EST: zt89c03.s1 Soares testis NHT Homo sapiens cDNA clone
487 CNS	0.8603262	0.3160376	0.265752	AA4 0.169878351	1192_a	EST: aa43f10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
488 CNS	0.8599824	0.3159898	0.265608	AB0 0.1697924.t	AB002304_a	Himm mona for Italana
480 CNG	0.0503042	1		RC	12370	ridinal linuvA tot NAAW30b gene, partial cds
490 CNS	0.8595918	0.3159038	0.265555	0.16968083 34 at		Golgi SNAP receptor complex member 2
		Į	0.203330	0.10939852 W25847	ज	Homo sapiens mRNA for GEF-2 protein
491 CNS	0.8588387	0.3156932	0.265364	0.16952276 57		Homo sapiens clone 23570 mRNA serii ence
492 CNS	0.8587751	0.3156571	0.265339	0.16945778 29 at	A2916	EST: z45f05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
493 CNS	0.8586209	0.3156269	0.265235	0.1693457 W60181_at	81_at	P311 protein
494 CNS	0.8583674	0.3156097	0.265107	0.1692594 M93426	at	PTPRZ Protein tyrosine phosphatase, receptor-tyne, zeta notynentida
495 CNS	0.8581185	0.3156079	0.28500			EST: zc30d03.r1 Soares senescent fibroblasts NbHSF Homo saniens
496 CNS	0.8570005		0.20203	N. 109 1 104 1 W46 192 at RC AA4 118		cDNA clone 323813 5', mRNA sequence. (from Genbank) EST: zt67c03.s1 Soares testis NHT Homo sanians CDNA clone
ONE ONE	0.001 3000	0.3133886	0.265009	0.16912585 25_s_at		727396 3', mRNA sequence. (from Genbank)
497 CNS	0.8575531	0.3155774	0.264968	RC_A 0.16902694 41_at	AA0533 3	RC_AA0533 381354 3' similar to contains Alu repetitive element; contains element 41 at MFR22 repetitive element in PNN securors (from Cartains element).
				Maria Company		ICINEZ TEPETITIVE GIGITICITI, IL TITIVA SEQUETICE. (ITOM GENDANK)

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498	498 CNS	0.8573443	0.3154531	0.264789	0.16893794	RC_AA4550 97 i at	RC_AA4550 EST; aa04f08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 97 i at 812295 3', mRNA sequence, (from Genbank)
499	499 CNS	0.8570634	0.3153619	0.264617	0.16886637	AA464639_a t	Ribosome binding protein 1 (dog 180kD homolog)
200	500 CNS	0.8564378	0.3153363	0.264546	0.16878209	RC_AA2868 07_at	· · · · · · · · · · · · · · · · · · ·
501	501 CNS	0.8562839	0,3152781	0.264451	0.16869104	>	Homo sapiens mRNA for KIAA0788 protein, partial cds
502	502 CNS	0.8558524	0.8558524 0.3152213	0.264347	0.16859502	RC_AA2060 23_at	EST: zq77c12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 647638 3', mRNA sequence, (from Genhank)
503	503 CNS	0.8558478	0.3152061	0.264324	0.16850731 W02253 at	N02253 at	EST: za57f05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 296673 5', mRNA sequence, (from Genbank)
504	504 CNS	0.8555413	0.3150941	0.264212	AA4 0.16844626 <u>a</u> t	55606_s	
505	505 CNS	0.8551045	0.3150696	0.264109	0.16834123 T86796 at	786796 at	EST: yd86e07.r1 Homo sapiens cDNA clone 115140 5' similar to contains TAR1 repetitive element: (from Genhank)
506	506 CNS	0.8549647	0.3149992	0.264041	A 0.16830519 t	VA418351_a	
507	507 CNS	0.8548502	0.314909	0.263969	0.16821444 26 at	RC_AA0763	Ribosomal profoin (32)
508	508 CNS	0.8547452	0.3148094	0.263928		RC_AA0562 47_at	Homo eanione closs 2464 mpNiA
509	509 CNS	0.85447	0.3145937	0.263857	0.16805875 38 s at	7	EST: x80b06.s1 Soares testis NHT Homo sapiens cDNA clone 728627 3' mRNA sequence (from Genhand)
510	510 CNS	0.854466	0.3143011	0.263817	0.16803373 t	152957_a	AA452957_a clone 788544 5' similar to gb:X52354 ZINC FINGER PROTEIN
511	511 CNS	0.8543346	0.8543346 0.3140812	0.263778	RC_A 0.16789782 02 at	C_AA4635	RC_AA4635 EST: zx72c09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 02 at
SUZIC	CNS	0.8539971	0.3140491	0.263695	0.16781375 D16181	at	PMP2 Perloheral myelin profein 2
513 CNS	CNS	0.8536553	0.3139249	0.263619	0.16769223 73 at	A4534	EST: zx45d07.s1 Soares testis NHT Homo sapiens cDNA clone 795181 3', mRNA sequence (from Genhank)
514 CNS	CNS	0.8534239	0.3139046	0.263609	RC_A 0.16759919 39_at	A2794	EST: zs85f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704297 31 mRNA sertience (from Goobson)
515 CNS	CNS	0.8530401	0.3134361	0.263497	RC_A 0.16751824 19 at	A4063	Midline 1 (Opitz/BBB syndrome)
516 CNS	SNS	0.8529968 0.3132913	0.3132913	0.263496	RC_A 0.16740824 72_at	A2624	EST: zs17g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685492 3', mRNA sequence. (from Genhank)

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517 CNS	0.8523769	9 0.3130742	0.263365	0.1673256	RC_AA4529 EST: zx41h05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 28 at clone 789081.31 mRNA sequence (from Centeral)
518 CNS	0.8521363	3 0.3130189	0.263313	0	-
519 CNS	0.851822	2 0.312805			YIG3e12.r1 Homo sapiens cDNA clone 162058 5' (from Controls)
520 CNS	0.8517499	9 0.3127979	0.263124	0.16709167 D81655 at	EST: Human fetal brain cDNA 5'-end GEN-181D03, mRNA sequence.
724 CNR	000000000000000000000000000000000000000		(1G3638- 1T3849_s	a la la la la la la la la la la la la la
02.0	0.0010000	0.312/483	0.26309	0.16702446 t	Amyloid Beta (A4) Precursor Protein, Alt. Splice 2, A4(751)
522 CNS	0.8511856	0.3127445	0.26303	RC_AA6090 0.16692969 11_at	
523 CNS	0.8509063	0.3126426	0.262916	RC_AA4648 0.16687898 44 at	
524 CNS	0.8506628	0.3125913	0.262904	0.1667924 10 f at	
525 CNS	0,8502092	0.3124628	0.262827	AA056681_a	
526 CNS	0.8501516	0.3124199	0.262785	0.16660722 F15210 at	Hexpsaminidase B (hota solvestida)
527 CNS	0.8500838	0.312153	0.262637	0.16654107 40 at	Carbonic anhydrase XI
528 CNS	0.8496226	0.3120626	0.262544	RC_AA0042 0.1664916711 at	RC_AA0042 EST: zh97c05.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
529 CNS	0.8495781	0.3118795	0.262489	0.16637972 97 at	Bone mornhogonatio and in 7 /
530 CNS	0.8491106	0.3118793	0.262465	AA465553 a	AA465553_a Aa33g05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
531 CNS	0.8489354	0.3117518	0.262405	RC_AA4896 0.1661839.87 at	
532 CNS	0.848788	0.848788 0.3116835	0.262311	0.16610803 R51401 at	Homo sapiens chromosome 19, fosmid 39554
533 CNS	0.84858	0.3115251	0.26225	RC_AA0695 0.16601504 71_at	Homo sapiens clone 24616 mRNA sequence
534 CNS	0.8485167	0.3114922	0.262184	0.16595986 46 at	
535 CNS	0.8484812	0.3114693	0.262158	0.16591097 t	
536 CNS	0.8481967	0.3113906	0.262115	0.16583134 1_at	GIF=growth inhibitory factor Ihuman brain Genomic 2018 at
			-		July 2010 Hy

 EST: zw91e01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA AA013042_a EST: ze35d03.r1 Soares retina N2b4HR Homo sapiens cDNA clone RC_AA5986 EST: ae39h03.s1 Gessler Wilms tumor Homo sapiens cDNA clone 0.16548029 62_at R13478 3', mRNA sequence. (from Genhank) EST: 12g4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA clone 646597 3', mRNA sequence. (from Genbank) AA419186_a EST: zv34f07.r1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zr65b05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA5043 EST: aa61e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone EST: zn20e08.s1 Stratagene neuroepithelium NT2RAMI 937234 3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1 0.1650733 68 at Genbank) RC_AA2054 | EST: zq66f07.s1 Stratagene neuroepithelium (#937231) Homo Homo sapiens clone 24703 beta-tubulin mRNA, complete cds IMAGE:825436 3', mRNA sequence. (from Genbank) clone 784344 3', mRNA sequence. (from Genbank) AFFX-HSAC07/X00351_M_at (endogenous control) Homo sapiens TRIAD1 type I mRNA, complete cds clone 755557 5', mRNA sequence. (from Genbank) sapiens cDNA, mRNA sequence. (from Genbank) 813478 3', mRNA sequence. (from Genbank) 668241 3', mRNA sequence. (from Genbank) 360965 5', mRNA sequence. (from Genbank) 898229 3', mRNA sequence. (from Genbank) Homo sapiens clone 24582 mRNA sequence 0.16516191 H83573 r at Tumor protein D52-like 2 0.16567186|0351_M_at-2|No info for gene Tetraspan 5 Genbank) RC AA4471 RC_AA2427 RC_AA1817 HSAC07/X0 HSAC07/X0 RC_AA4278 0.16485949 W07097 at AA287973_a 0.16557819|0351_M_at 0.16527882 W26770 at RC_AA2361 0.16497926 99_s_at AFFX-AFFX-0.16574931 20_at 0.16546215 57 at 0.16536698|24 at 0.16490059 60_at 0.16475065|50 at 0.16467585|26_at 0.165799|89 0.16509610.16464923 0.16453023 0.261956 0.26205 0.261713 0.261658 0.261841 0.261491 0.261867 0.261841 0.261592 0.261437 0.261189 0.261126 0.261124 0.261079 0.260999 0.260835 0.260756 0.260894 0.8473674 0.3113439 0.311379 0.8471552 0.3112805 0.8470684 0.3110745 0.8473674 0.3113068 0.8463649 0.3109135 0.8477377 0.3113883 0.3110506 0.3108082 0.8455775 0.3105439 0.8453791 0.3103805 0.8447517 | 0.3102813 0.3107384 0.8455679 0.3105175 0.8455085 0.3103857 0.8445458 0.3100374 0.8442358 0.3099558 0.8446667 0.3102381 0.8476792 0.8468567 0.846257 0.8462 537 CNS 538 CNS 539 CNS 540 CNS 541 CNS 542 CNS 543 CNS 544 CNS 545 CNS 546 CNS 547 CNS 548 CNS 549 CNS 550 CNS 552 CNS 551 CNS 553 CNS 554 CNS

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

FIG. 3C.

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

		,					
555 CNS	NS	0.8441979	0.3099062	0.26069	0.16448729 t	AA091017_a t	AA091017_a EST: yy1646.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)
556 CNS	NS	0.8441081	0.3098175	0.260595	RC 0.1644242 51	RC_AA4122 51_at	EST: zu10a07.s1 Soares testis NHT Homo sapiens cDNA clone 731412 3', mRNA sequence. (from Genbank)
557 CNS	SZ	0.8439533	0.3096205	0.26049	RC 0,16439494 80	RC_AA1730 80_at	RC_AA1730 EST: zp21g07.s1 Stratagene neuroepithelium (#937231) Homo 80 at sapiens cDNA clone 610140 3', mRNA sequence. (from Genbank)
558 CNS	۸S	0.8438715	0.3094766	0.260432	0.16430289t	AA478704_a t	Interleukin 13 receptor, alpha 1
559 CNS	ZS S	0.8432761	0.3094406	0.260363	RC_A 0.16416588 29_at	43507	EST: EST58150 Infant brain Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)
560 CNS	4S	0.8428872	0.309363	0.260262	RC 0.1640817178	45999 at	EST: ag28g07.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1090908 3', mRNA sequence. (from Genbank)
561 CNS	4S	0.8426119	0.3093524	0.260262	RC_AA1 0.16400689 64_f_at	761	EST: zp23h11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610341 3', mRNA sequence. (from Genbank)
562 CNS	4S	0.8426043	0.3091897	0.260153	RC_A 0.16390994 13_at	A6092	EST: af12f09.s1 Soares testis NHT Homo sapiens cDNA clone 1031465 3', mRNA sequence. (from Genbank)
563 CNS	4S	0.8425161	0.3090431	0.260142	0.16384247	Z68092 s_at	0.16384247 Z68092_s_at Cell division cycle 25B
564 CNS	Ş	0.8423365	0.3090026	0.260069	RC_A 0.16372354 45_at	41363	EST: zn89h06.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565403 3', mRNA sequence. (from Genbank)
565 CNS	ş	0.8421232	0.3089875	0.260015	RC 0.16364752 61	_AA1123 at	EST: zn68c10.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 563346 3', mRNA sequence, (from Genbank)
566 CNS	ફુ	0.8419783		0.259965	RC_A 0.1635746 71_at	A6214	EST: af92d09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 1055249 3', mRNA sequence, (from Genhank)
267 CNS	25	0.8414637	0.3088441	0.259935	0.16351797 T34963_at		Homo sapiens clone 24523 mRNA sequence
568 CNS	{S	0.8410502	0.3087117	0.259816	0.16342008 t	AB002324_a	Human mRNA for KIAA0326 gene, partial cds
569 CNS	ङ	0.8408773	0.3086928	0.259815	0.16336168 79 s at	RC_AA4258 79 s at	RC_AA4258 EST: zw49e02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 79 s at clone 773402 31, mRNA sequence, (from Genhank)
570 CNS	S	0.8408421	0.3086294	0.259698	0.16328335 t	88 a	Secretory carrier membrane protein 2
571 CNS	S	0.8407771	0.3085646	0.259674	0.16320334 t-2	6062_s_a	Human mRNA for KNP-lb, complete cds
572 CNS	হ্য	0.8407771	0.3084042	0.259591	0.16303906 t)86062_s_a	KNP-Ib
573 CNS	S	0.840645	0.840645 0.3083106	0.259547	0.16299616	RC_D51172 _at	EST: Human fetal brain cDNA 3'-end GEN-015G07, mRNA sequence. (from Genbank)

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	0.8401902	0.3081848	0.259513	0.16288611 R23293 at	FK506-hinding profein 2 (13kD)
	0.8400458	0.3081639	0.259459		-
		}		RC_AA4549	
	0.8396528	0.3081607	0.259373	0.16277693 37_at	IMAGE:814764 3', mRNA sequence, (from Genbank)
	0.839603	0.308064	0.259277	0.16273163 N23801 at	EST: yx36b12.r1 Homo sapiens cDNA clone 263807 5', (from Genbank)
	0.8395087	0.3079699	0.259274	U00802 s 0.16263796 t	ന_
	0.8390283	0.3079161	0.259176	RC_AA4418 0.16259329 02 at	
	0.8388993	0.3078571	0.259159	C01688_s 0.16249704 t	ω.
	0.8388622	0.307803	0.259141	RC_AA4525 0.16235134 36 at	
: 1	0.8384658	0.3077509	0.259122	0.16231601 58 at	AA0393 EST: zf05d10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA at clone 376051 3', mRNA sequence, (from Genbank)
	0.8380725	0.3077364	0.259063	0.16226761 N98799 at	
. 1	0.8379745	0.8379745 0.3077118	0.258961	0.16214316 R54897 at	
	0.8377281	0.3076383	0.258961	AA484997_a 0.1620365 t	_a Manic fringe (Drosophila) homolog
i i	0.8376226	0.3075781	0.258925	0.16197784 R69700_at	
	0.8370836	0.8370836 0.3075253	0.258793	0.16196665 S72422 s	at
	0.8365548	0.8365548 0.3074768	0.258715		
	0.8365279	0.3074643	0.258664	0.1617889 W27237_at	
1	0.8360968	0.307357	0.258604	RC_AA2838 0.16175145 23 at	
- 1	0.8360176	0.3073144	0.258495	AA426168_a	-
	0.8360081	0.307299	0.258468	RC_AA3572 0.16165869 04 s at	
1	0.8359247	0.3072293	0.258425	RC_AA1498 0.16158219 33_at	
	0.8358825	0.3070409	0.258409	0 1615138 08 at	RC_AA2583 EST: zr60g11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
1	2-00000	2010	0.200100	0.1013130 00 at	100/044 3, MKINA sequence, (from Genbank)

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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						3C AA2526	All Addition of the contract o
707	595 CNS	0.8352098	0.3070316	0.258341	0.16141166 30 at	30 at	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
596	596 CNS	0.8346335	0,306995	0.258305	0.161329281	AA248283_a l	AA248283_a EST: csg2234.seq.F Human fetal heart, Lambda ZAP Express Homo t sapiens cDNA 5', mRNA sequence. (from Genbank)
507	507 CNS	0 8335921 0 306777	0.3067779	0.258263	0.161329281	D83883_s_a	Human tip associating protein (TAP) mRNA, complete cds
3	2					AA096491_a	AA096491 a EST: k0190.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
298	598 CNS	0.8334558	0.3067616	0.258238	0.1612344 t		cDNA 5, mKNA sequence. (Irom Senbank)
				1	L C	A437171_a	Homo sapiens transcriptional regulatory protein p54 mKNA, complete
299	599 CNS	0.8333895	0.3066787	0.258063	0.161206/51		COS ECT 7/662 Home canisas cDNA 5' and similar to None (from
009	600 CNS	0.8325222	0.3065542	0.258037	0.16111238 T34752	s at	s at Genbank)
904	601 CNS	0.8325188		0.258015	0.16096246	143286_s_a	Gamma-aminobutyric acid (GABA) B receptor, 1
						A259021_s	EST: zs33b03.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone
602	602 CNS	0.8324813	0.3064551	0.257811	0.16087097		IMAGE:686957 5', mRNA sequence. (from Genbank)
603	603 CNS	0.8323581	0.3062807	0.257705	RC_A 0.16081205 00 at	A2529	EST: zr76f01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669337 3', mRNA sequence. (from Genbank)
3	2					A2353	EST: zt30h10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
604	604 CNS	0.8323335	0.3062381	0.257639	0.1608087385 at		clone 723907 3', mRNA sequence, (from Genbank)
605	SNO	0.8324360	0.3062159	0.257631	RC_AAZ 0.16073544 04 s. at	801	EST: ztd5h09.s1 NCI_CGAP_GCB1_H0m0 sapietis cDNA cione IMAGE:712289 31, mRNA sequence. (from Genbank)
909	606 CNS	0.8317393	0.3061822	0.257606	0.16054262 Y12478 at	Y12478 at	CHD5 protein
5						AA379742 a	AA379742 a EST: EST92623 Skin tumor I Homo sapiens cDNA 5' end, mRNA
09	607 CNS	0.8317165	0.8317165 0.3061796	0.257581	0.16043402 t		sequence. (from Genbank)
				1			Zc29g11.r1 Soares senescent fibroblasts NbHSF Homo sapiens
00	608 CNS	0.8306666	0.3060078	0.257496	0.16035496 W44681	at	cDNA clone 323780 5', mKNA sequence. (from Genbank)
							clone 291413 5' similar to PIR:S33957 S33957 coat protein gamma-
906	609 CNS	0.8306291	0.3059836	0.257404	0.16033968 W03008	W03008_at	COP - bovine ;, mRNA sequence. (from Genbank)
		1	i		11000	, doodin	EST: zd82b12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
61	610 CNS	0.8305032	0.3059652	0.25/391	0.16031/4	0.16031/4 W80658 at	CIONE 34/135 5, IIIKINA SEQUETICE. (TOTAL GETIOATIN)
	611 CNS	0.8304488	0.3058153	0.25739	0.16031574	H89133_s_a	KIAA0618 gene product
			1				EST: yg77g09.r1 Homo sapiens cDNA clone 39567 5'. (from
61	612 CNS	0.8303629	9 0.305801	0.257313	0.16021173	0.16021173 R51809_at	Genbank)
9	613 CNS	0.830255		0.257306	0.16008936	RC_D52154	Iduronate 2-sulfatase (Hunter syndrome)
5	21.0			ŀ			

FIG. 3F

				1.0	4 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	The strong set of the strong s
614 CNS	0.8298565	0.3057225	0.257296	RC_AA0791 0.15999512 35_at	RC_AA0791 35_at	EST: zm98f06.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone 545987 3', mRNA sequence. (from Genbank)
615 CNS	0.829702	0.3055946	0.257213	RC_A 0.15995744 40_at	RC_AA6001 40_at	Deleted in oral cancer-1
616 CNS	0.8290605	0.3055408	0.256933	0.15990305 t	AA095812_a t	Density-regulated protein
617 CNS	0.8290556	0.3054445	0.256876	RC_A 0.15990305 _{42_at}	A2329	EST: zr46e02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666458 3' similar to contains element L1 repetitive element ;; mRNA sequence. (from Genbank)
618 CNS	0.8289711	0.3053838	0.256852	0.15977687 T31862 at	T31862 at	EST: EST40163 Horno sapiens cDNA 5' end similar to None. (from Genbank)
619 CNS	0.8289131	0.3050947	0.256769	0.15974285	AB002313_a t	Human mRNA for KIAA0315 gene. partial cds
620 CNS	0.8286154	1	0.256741	0.15964518 22 at	RC_AA3985 22_at	RC_AA3985 EST: zt47d11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 22 at clone 725493 3', mRNA sequence. (from Genhank)
621 CNS	0.8286033	0.3049647	0.256714	0.15957911 W26984	व्य	Calmodulin 1 (phosphorylase kinase, delta)
					AFFX- HUMGAPDH /M33197_5_	
022 CINS	0.8286032	0.3049378	0.256682	0.15943897	at AFEX.	AFFX-HUMGAPDH/M33197_5_at (endogenous control)
					HUMGAPDH	
623 CNS	0.8286032	0.3049011	0.256651	/M3; 0.159379 at-2	/M33197_5_ at-2	Glyceraldehyde-3-phosphate dehydrogenase
624 CNS	0.8283285	0.3047462	0.256591	0.15929787	AA033543_a t	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12
625 CNS	0.8281773	0.3046939	0.256558	RC_A 0.15922712 73 at	A4560	Human amino acid fransport-related protein mRNA complete ode
626 CNS	0.8281543	0.3046188	0.256551	0.15922263 R83496 at		EST: yp15c07.r1 Homo sapiens cDNA clone 187500 5' (from Genbank)
627 CNS	0.8280532	0.3045814	0.256515	RC_A 0.15915386 46_at	A0355	EST: ze24c07.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 359916 3', mRNA sequence. (from Genbank)
628 CNS	0.8279582	0.3044593	0.256404	RC_A 0.15907359 62_at	A0708	EST: zm58c10.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone 529842 3' similar to TR:G998813 G998813 TIF1. [1];, mRNA sequence. (from Genbank)
629 CNS	0.8279355	0.3043807	0.256362	0.15899748 W69964_at		Homo sapiens mRNA, chromosome 1 specific transcript KJAA0495
630 CNS	0.8278584	0.3043257	0.256346	0.15890592 L11373 at		Protocadherin 43 mRNA for abbreviated PC43

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631	631 CNS	0.8275738	0.3043096	0.256312	0.15886128 49_	RC_AA2325 49_i_at	EST: zr24c06.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664330 3', mRNA sequence, (from Genbank)
632	632 CNS	0.8273299	0.3042676	0.256253	0.15877318 R80333_at	R80333_at	EST: yi96b06.r1 Homo sapiens cDNA clone 147059 5'. (from Genbank)
633	633 CNS	0.8269027	0.3042376	0.256251	RC_A 0.15862796 94 at	RC_AA4285 94_at	EST: zw75g12.s1 Soares testis NHT Homo sapiens cDNA clone 782086 3', mRNA sequence. (from Genhank)
634	634 CNS	0.8267392	0.3042368	0.256119	0.15855484	AA149543_a t	
							EST: zt28g07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 714492 3' similar to TR:E91187 E91187 NMDA RECEPTOR
635	635 CNS	0.8263632	- 1	0.256093	0.15850711 27_s_at	KC_AA2924 27_s_at	GLUTAMATE-BINDING SUBUNIT.;, mRNA sequence. (from Genbank)
930	CNS	0.8261754	0.3037881	0.256087	0.15847576 D82534	D82534_at	Homo sapiens clone 23765 mRNA sequence
289	CNS	0.8261409	0.3037502	0.25607	0.158348	0.158348 R15268_at	EST: yf89f02.r1 Homo sapiens cDNA clone 29665 5' (from Genhank)
638 CNS	CNS	0.8259348	0.3034252	0.256001	0.15829577	AA256355_a t	EST: zr80b02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 681963 5'. mRNA sequence. (from Genhank)
639 CNS	CNS	0.825903	0.3033613	0.255951	RC_A 0.15825278 54_at	A0260	EST: ze86b05.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 365841 3', mRNA sequence, (from Genhank)
640 CNS	CNS	0.8257268	0.3032471	0.255938	0.15816386	RC_AA1483 18 s at	Human mRNA for KIAA0069 gene partial cds
641 CNS	SNS	0.8255546	0.3031608	0.255883	RC_A 0.15812258 89_at	A4217	EST: zu26e07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739140.31 mRNA sequence (from Genhant)
642 CNS	SNS	0.8254309	0.3030926	0.255796	RC_A 0.15805726 43 at	RC_AA4259 43 at	Acyl-Coenzyme A dehydrogenase yenylong chain
643 CNS	SNS	0.8253813	0.3030733	0.255702	0.15801959 W26589 at		EST: 33d9 Human retina cDNA randomly primed sublibrary Homosapiens cDNA, mRNA sequence, (from Genhank)
644 CNS	SNS	0.8252641	0.3030448	0.255632	RC_A 0.15787694 77_at	A4820	EST: zv43d08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756399 3", mRNA sequence, (from Genbank)
645 CNS	SNS	0.8250298	0.3030217	0.255574	RC_AA4 0.15780035 82_s at	RC_AA4314 82_s at	Homo sapiens mRNA for KIAA0465 protein partial cds
646 CNS	SNS	0.8249951	0.302834	0.255532	RC 0.15772638 53	548	EST: zx79e11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809996 31, mRNA sequence, (from Genbank)
647 CNS	SNS	0.8241409	0.3028197	0.255446	0.15759073 H29992 at		EST: yp44g05.r1 Homo sapiens cDNA clone 190328 5'. (from Genbank)
648 CNS	SNS	0.8240151	0.3027892	0.255333	0.15747163 D45278_at	D45278_at	EST: Human brain cDNA, mRNA sequence. (from Genbank)
649 CNS	SNS	0.8239818	0.8239818 0.3026509	0.255147	RC_A 0.15740249 63_at	RC_AA4959 63_at	RC_AA4959 EST: zw06b08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 63_at 7684713', mRNA sequence. (from Genbank)

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650 CNS	0.823882	0.3025819	0.255044	0.45737307	3C_AA4777	RC_AA4777 Breakpoint cluster region protein, uterine leiomyoma, 1; barrier to
651 CNS	0.8238664	0.8238664 0.3025027			20811 at	autolitiegration factor
652 CNS	0.8238664	0.8238664 0.3024769		0.157236371.90644	20014 81	GRIAZ GIutamate receptor, ionotropic, AMPA 2
				0.10720037	Z0014 al-Z	Giutamate receptor, ionotropic, AMPA 2
653 CNS	0.8238363	0.3023984	0.254841	0.15722528 T30687 s	30687_s_at	at Human PDGF associated protein mRNA. complete cds
654 CNS	0.8234683	0.3023061	0.254837	0.15714197 t	A046865_a	AA046865_a EST: zf12b09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
655 CNS	0.823076				RC_AA3507	EST: EST58251 Infant brain Homo sapiens cDNA 3' end. mRNA
656 CNS	0.023010	0.3021700			6 at	sequence. (from Genbank)
	0.0441 333	- 1	0.254625	0.1569892 L13435 at		Human chromosome 3p21.1 gene sequence
657 CNS	0.8226515	0.3021401	0.254621	0.1568895 t	M60346_s_a t	a ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2
658 CNS	0.8225755	0.3020018	0.254592	0.15687397 R77159	77159 at	EST: yi65a07.r1 Homo sapiens cDNA clone 144084 5'. (from Genbank)
659 CNS	0.8224721	0.3019881	0.254545	0 1568171	R87373 s a	i i i i i i i i i i i i i i i i i i i
		1			ABOO374 2	indionate z-sullatase (Hunter syndrome)
960 CNS	0.8224141	0.3019762	0.254505	0.15674943	D006314_a	Human mRNA for KIAA0376 gene partial cds
661 CNS	0.8220636	0.3018619	0.254256	RC 0.156674 41	RC_AA4784 41 at	Cathensin F
662 CNS	0.8220327	0.3018507	0.254219	O 15665907 49	RC_AA4854	
				77.000000.00	, a	riomo sapiens hypothetical SBBI03 protein mRNA, complete cds
- to						7032008 rd Gershama and an and an an an an an an an an an an an an an
663 CNS	0.8220047	0.3015831	0.254202	0.1565604 t	4147144_a	AA147144_a 588586 5' similar to WP:C14B1.4 CE00901 GUANINE NUCLEOTIDE
664 CNS	0.8219892	0.301553	0.25415	0 15649949 84	AA4029	EST: 2u55b08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
665 CNS	0.894728	0.000	1			EST: yx88c08.r1 Homo sapiens cDNA clone 268814 5' (from
666 CNS	0.021100	0.301447	0.254016	0.15643784 N36619	at	Genbank)
	0	+0++10000	700407.0	U.1563126 N2/670	at	Homo sapiens mRNA for putative progesterone binding protein
967 CNS	0.8213707	0.3014148	0.253988	0.15627375 51_at	A0564	EST: zl69d05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509865 3', mRNA sequence. (from Genhank)
668 CNS	0.821304	0.3013967	0.2539	0.15619285 t	AA046768_a t	Homo sapiens clone THA8 Cri-du-chat racion mDMA
669 CNS	0.8212514	0.3013807	0.253736	0.15610074	490648_a	AA490648_a Aa01g06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 812026
670 CNS	0.8212333	0.3012483	0.253577	0.15602048 37 s	A5990	SWI/SNF related, matrix associated, actin dependent regulator of
					5	and manners of the ma

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		Contraction of the Contraction o			N. dust that M. Mark their		thost West trade made thest Made that
671 CNS	တ	0.821083	0.3012019	0.253545	0.15594865	1	_AA4881 EST: ad08b01.s1 Soares NbHFB Homo sapiens cDNA clone 877609 s at 3', mRNA sequence. (from Genbank)
672 CNS	S	0.8208385	0.3011568	0.253524	0.1558727	RC_D60296 _at	EST: Human fetal brain cDNA 3'-end GEN-097D06, mRNA sequence. (from Genbank)
673 CNS	S	0.8204764	0.3010707	0.253456	0.1558075	RC_AA0226 15_at	EST: ze72h10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364579 3', mRNA sequence. (from Genbank)
674 CNS	(0)	0.8203406	0.3009537	0.253417	0.15573676 19	_AA1477 at	EST: zo44b06.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 589715.3' mRNA secilence (from Ganhank)
675 CNS	(0	0.82015	0.3008483		0.1556185	RC_AA4282 04 at	EST: zw51c11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
676 CNS		0.8199686	0.3007678	0	0	W38663 at	Galactokinase 1
677 CNS		0.8198898	0.3007077	0.253157	0.15551578 48	AA04	EST: zk54a10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486618 31 mRNA sequence (from Genhank)
678 CNS		0.8196563	0.3006394	0.253157	RC_A 0.1554966943 at	A4045	EST: zw37h03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 772277 3' mRNA sequence (from Genhank)
679 CNS		0.8194774	0.3006275	0.253109	RC_A 0.15542647 68_at	A2580	EST: zs76d12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703415 3' similar to contains MER28.t1 MER28 repetitive element;, mRNA sequence. (from Genbank)
680 CNS		0.8193989	0.3004805	0.253104	0.1553556 H19063 at	H19063 at	EST: yn51b01.r1 Homo sapiens cDNA clone 171913 5'. (from Genbank)
681 CNS		0.8193691	0.3004341	0.253047	RC 0.15529554 77	AA4881 at	EST: ad08c03.s1 Soares NbHFB Homo sapiens cDNA clone 877636 3', mRNA sequence, (from Genbank)
682 CNS		0.8188886	0.3003271	0.25297	0.15524507	AA436102_a t	EST: zu03b11.r1 Soares testis NHT Homo sapiens cDNA clone
683 CNS		0.8188499	0.8188499 0.3002946	0.252903	0.15521008	A4958	EST: zwo5b10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 768379.31 mRNA sequence (from Genhank)
684 CNS		0.8187499	0.8187499 0.3002751	0.252865		R82229 at	Homo sapiens clone 23956 mRNA partial cds
685 CNS		0.8186795	0.3000532	0.252771	0.15503395	A4525	EST: zx35f06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788483 3', mRNA sequence (from Genhank)
686 CNS		0.8186256	0.3000451	0.252765	RC_A 0.15492807 73 at	A4497	EST: zx07h07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785821.31 mRNA sequence (from Genhank)
687 CNS		0.8185136	0.2999589	0.252719	RC_A 0.1549017 08_at	A4302	EST: zw59e02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774362 3', mRNA sequence. (from Genhank)
688 CNS		0.8184393	0.2998772	0.252638	0.15483402 t	AA127605_a t	Homo sapiens mRNA for KIAA0829 protein, partial cds
689 CNS		0.8181421	0.2998648	0.252551	0.15480909 D31134	at	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)
690 CNS).8175545	0.8175545 0.2998346	0.252538	RC 0.15472803 49	_AA0695 at	EST: zm52e03.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone 529276 3', mRNA sequence. (from Genbank)

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691 CNS	0.817362	0.2998277	0.252479	0.1546834	RC_AA4121	RC_AA4121 EST: zt69a05.s1 Soares testis NHT Homo sapiens cDNA clone
692 CNS	0.8171154		0	0	Z95636 at	Hanjens mRNA for lamining other 5 chain
693 CNS	0.817001	0.2993721	0.252311		H60501 at	EST: yr42g01.r1 Homo sapiens cDNA clone 207984 5. (from Genhank)
694 CNS	0.816563	0.2993583	0.252271	0.15448625	AA313653_a	AA313653_a EST: EST185526 Colon carcinoma (HCC) cell line Homo sapiens t
695 CNS	0.8165445	0.2992305	0.252208	RC 0.15435196 41	RC_AA4438 41_at	Homo sapiens Sprouty 2 (SPRY2) mRNA complete ode
696 CNS	0.8165259	0.2990672	0.252125	0.15427282 W76399 at	N76399 at	EST: zd66d05.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345609 5' similar to SW:A33_PLEWA Q02084 ZINC-BINDING PROTEIN A33_f11: mRNA seminance (from Conhact)
697 CNS	0.8162547	0.2990464	0.252058	0.15425204	S76942_s_at 2	Dopamine recentor D4
698 CNS	0.8162547	0.2989794	0.252013	0.15419286 S76942 s		Dopamine D4 receptor (exon 1) [human, brain tumor tissue, mRNA at Partial Mutant, 386 nt]
699 CNS	0.8162507		0.251922	0.15403028 97	3C_AA2793	RC_AA2793 EST: zs85d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
700 CNS	0.8161736	0.2987502	0.251853	1	301949 at	Homo sapiens mRNA for KIAAAASE protein rectical color
701 CNS	0.8159177	0.2987489	0.251826	RC_AA47 0.153949 04 i at	RC_AA4766 04 i at	EST: zx03d08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785391.3° mRNA sequence (from Coubon)
702 CNS	0.8156514	0.2986366	0.251785	0.15392488	AA091467_s _at	Homo sapiens CAGH1a (CAGH1) mRNA, partial cds
703 CNS	0.8156021	0.298605	0.251733	0.153819 L44334 at		EST: Homo sapiens thymus mRNA (randomly primed, normalized),
704 CNS	0.8154852	0.2985106	0.251703	A 0.15376309 t	w,	CASP8 and FADD-like anontosis regulator
705 CNS	0.8154646	0.2984948	0.251622	0.15371522	AA442054_s at	Phospholipase C. damma 1 (formanty culpture 140)
706 CNS	0.8148758	0.2983965	0.251537	0.15365468 N46577	at	EST: yy48b04.r1 Homo sapiens cDNA clone 276751 5'. (from Genbank)
707 CNS	0.814853	0.2983666	0.25151	0.15354574 t	A094999_a	AA094999_a Homo sapiens zinc finger protein 216 splice variant 2 (ZNF216)
708 CNS	0.8147036	0.2983133	0.25149	0.15349714		EST: zx88g08.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810878 5', mRNA sequence. (from Genhank)
709 CNS	0.8145073	0.2982905	0.251426	RC_A 0.15345654 38_at	A3985	EST: zt73c02.s1 Soares testis NHT Homo sapiens cDNA clone 727970 3', mRNA sequence. (from Genbank)
710 CNS	0.8144894	0.298214	0.251287	A 0.153384011	AA454214_a t	Homo sapiens clone 23631 mRNA sequence

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						4A447349 a	AA447349 a EST: zw93g08.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
711 CNS	CNS	0.8144709	0.8144709 0.2981073	0.251261	0.1533421 t		clone 784574 5', mRNA sequence. (from Genbank)
				The state of the s		A0636	EST: ze87g04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
712	712 CNS	0.8144354	0.298103	0.251176	0.15333316 18_at		clone 366006 3', mRNA sequence. (from Genbank)
						A1581	EST: zo55h11.s1 Stratagene pancreas (#937208) Homo saplens
713	713 CNS	0.8140076	0.2980999	0.251103	0.15325634 62	at	cDNA clone 590853 3', mRNA sequence. (from Genbank)
						A6203	EST: af07d01.s1 Soares testis NHT Homo sapiens cDNA clone
714	714 CNS	0.8139586	0.2980237	0.250998	0.15316522 55_at	55_at	1030945 3', mRNA sequence. (from Genbank)
7.15	715 CNS	0.8136003	0.2979746	0.250928	0.15304327	AA291444_a t	Novel centrosomal protein RanBPM
			1			AB002306 a	
716	716 CNS	0.8135234	0.2979568	0.250879	0.15300635	ر ا	Human mRNA for KIAA0308 gene, partial cds
717	747 CMS	0.8423050	0.2078435	0.250846	0 15205824	AA449376_a	AA449376_a EST: zx04c11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
	2	0.0	ı	0.50003.0		s 07727W	EST: 7477c10 r1 Soares fetal heart NhHH19W Homo saniens cDNA
718	718 CNS	0.8131968	0.2977865	0.250795	0.15286915 at		clone 346674 5', mRNA sequence. (from Genbank)
						U32169 rna	The same of the sa
719	719 CNS	0.8131241	0.2976297	0.250746	0.15279359 2_s_at		Collagen, type XI, alpha 2
						831	EST: zt17c12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
720	720 CNS	0.8130422	0.2975648	0.250619	0.15276536 80_at	80_at	clone 713398 3', mRNA sequence. (from Genbank)
					1	RC_AA4358	
721	721 CNS	0.8126917	0.2974907	0.250572	0.15275177 99_at		Homo sapiens mKINA for KIAAU462 protein, partial cds
1	9	070070		0	0.47074	A6096	EST: af15f12.s1 Soares testis NHT Homo sapiens cDNA clone
77./	722 CNS	0.8126193	0.29/4826	0.250566	0.152/162 14 at	14 at	1031/59 3, MKINA sequence. (Iroin Genoank)
							EST: zn21f01.s1 Stratagene neuroepithelium NT2RAMI 937234
				:		RC_AA0820	RC_AA0820 (Homo sapiens cDNA clone 548089 3', mRNA sequence. (from
723	723 CNS	0.8125814	0.2973941	0.250559	0.1525916 57_at	57_at	Genbank)
						RC AA5984	EST: ae48f01.s1 Stratagene lung carcinoma 937218 Homo sapiens
724	724 CNS	0.8120902	0.2973632	0.250516	0.15253317 41	at	cDNA clone 950137 3', mRNA sequence. (from Genbank)
						2	EST: Human fetal brain cDNA 3'-end GEN-120A10, mRNA sequence.
725	725 CNS	0.81174	0.2973608	0.25051	0.15245025	at	(from Genbank)
706	70E CMS	0.8442774	0.2072058	0.250.432	RC 0.45242224 0.4	RC_AA2871	Homo eanians mRNA for DRP8 protain complete cds
7	2,5	0.011211			0.10272217	AA486831 s	
727	727 CNS	0.8109133	3 0.2972147	0.250361	0.15242274	i T	KIAA0618 gene product
					1	RC_AA4494	RC_AA4494 EST; zx05b03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
728	728 CNS	0.8108686	0.8108686 0.2968683	0.250225	0.15227762 19 at	19 at	clone 785549 3', mRNA sequence. (from Genbank)

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729 CNS	SNS	0.8108075	5 0.2968556	3 0.250212		0.152163\W24319_at	EST: zb81b11.r1 Soares senescent fibroblasts NbHSF Homo sapiens
730 CNS	NS	0.8106909	0.2968284		0.		RC_C21123 EST: HUMGS0002071, Human Gene Signature, 3'-directed cDNA_at sequence, mRNA sequence, (from Genhank)
731 CNS	NS	0.8103234	0.2968175	5 0.25017	0.15206029	W79850 at	EST: zd75e07,r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346500 5' mRNA sequence (from Canhart)
732 CNS	NS	0.8099455	0.2968099	0.250136	0.15205514 46 at	A1327	EST: zo21a03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587500 31 mRNA sequence (from Genhank)
733 CNS	SN SN	0.8098899	0.296799	0.250134		RC_AA4060 56 at	Homo sanjens CAGH32 mBNA martial Ada
734 CNS	NS	0.8098409	0.2967913	0.250019	0.1519263	RC_D59316 _f_at	EST: Human fetal brain cDNA 3'-end GEN-014B03, mRNA sequence. (from Genbank)
735 CNS	NS	0.809783	0.2967666	0.249945	0.15189499	0.15189499 M57399 at	PTN Pleiotrophin (heparin binding growth factor 8, neurite growth- promoting factor 1)
736 CNS	NS	0.8095502	0.2966725	0.249794	0.151788		AA135328_s EST: zo28e08.r1 Stratagene colon (#937204) Homo sapiens cDNAat clone 588230 5', mRNA sequence. (from Genhank)
737 CNS	NS	0.8093398	0.2966647	0.249761	0.1517824 M63379	M63379_at	CLU Clusterin (complement lysis inhibitor; testosterone-repressed prostate message 2; apolipoprotein (1)
738 CNS	NS	0.8092362	0.2962177	0.249673	0.15174271 H44269 at		EST: yp17b05.r1 Homo sapiens cDNA clone 187665 5' similar to
739 CNS	٧S	0.8092039	0,2962093	0.249655	RC_A 0.15173368 55_at	A4486	H.sapiens mRNA for RP3 gene
740 CNS	NS NS	0.8091561	0.2960731	0.249597	0.15165432	Z11584 s at	0.15165432 Z11584 s. at H saniens NuMA cond (Clana T22)
741 CNS	4S	0.809099	0.2959747	0.249574	RC_A 0.15157907 78 at	RC_AA4500 78 at	RC_AA4500 EST: zx42a07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 78 at
742 CNS	SN	0.8089281	0.2959734	0.249558	0.1515625 t	3376_a	Sjogren syndrome antigen A2 (60kD, ribonucleoprotein autoantigen SS-A/Ro)
743 CNS	S	0.8088711	0.2959734	0.249555	0.1514404 t	A251693_a	EST: zs04a09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684184 5' mRNA sequence (from Garbank)
744 CNS	S	0.8088388	0.2958687	0.249495	RC_A 0.1513642 18 at	A4501	EST: zx42e09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 789160.31 mRNA sequence (from Conhact)
745 CNS	S	0.8086565	0.2958662	0.249449	0.15125836 85 at	A2624	EST; zs17h07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
746 CNS	S	0.8085643	0.2958061	0.24936	D 15118250+	A307471_a	The control of the NA Sequence, (from Genbank)
747 CNS	S	0.8084993	0.2957328	0.249333	0.15110232	T95813 f at	0.15110232 T95813 f at Karvonherin alnha 4 (imnortin alnha 3)
748 CNS	S	0.8084518	0.2956044	0.249305	0.15103455 24 at	RC_AA2339 124 at	RC_AA2339 EST: zr49e08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
							occion o, illinia sequelice. (Iloni Genbank)

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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e product	EST: yw29b04.r1 Homo sapiens cDNA clone 253615 5'. (from Genbank)	EST: hfe0150.seq.F Human fetal heart, Lambda ZAP Express Homo	EST: zk96e11.s1 Soares pregnant uterus NbHPU Homo sanians	CDNA clone 490700 3', mRNA sequence. (from Genbank)	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds	EST: ym86a02.r1 Homo sapiens cDNA clone 165770 5'. (from Genhank)		Nuclear lactor I/A (CCAA1-binding transcription factor)	EST: ab13a09.r1 Stratagene lung (#937210) Homo sapiens cDNA	EST: za52d12.r1 Soares fetal liver spleen 1NFLS Homo sapiens	CUINA clone 296183 5', mRNA sequence. (from Genbank) Homo sapiens clone 23675 mRNA sequence		EST: zc67a06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA	RC_AA6093 EST: zu71b11.s1 Soares testis NHT Homo sapiens cDNA clone 46 at 743421.31 mRNA society (2000)	EST: zw96h10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784867 51 mPNA scanner fetus Nb2HF8 9w Homo sapiens cDNA	and sequence. (Hottl Genbank)	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence.	EST; zw86c05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 783848 3' mRNA seguence (feet of the contract of the cont	oroduct
KIAA0351 gene product	EST: yw29b04.r1 Homo sap Genbank)	SST: hfe0150.seq.F Human	ST: zk96e11.s1 Soares pre	DNA clone 490700 3', mRN RANSCRIPTION INITIATIVE	Homo sapiens branched cha precursor, mRNA, nuclear g complete cds	EST: ym86a02.r1 Homo sap	infloor foots 100 on a second	ucieal lactor I/X (CCAAL-b	EST: ab13a09.r1 Stratagene It	ST: za52d12.r1 Soares feta	omo sapiens clone 23675 n	ii i anaines	ST: zc67a06.r1 Soares fetal	ST: zu71b11.s1 Soares test	5T: zw96h10.r1 Soares tota	M cytotoxic granulo cooper	EST: Human fetal-lung cDNA (from Genhank)	T: zw86c05.s1 Soares tota	KIAA0307 gene product
\B002349_a	at	AA249175_a t	RC_AA1017		A4210	to	A4364	2_s_a	A486335_a	7	ज ह		Ø.	3C_AA6093 E	456_a	A4650	3 s a	A4436	AB002305_a t KL
0.1509965 t	0.15093213 H91564	0.15086646		0.15074073 H06982 at	RC A 0.15064792 52_at	0.15059124 R86859	0.15052259159 at	0.150522591	0.150478991	0.15034464 34/00004	0.1502955 N23817 at	0.15023437 D31381_at	0.15016064 t	RC_A 0.15011425 46_at	0.15009287 t	RC_A 0.14999449 93 at	0.1499445 t	RC_A 0.1499408 76_at	0.14980794 _t
0.249267	0.249138	0.249079	0.248984		0.248774	0.248774	0.24871	0.248624	0.248556	0.248552	0.248463	0.248396	0.248337	0.248321	0.248314	0.248313	0.248259	0.248219	0.248076
0.29557	0.2955176	0.2953989	0.2953879	1 1	0.2952259	0.2951218	0.2950774	0.2950059	0.2949879	0.2949433	0.2949147	0.294886	0.2948833	0.2948734	0.2945857	0.2945691	0.2945454	0.2944939).2944721
0.808348	0.8081766	0.808082	0.8078888	0.8075836	0.8075659	0.807376	0.8071907	0.8068485	0.8068011	0.8067973	0.8065688	0.8065649	0.8064374	0.8061346	0.8061283	0.8059463 (0.8058006	0.8056954 (0.8053963 0.2944721
749 CNS	750 CNS	751 CNS	752 CNS	753 CNS	754 CNS	755 CNS	756 CNS	757 CNS	758 CNS	759 CNS	760 CNS	761 CNS	762 CNS	763 CNS	764 CNS	765 CNS	766 CNS	767 CNS	768 CNS

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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0140	9770900	0.00000446	0 247984	AB002369_a 0.14976819 t	
769 CNS	0.8030140	0.2343372	0.5		EST: yi36c12.r1 Homo sapiens cDNA clone 141334 5. (IIOIII
770 CMS	0 8048108	0.2943849	0.247922	0.14964971 R64534 at	Genbank)
CNOCIA	2000	1		AA248582_a	
774 CNS	0 8046038	0.2943849	0.247859	0.1496261 t	KIAA0737 gene product
ONIO OTTO	0 0044034	1	0 247847	AB002378_a	RIAA0380 gene product
(12 CN3	0.00			AA478512_a	-
773 CNS	0.8042371	0.2943177	0.247776	0.14946802 t	Homo sapiens Evid nominory in vivy, compress con
774 CNS	0.8041161	0.2943097	0.247702	RC_AA4304 0.149391 96_f_at	
775 CNS	0.8039966	1	0.247681	RC_AA4339 0.14934379 13_at	
776 CNS	0.803987;	0.8039872 0.2942532	0.247619	0.14931679 D82399 at	D82399 at Homo sapiens clone 23/14 IIINNA Sequence
777 CNS	0.8037524	4 0.2941536	0.247619	0.14927964 t	752793 5', mRNA sequence. (from Genbank)
778 CNS	0.8036697	1	0.247563	0.14924994 40_at	6 Homo sapiens mRNA for KIAA0643 protein, partial cds
		1		0 44046549 1 44403 af	
779 CNS	0.803497	0.2939619	0.24734	N. 149 10342 E44409 CK	9
780 CNS	0.8033435	15 0.2939595	0.247499	0.14910783 92_at	
781 CNS	0.8028711	11 0.2938561	0.247449	RC_AA5995 0.14905417 52_s_at	
782 CNS	0.8028511	11 0.2938471	0.247383	AA281677 0.14902623 t	a'
783 CNS	0.8028113	l	0.2473	0.14900622 N91193	at cDNA clone 292397 5', mRNA sequence. (from Genbank)
784 CNS	0.8026431	31 0.2938411	0.247205	0.14898409 H15314	at Genbank)
785 CNS	0.8025617	17 0.293812	0.247184	0,1489192	
786 CNS	0.8025582	0.293781	4	RC 0.14884889 77	81 EST: zw83b12.s1 Soares testis NH1 Homo sapiens converged 782783 3', mRNA sequence. (from Genbank)
787 CNS	0.80252	0.8025266 0.2937437	7 0.247044	RC_AA5989	

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					H. Mart Kort H. Tank South		પ્રાથમ પાતામ પાતામ તામામ સામામ પ્રાથમ
788	788 CNS	0.8024967	7 0.2936523	0.247023	0.14874522	14290_s_a	C14290_s_a EST: Human fetal brain cDNA 5'-end GEN-043C09, mRNA sequence.
788	789 CNS	0.8019133	3 0.2936039	0.24696	0.1487379	RC_AA6098 69 at	
790	790 CNS	0.8018169	9 0.2935399	0.246913	0 14860001	RC_AA0842	(Alibaino illori) conceptos vasturis de la
791	791 CNS	0.8018161	0.2935148	1 1		24039 at	Homo sapiens clone 24700 unknown mbNn
792	792 CNS	0.8017443	3 0.2934496	0.246823		1 1	EST: ym87d05.r1 Homo sapiens cDNA clone 165897 5'. (from Genbank)
793	793 CNS	0.8016132	0.2934448	0.246782		C +c 7020.	11
794	794 CNS	0.8016132	1 1			2507 at	0.14844613 U72507 at 40871 mRNA partial sequence, (from Genbank)
795	795 CNS	0.8015544	0.2932595	0.246696	0.14831293	AA236441_a	Home earling observed to the control of the control
796	796 CNS	0.8014099	0.2932074	0.246643		5018 at	Overlaing and aluming sign
797	797 CNS	0.8012898	0.2932045	0.246576	0.1482562	RC_D59981 s_at	EST: Human fetal brain cDNA 3'-end GEN-079C04, mRNA sequence.
798	798 CNS	0.801284	0.2932003	0.246501	0.14813866 t	214085_a	AA214085_a EST: zn57h08.r1 Stratagene muscle 937209 Homo sapiens cDNA
799	799 CNS	0.8010261	0.2931294	0.246443	RC_A 0.1480573 20 at	A4657	EST: aa32f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
800	800 CNS	0.8000084	0.00000				EST: za76b09.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 298457 5' similar to contains element MFR22 repetitive alement
		10000000		0.246361	0.14803538 W04732 at RC AA4655		., mRNA sequence. (from Genbank)
801	801 CNS	0.8007942	0.2929077	0.246331	0.14799511 40_at	7	IMAGE:814229 3', mRNA sequence (from Genhank)
802	802 CNS	0.8002412	0.2928934	0.24628	0.14789902 at	34178_s	EST: 2018f10.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 587275 5' mRNA socione (from Control)
803	803 CNS	0.7999758	0.7999758 0.2928348	0.24624	RC_A	A6091	EST: af11g09.s1 Soares testis NHT Homo sapiens cDNA clone
804	804 CNS	0.7999215	0.7999215 0.2928279	0.246186	0.14780673 X74142	12 at	1031392 3, mKNA sequence. (from Genbank) HRE-1 mRNA for transmitting 6-4
SNO COS	CNS	0.7999215	0.2928088	0.246184	0.14774841 X74	142 at-2	0.14774841 X74142_at-2 Forkhead (Drosophila)-like 1
806 CNS	CNS	0.79992	0.2927665	0.246137	0.14768411 W27984 at	7984 at	EST: 40f11 Human retina cDNA randomly primed sublibrary Homo sabiens cDNA, mRNA securence, (from Conhank)
807 CNS	CNS	0.7998202	0.2926448	0.246097	RC_A 0.14763619 14_at	A4786	EST: zv19c10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754098 3', mRNA sequence (from Genhank)
808 CNS	SNS	0.7997556	0.2926099	0.245953	0.14759286 t	746908_a	AA046908_a EST: zf47f09.r1 Soares retina N2b4HR Homo sapiens cDNA clone t 380105 5', mRNA sequence (from Genhank)
							(in an online)

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Docke	t No.: 2825.2020-002
Title:	Genetic Markers for Tumors
Invento	ors: Sridhar Ramaswamy, et al.

809 CNS	ONS	0.7994891	0.2925932	0.245904	RC_AA 0.14749941 60_i_at	1366	EST: zk99a04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490926 3', mRNA sequence. (from Genbank)
810 CNS	CNS	0.7993264	0.2924895	0.245896	RC_A 0.14745213 73 at	A4317	Homo sapiens clone 23716 mRNA sequence
							EST: yy38c09.r1 Homo sapiens cDNA clone 273520 5' similar to
811 CNS	CNS	0.7993043		0.245862	0.14732514 N44756	at	contains Alu repetitive element;. (from Genbank)
812 CNS	CNS	0.7992892	0.2924341	0.245835	0.14729407 D87458		KIAAU282 gene, partial cds
813	813 CNS	0.7991949	0.2923353	0.24579	0.14726983 X78932_f_at		H.sapiens HZF9 mRNA for zinc finger protein
- 3		20000		77.00	A 17050571	AA112941_a	in the second se
0 14	CNO	0.7 99000	0.2923112	0.2437.33	0.147.23034 1		חוומום אוווומפם
815	815 CNS	0.7987962	0.7987962 0.2922759	0.245688	0.14725018	(95073_at-2	0.14725018 X95073_at-2 H.sapiens mRNA for translin associated protein X
816	816 CNS	0.7987962	0.7987962 0.2922645	0.245662	0.14716852 X95073_at		Translin associated protein X
					LL.	A5985	EST: ae35e11,s1 Gessler Wilms tumor Homo sapiens cDNA clone
817	817 CNS	0.79853	0.2921798	0.245622	0.14708227 75_at		897836 3', mRNA sequence. (from Genbank)
					<u>LL</u>	A4117	EST: zv16d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
818	818 CNS	0.7984864	0.2921749	0.245433	0.147022 11_at		753807 3', mRNA sequence, (from Genbank)
	77.7				<u> </u>	A2367	EST: zr76e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
819	819 CNS	0.7981759	0.2921284	0.24541	0.1469538 90_at		669358 3', mRNA sequence. (from Genbank)
					<u>+</u>	RC_AA4614	EST: zx68d06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
820	820 CNS	0.7981136	0.2921042	0.245316	0.1468983 58_at		clone 796619 3', mRNA sequence. (from Genbank)
					1	A324825_a	AA324825_a Homo sapiens polyadenylate binding protein-interacting protein-1
821	821 CNS	0.79803	0.2920942	0.245267	0.14684244 t		(PAIP1) mRNA, complete cds
				- 11-1	<u></u>	AA4422	EST: zv61h04.s1 Soares testis NHT Homo sapiens cDNA clone
822	822 CNS	0.7979968	0.2920861	0.245251	0.1468264561	at	758167 3', mRNA sequence. (from Genbank)
							EST: yb39g06.r1 Homo sapiens cDNA done 73594 5'. (from
823	823 CNS	0.7978979	0.2919534	0.24524	0.14672877 T55688_s	at	at Genbank)
824	807 CNS	0.70788	0.2947496	0.245204	RC_A 0.146659 22 at	A4000	EST: zu68e12.s1 Soares testis NHT Homo sapiens cDNA clone 743182 31 mRNA sequence (from Genbank)
2				100		RC AA4278	
825	825 CNS	0.797752	0.2917179	0.245168	0.14663151 89_at		H.sapiens gene from PAC 42616, similar to syntaxin 7
826	826 CNS	0.7976823		0	0.146527921	J37408_at-2	0.14652792 U37408_at-2 C-terminal binding protein 1
827	827 CNS	0.7976823	3 0.2914804	0.24507	0.14647587 U37408	at	CtBP mRNA
828	828 CNS	0.7974007	0 2914502	0.244943	RC_A 0.14640293 95_at	A4117	EST: zt67d11.s1 Soares testis NHT Homo sapiens cDNA clone 727413.3' mRNA seguence (from Genhank)
			1			RC. AA2626	FST: 7521h09.51 NCI CGAP GCB1 Homo sabiens cDNA clone
829	829 CNS	0.7971985	5 0.2914463	0.244917	0.14635049 59_at	59_at	IMAGE:685817 3', mRNA sequence. (from Genbank)
			1	177.00	100170077		EST: 43h8 Human retina cDNA randomly primed sublibrary Homo
830	830 CNS	0.797021	0.2914377	0.244781	0.14631/6Z WZ8Z35	WZ8Z35_at	Sapiens CUNA, MKNA sequence. (Iloni Genbank)

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1 353 14 3, HINNA Sequence. (from Genbank)				
RC_AA4061 EST: zu20a06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	0.243839	0.2905922	0.7941078 0.2905922	849 CNS
RC_AA2281 ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha 0.14520562 22_at polypeptide, 70kD, isoform 1	0.243854 (0.2906041	0.7941172	848 CNS
	0.243908	0.2906424	0.7941307	847 CNS
0.14531973 68_at sequence. (from Genbank)	0.243945 (0.2906865	0.7941835	846 CNS
EST: zs82a03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone				
0.14535981 40 s_at ADP-ribosylation factor-like 2	0.244013	0.2907926	0.7942234	845 CNS
	0.244013	0.2908313	1	844 CNS
	0.244031	0.2908929	0.7947477	843 CNS
0.1455829 C01750_at sequence, mRNA sequence, (from Genbank)	0.244186	0.2909977	0.7947549	842 CINS
ADAP III MCCOASS II (from Genbank)	2			
A2816	0.944072	0.2940888	0.7948155	841 CNS
0.14573152 M24899_at viral (v-erb-a) oncogene homolog)	0.244289	0.29111	0.7950217	840 CNS
0.14580399 t clone 784160 5', mRNA sequence. (from Genbank)	0.244295		000100	
AA446785_a EST: zw89e05.r1 Soares total fetus Nb2HF8 9w Homo carriene cDNA		0.2044.00	0.7051386	839 CNS
0.14584789 55 s at Iclane 773235 3' mbn/ secures total fetus Nb2HF8 9w Homo sapiens cDNA	0.244485	0.2911394	0.7952884	838 CNS
1	0.244528	0.291157	0.7960093	837 CNS
0.14596465 C00100 at securing 2005724, Human Gene Signature, 3'-directed cDNA	0.244552	0.2911871	0.7962375	836 CNS
0.14597984 W28406_at_sapiens_cDNA, mRNA sequence. (from Genbank)	0.244574	0.2912249	0.7963432	835 CNS
0.146002 86_at cDNA clone 504316 3', mRNA sequence. (from Genbank)	0.244592	0.2912573	0.7965123	834 CNS
	0.244695	0.2912585	0.7965409	COLO COCO
RC AA4260 757254 31 circulates testis NHT Homo sapiens cDNA clone				1
	0.244712	0.2913662	0.796841	832 CNS
0.14626573 17 at clone 796954 3', mRNA sequence. (from Genbank)	0.244764	0.7969728 0.2914265	0.7969728	021 CN2
RC_AA4634 EST: zx71q06.s1 Soares total fetus Nh2HF8 9w Homo sanions annian			10001	934 CNIS

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. gent, pers, gent, press press press, const, gent, gent, gent, gent, all gent, pers, etc.,

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850 CNS	0.7938355	0.2904645	0.243827	X988 0.14511038 1_at	(98834_rna 1_at	X98834_rna Zinc finger protein Hsal2 gene extracted from H.sapiens mRNA for
851 CNS	0.7935988	0.2904433	0.243704	RC_A 0.14509714 40_s	RC_AA4548 40_s_at	EST: zx79d09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809969 3', mRNA sequence. (from Genbank)
852 CNS	0.7935311	0.2904395	0.24369	0.14499152 U43083	J43083_at-2	at-2 Guanine nucleotide binding protein (G protein), q polypeptide
853 CNS	0.7935311	0.2904395	0.243611	0.1449714 U43083 at	J43083 at	GNAQ Guanine nucleotide hinding protein (G protein) a polymontide
854 CNS	0.7934907	0.2904244	0.243564	RC_A 0.1449316 80_at	RC_AA2561 80_at	Dihydropyrimidinase-like 2
855 CNS	0.7931503	0.290382	0.243508	0.14490317 t	\A282702_a	AA282702_a EST: zt15d02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
856 CNS	0.7931114	0.2903816	0.2435	0.14483695	3C_AA6003	RC_AA6003 EST: ag04a07.s1 Gessler Wilms tumor Homo sapiens cDNA clone
857 CNS	0.7930369	0.7930369 0.2903816	0.24349	1	66762 at	Homo sabiens clone 23914 mRNA secretore
858 CNS	0.7929705	0.2903469	0.2434	RC_A 0.14468367 34_at	RC_AA0470 34_at	EST: zf50b11.s1 Soares refina N2b4HR Homo sapiens cDNA clone 380349 3', mRNA sequence. (from Genhank)
859 CNS	0.7929339	0.2903374	0.243243	0.14463335 t	AA258286_a t	Homo sabiens mRNA for KIAA0877 protein partial cde
860 CNS	0.792861	0.2903341	0.243189	0.14456643 16	_AA4437 at	EST: zw88c05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784040.31 mRNA sequence (from Centrally)
861 CNS	0.7928296	0.2902932	0.243116	0.14450252 t	248734_a	EST: hfe0796.seq.F Human fetal heart, Lambda ZAP Express Homo
862 CNS	0.79251	0.2902331	0.243076	RC_A 0.14443891 10_at	A4566	EST: 2X75b09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809561 3', mRNA sequence. (from Genbank)
863 CNS	0.7924936	0.2901875	0.243038	RC 0.14440922 24	_AA2243	EST: zr12e05.s1 Stratagene hNT neuron (#937233) Homo sapiens
864 CNS	0.7911196	0.2900868	0.242964	0 1443244 70	_AA4053	EST: zu66b01.s1 Soares testis NHT Homo sapiens cDNA clone
865 CNS	0.7910059			0.1442823 1.142390	to	742921 3, IIIRNA Sequence. (Ifom Genbank)
866 CNS	0.7906377	0.2899146	0.242785	0.144206 W28462	at	Secreted protein, acidic, cysteine-rich (osteonectin)
867 CNS	0.7903458	0.2899036	0.24278	0.14415523 t	7_a	EST: zv03b07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 752533 5', mRNA sequence. (from Genhank)
868 CNS	0.7901512	0.2896226	0.242776	RC_A 0.14411739 56 at	A0567	EST: zk81g03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489268 3. mRNA seguence (from Genhank)
869 CNS	0.7901413	0.2895369	0.242761	RC_A 0.14405075 82_at	A4004	EST: zu64g10.s1 Soares testis NHT Homo sapiens cDNA clone 742818 3', mRNA sequence. (from Genbank)
870 CNS	0.789775	0.2894742	0.242738	RC_A 0.14400978 62_at	A2911	EST: zs46d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700525 3', mRNA sequence, (from Genbank)

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871	cns	0.7897602	0.2893994	0.242658	RC_AA0859 0.14393917 18_at	9 H.sapiens HUNKLmRNA
872	872 CNS	0.789265	0.28926	0.242523	H19570_s_a 0.1438543 t	EST: yn59b03.r1 Homo sapiens cDNA clone 172685 5' similar to contains Alu repetitive element; contains PTR5 repetitive element; (from Genbank)
873	873 CNS	0.7889618	0.289226	0.242497	RC_AA6095 0.14383705 40_at	5 EST: af14h01.s1 Soares testis NHT Homo sapiens cDNA clone 1031665 3', mRNA sequence. (from Genbank)
874	874 CNS	0.7888299	0.2891739	0.242495	0.14379609 R61154_at	EST: yh10d07.r1 Homo sapiens cDNA clone 43071 5'. (from Genbank)
875	875 CNS	0.7886787	0.2891345	0.242455	0.14373153 H19378_at	EST: ym46e01.r1 Homo sapiens cDNA clone 51292 5'. (from Genbank)
876	876 CNS	0.788366	0.2891033	0.242418	0.14369497 C00180 f	0.14369497 C00180 f at Synantic divronnatein SC2
877	877 CNS	0.7875977	0.2890145	0.24214	0.1435807 D56558 at	H.sapiens mRNA for p40
878	878 CNS	0.7875876	0.2889892	0.242118	RC_AA2787 0.14356026 20 at	
879	879 CNS	0.7875552	0.288822	0.242063	0.14343849 L43631 at	Scaffold attachment factor (SAE-R) case nortial add
880	880 CNS	0.7875552	0.2887696	0.242044		
881	881 CNS	0.7875167	0.28875	0.242043	RC_AA0016 0.14324279.04 at	
						EST: zc91g02.r1 Pancreatic Islet Homo sapiens cDNA clone 338546
882	882 CNS	0.7873678	0.2886144	0.241954	0.14319625 W52581_at	
883	883 CNS	0.7871386	0.2885805	0.241944	AA024641 0.143086 t	AA024641_a EST: ze79a04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA to clone 365166 5', mRNA sequence, (from Genbank)
884	884 CNS	0.787109	0.2885481	0.24188	AA316272_a 0.14305142 t	
885	885 CNS	0.7868788	0.2885302	778176 0	RC_AA4289	1
886	886 CNS	0.7865008	1	0.241794	0.14294165 C02050 at	H.sapiens mRNA for nuclear protein SA-2 Homo sapiens mRNA for hete tribulin folding confector D
887	887 CNS	0.7864874	0.2885086	0.241785	0.14284727 t	AA278243_a EST: zs77b11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
888	888 CNS	0.7862121	0.2884736	0.241778	AA253232 0.14280447 t	AA253232_a EST: zr53e12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t
883	889 CNS	0.7861354	0.28836	0.241666	0.14276288 X81006 at	H.sapiens HCG I mRNA
890	890 CNS	0.7861137	0.2883279	0.24164	AA044781_ 0.14262506 t	AA044781_a EST: zk74b09.r1 Soares pregnant uterus NbHPU Homo sapiens t cDNA clone 488537 5', mRNA sequence. (from Genbank)
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				M. Thatt Tarist W. Thaist Sand	-	માતમ પાતા પાતા વાતરા પ્રતારે કેતા? કેતાય માતા પાતા પાતા પાતા પાતા પાતા પાતા પાતા
891 CNS	0.786096	0.7860966 0.2882715	5 0.241612	2 0.14256547 W37583 at	V37583 at	EST: zc10e03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321916 5' similar to contains Alu repetitive element;, mRNA seguence (from Genhank)
892 CNS	0.7858892	2 0.2882437	7 0.241604	0.14249413	AA436291_a t	
893 CNS	0.7857466	6 0.2882239	9 0.241551	0.14246006	RC_AA4026 37 at	
894 CNS	0.7856637	7 0.2882152	2 0.241537		779265 at	EST: yi84b08.r1 Homo sapiens cDNA clone 145911 5', (from Genbank)
895 CNS	0.7856381	0.2881519	0.241531	0.14233994	RC_AA1653 69 at	
896 CNS	0.7853615	0.2881504	0.241473	0.14225884	RC_AA4960 45 s at	
897 CNS	0.7850788	0.2881426	0.241455	0.14216	A131547_a	AA131547_a Homo sapiens phosphatidylinositol synthase (PIS) mRNA, complete to
898 CNS	0.7849888	0.2881242	0.241351	0.14213224	RC_AA2340 94_at	omorphism of the control of the cont
888 CNS	0,7843437	0.2881106	0.241334		at	Ribosomal protein 1 27
900 CNS	0.7843323	0.2881069	0.24131	0.14204784 H15219 at	1	EST: ym30f02.r1 Homo sapiens cDNA clone 49693 5'. (from Genbank)
901 CNS	0.7841904	0.288061	0.241258	RC_A 0.142023.74_at	80	
902 CNS	0.7841194	0.2880256		0.14196818 46	AA2555	EST. zr85c12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
903 CNS	0.7838343	0.2879909		0.141938031	5238_s_a	EST: yz/3112.r1 Homo sapiens cDNA clone 288719 5' similar to
904 CNS	0.7835919	0.2879909	0.24		A4764	Contrains Atu repetitive element;, (from Genbank)
905 CNS	0.7834707	0.2879443	0.241026	AB AB	2300_a	nomo sapiens cyclophilin-33A (CYP-33) mRNA, complete cds
906 CNS	0,7834551	0.2878872	0.241007	RC A 0.1418429 12 at	AA4790 I	RC_AA4790 EST: zu39e05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
907 CNS	0.783259	0.2878077	0.240985	0.14182705 87	A4465	EST: zw84e01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
908 CNS	0.7831872	0.2877817	0.240982	R5(0.14173692 t	R50247_s_a E	EST: yj58b01.r1 Homo sapiens cDNA clone 152905 5'. (from Genbank)
909 CNS	0.7828515 0.2877749	0.2877749	0.240955	RC_A 0.14173166 70 at	A4257	EST: zw47g06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
						one 113242 3, mKNA sequence. (from Genbank)

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					And the first of t	fig. fig. fig. fig. fig. fig. fig. fig.
910 CNS		0.7825069	0.2876664	0.240933	0.14169355 W28167 at	
911 CNS		0,7820613	0.2876557	0.240922	0.1416808448 at	Suppressor of actin mutations 2, yeast, homolog-like Suppressor of actin mutations 2, yeast, homolog-like
912 CNS		0.7818281	0.2876338	0.240778	0.14161229 t	
913 CNS	SNS	0.7817494	0.2875974	0.240768	RC_AA4418 0.14157207 00 at	
914 CNS	SNS	0.7816512	0.2875651	0.240735	RC_AA4238 0.14147417 38 at	
915 CNS	CNS	0.7815679	0.2874509	0.240735	RC_AA4960 0.14143275 48_at	
916	916 CNS	0.7815552		0.24073		
917	917 CNS	0.7814773	0.2874133	0.240678	0.14132595 U5/316	at GCND (HGCND) Bare
918	918 CNS	0.7814773	0.2873927	0.240617	0.14120653 U57316	0.14120653 U57316 at-2 Homo sapiens histone acetyltransferase (GCN5) mRNA, partial cds
919	919 C.N.S	0.781007	0.287369	0.240546	RC_AA4881 0.1411887 99_at	
	ON OCC	0 7808299	C	0.240521	AA247453_a 0.14109704 t	
920		0.7807418	1	0.240442		2 a EST: aa39b02.r1 NCI_CGAP_GCB1 Homo sapiens conversions and an arrange in IMAGE:815595.s1, mRNA sequence, (from Genbank)
921	921 CINS	0.1001.0	1		RC_AA2533	
922	922 CNS	0.7805461	0.2872551	0.240423	0.14104229 90 s at	Tetraspan 5
923	923 CNS	0.7802509	0.7802509 0.2872551	0.240411	0.14103632 77 at	
924	924 CNS	0.7800378	3 0.2871554	0.240378	RC_AA2825 0.1409082 21_at	
360	ONE CINC	0.779781		0.240331	RC_AA2620 0.14085378 32_at	
900		0.779748	9 0.287107	1		650
927	927 CNS	0.779635	0.7796359 0.2868305	0.240267	0.14064182 C01169	at Karyopherin alpha 4 (Importin alpha 3)
908	928 CNS	0.7793308	8 0.2868064	0.240184	0.14054224	
020	CNS	0.7792648	8 0.2867799	0.240166	0.14053299	מ
93(930 CNS	0.7790957	1	0.240022	RC AA1502 0.14048833 62 at	1502 EST; zl07e02.s1 soares pregnant uterus nom Cenbank) cDNA clone 491642 3', mRNA sequence. (from Genbank)
- Inches						

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					The first fi	E. C. C. C. C. C. C. C. C. C. C. C. C. C.
700	ONC	0.7787081	0.2866019	0.240016	0.14038512 02_at	clone 756981 3', mRNA sequence. (from Genbank)
2 6	2	0.7705206		0 240015	0.14038512 14 at	IMAGE:814210 3', mRNA sequence. (from Genbank)
932 CNS	NS.	0.7703730	- 1			EST: yx51a06.r1 Homo sapiens culva cione zozzon o (minima zozzon o kanala zozen o kanala zen
033 CNS	N.S	0.7784938	0.2865575	0.239996	0.14033404 N30998 at	-
200				0 230002	RC_AA599Z 0 1402985 11 at	Short-chain dehydrogenase/reductase 1
934 CNS	NS	0.//84/48	0.280301.0	0.50005		1
935 CNS	NS	0.7783558	0.2864201	0.23995	0.14029352 W26958 a	-
936 CNS	NS	0.778171	0.2863807	0.239937	0.14026922 36 s at P	Homo sapiens mRNA for KIAA0795 protein, partial cds Homo sapiens cDNA BE EST: #RR412 s1 Soares fetal heart NbHH19W Homo sapiens cDNA
937 CNS	NS NS	0.7778792	0.2863567	0.239931	0.14019565 95 at	
SINO	OIN	0 7774258	0 7774258 0 2863567	0.239911	RC_AAU3 0.14014171 54_at	
939 CNS	SNS	0.777338	0.777338 0.2863043		0.14006734 W27503 at	Homo sapiens mKNA for NIAA0013 process, particular cone
940 CNS	SNS	0.7773348	8 0.2862876	0.239794	0.13999467 82 at	
941 CNS	SNS	0.776992.	2 0.2862852	0	0.13997345 07 s. at	
942 CNS	SNS	0.776945	0.7769451 0.2862736	0.23964	0.1399609 M9725Z	at KALLIWAININ STRUCTURE TO STR
943	943 CNS	0.7769451	0.286258	0.239622	0.13986395	0.13986395 M97252 at-2 Kallmann syndrome 1 sequence
944	944 CNS	0.7768155	55 0.2862105	5 0.239479	0.1398353	49 at clone 810992 3', mRNA sequence. (from Genbank)
945	945 CNS	0.776715	15 0.286201	0.239459	0.13981009	clone 786058 3', mRNA sequence. (from Genbank)
946	946 CNS	0.7767122	22 0.2861985	5 0.239421	0.13974254	Homo sapiens mRNA for KIAA0639 protein, partial cds
947	CNS	0.776687		8 0.239379	RC_AA2800 0.13969864 32_at	
948	948 CNS	0.7766538	38 0.2861658	8 0.239275		
949	949 CNS	0.776552	0.28611	49 0.239275	0.13957366	
950	950 CNS	0.77650	0.7765047 0.2861035	35 0.239163	RC_0.1395410914	AA0592 381764 3' similar to TR:G508424 G508424 NEUROPHILIN: ;, mRNA sequence. (from Genbank)

FIG. 3W2

The principle of the control of the

0.776407 0.2860858
0.7763682 0.2860685 0.239107 0.1394616 47 at
0.7761444 0.2858928 0.239094 0.13941881 U35234
0.7761444 0.2857713 0.239066 0.13939281 U35234_at-2 Protein tyrosine phosphatase, receptor type, S
0.7758534 0.2857562 0.239064 0.13934022 98_at
0.7757993 0.285754 0.238992 0.13929884 W92836
0.7757189 0.2856855 0.238992 0.13917425 04 at
0.7755565 0.2856752 0.238785 0.13910772 77 at
0.7755209 0.285663 0.238785 0.13910772 76_at
0.7753943 0.2855165 0.238715 0.13906229 37 at
0.7753196 0.2854844 0.23862 0.13904567
0.7753158 0.2853704 0.238603 0.13896662_at
0.7751086 0.2853686 0.238579 0.1389276 80 at
0.7749978 0.2853333 0.238568 0.13891321 28_at
0.7748278 0.2852866 0.238559 0.1388707577 at
0.7745657 0.2852629 0.23853 0.13883941t
0.7744977 0.2852601 0.238499 0.13880026 59 at
0.7744122 0.2852188 0.23844 0.13876756 40_at
0.7739148 0.2852054 0.238428 0.1387426 W86706 at

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	10					EST: zv75e04.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759486 5' similar to contains Alu repetitive element; contains
070	0 7700000				AA452003_a ele	element MER22 repetitive element ;, mRNA sequence. (from
970 CN3	0.1738323			0.138625071	-	Genbank)
971 CNS	0.7737186		0.238368	0.13853648 S69790_at		Brush-1
9/2 CNS	0.7736881	0.2850699	0.238296	0.13845417 W69582 at		Homo sapiens mRNA for KIAA0696 protein, partial cds
973 CNS	0.7735992	0.2850409	0.238292	0.13840705 W26520_at		EST: 32g10 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
(AA26;	3028_a Hc	AA263028_a Homo sapiens malate dehydrogenase precursor (MDH) mRNA,
974 CNS	0.7733082		0.238261	0.13835496 t	급	nuclear gene encoding mitochondrial protein, complete cds
975 CNS	0.7731788	0.285026	0.238109	0.13832414 W27299 at	99 at Hc	Homo sapiens clone 23685 mRNA sequence
976 CNS	0.773162	0.2849931	0.238027	RC_A 0.13825244 90 at	A2922 Et	RC_AA2922 EST: zt51c08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725870 3', mRNA sequence. (from Genhank)
977 CNS	0.7726568	0.284988	0.237937	AA232 0.1382138 t	AA232156_a t	Insulin-like growth factor 2 (somatomedin A)
070	0 4100			RC_A	1437	EST: zw86e09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
9/8 CNS	0.7725179	0.2849739	0.237914	0.1381877 91 f at		clone 783880 3', mRNA sequence. (from Genbank)
979 CNS	0.772334	0.772334 0.2848958	0.237905	0.13813432 M28219	at-2	Homo saplens low density lipoprotein receptor (FH 10 mutant causing at-2 familial hypercholesterolemia) mRNA, 3' end
980 CNS	0.772334	0.2848958	0.237861	0.1380858 M28219 at		LDLR I ow density linourotein recentor (familial hynarchylaefarolamia)
981 CNS	0.7722658	0.2848463	0.237842	0.13806406 W27054 at		APOLIPOPROTEIN AI REGULATORY PROTEIN-1
GROCING	0.770949	10000100	7077600	AA30	4566 a Et	AA304566_a EST: EST17372 Aorta endothelial cells, TNF alpha-treated Homo
000 000	0.7701000	0.2040201	0.23/19/	1 3803005 1		sapiens cDNA 5' end, mRNA sequence. (from Genbank)
983 CNS	0.7721638	0.2848311	0.237741	0.13797128 D52791 at		Human clone iota unknown protein mRNA, complete cds
984 CNS	0.7721435	0.2847193	0.237675	RC_A 0.13793764 38_at	A3995	EST: zt88e11.s1 Soares testis NHT Homo sapiens cDNA clone 729452 3', mRNA sequence, (from Genbank)
985 CNS	0.771937	0.2847083	0.237637	0.13785812 R62894	,क	EST: yi11h08.r1 Homo sapiens cDNA clone 138975 5'. (from Genbank)
986 CNS	0.7718838	0.2846035	0.997694	RC_A	169	
			0.4.01	0.13/000103 s at	270	Gap Junction protein, alpha 1, 43kD (connexin 43)
987 CNS	0.7717063	0.2846898	0.237586	0.13776186 86_at	6177	E-51. 2130C12.51 30aftes NnHMPU 51 Homo sapiens cUNA clone 667606 3', mRNA sequence. (from Genbank)
988 CNS	0.7717017	0.2845522	0.237586	X58431 0.13769595 2_s_at	rna	HOX 2.2 gene extracted from Human Hox2.2 gene for a homeobox protein
989 CNS	0.7717017	0.2845313	0.237496	X58431 0.13767721 2_s_at-2	rna	HOMEOBOX PROTEIN HOX-B6::HOMEOBOX PROTEIN HOX-B6
0	01001110		0	RC_A	A1913	EST: zp88c05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 627272 3' similar to contains Alu repetitive element;,
aan CNS	0.7713846	U.Z845313	0.237412	0.13761114 36 at		mRNA sequence. (from Genbank)

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700	0	1				RC_AA4322	RC_AA4322 EST: zw69e03.s1 Soares testis NHT Homo sapiens cDNA clone
SNO LEE	אַמ	0.7713515	0.1713515 0.2844337	0.237373	0.13757862	92_at	781468 3', mRNA sequence. (from Genbank)
						RC_AA4120	
992 CNS	NS	0.7711845	0.7711845 0.2844117	0.237298	0.13754289 28_s_at	28 <u>.</u> s_at	Homo sapiens mRNA for Fe65L2, complete cds
	9	1				AF007165_a	AF007165_a Homo sapiens nuclear DEAF-1 related transcriptional regulator
SAS CNS	202	0.77710287	0.1710287 0.2843574	0.237275	0.13747811		protein mRNA, complete cds
	2	1				AA247455 a	AA247455_a EST: csg2890.seq.F Human fetal heart, Lambda ZAP Express Homo
000 488	20	0.1709872	0.7709872 0.2843531	0.237197	0.13747366		sapiens cDNA 5', mRNA seguence. (from Genhank)
L	9					RC_AA4372	RC_AA4372 EST: zv62b04.s1 Soares testis NHT Homo saniens cDNA clone
SNO CAR	NG	0.770958	0.770958 0.2843426	0.23715	0.13742611	78_at	758191 3', mRNA sequence. (from Genhank)
000	2	1				AA039762_a	AA039762_a EST: zf10a09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
CNIO	22	0.770297	0.770297 0.2842931	0.237146	0.13738962	٠	clone 376504 5', mRNA sequence, (from Genhank)
200	Q	0.4400040		1		RC_AA4468	RC_AA4468 EST: zw84h11.s1 Soares total fetus Nb2HF8 9w Homo sapiens CDNA
SAL CINO	02	0.1102819	0.284291	0.237111	0.13725737	58_at	clone 783717 3', mRNA sequence. (from Genbank)
Č	Ç	11	; ; ;				EST: yx80g06.r1 Homo sapiens cDNA clone 268090 5'. (from
SAC CINS	22	0.7701257	0.7701257 0.2842826	0.237099	0.1372234	0.1372234 N40320_at Genbank)	Genbank)
9NO 000	<u>o</u>	00 10077 0	00000	(RC_AA4421	RC_AA4421 EST: zw56h02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
0 666	2	0.7700138	0.1100138 0.2842288	0.236811	0.13717082 42_at	42_at	clone 774099 3', mRNA sequence. (from Genbank)
1000	Ç	1	6			RC_AA2566	RC_AA2566 EST: zr86g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
1000 CNS	2	0.7700077	0.1700077 0.2842197	0.236729	0.1370803 06_at	06_at	682614 3', mRNA sequence. (from Genhank)

FIG. 3Z

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1.3304546 0.6979361 0.61841	0.61841	0.61841 (_	0.61841 0.46926254 at	Galectin-4
0.9893228 0.6466596 0.573452	0.573452	0.573452 0	0	.43697375 U51095 at	0.43697375 U51095 at CDX1 Caudal type homeo box franscription factor 1
0.9447319 0.6240295 0.551708	0.551708	0.551708 0.4	0.4	0.42068958 X83228 at	LI-cadherin
0.9219171 0.6074118 0.539086	0.539086			10901852 M29540 at	0.40901852 M29540 at CARCINOEMBRYONIC ANTIGEN PRECURSOR
0.8310602 0.5984152 0.52723	0.52723			40071398 M35252 at	0.40071398 M35252 at TUMOR-ASSOCIATED ANTIGEN CO-029
0.7965425 0.5912129 0.520434	0.520434		0.	39418483 D14520 at	0.39418483 D14520 at GC-Box binding protein BTEB2
7 Colorectal 0.772929 0.5859177 0.514771 0.3	0.514771		0	38826877 X98311_at	0.38826877 X98311_at Carcinoembryonic antigen family member 2. CGM2
	-	-		X74929 s a	
0.7369248 0.5797341 0.509057	0.509057		0	0.38285961	KRT8 Keratin 8
9 Colorectal 0.710591 0.5760404 0.503801 0.3	0.503801		0.3	7822562 M10050_at	0.37822562 M10050_at HBG2 Hemoglobin gamma-G
					LGALS3 Lectin, galactoside-binding, soluble, 3 (galectin 3) (NOTE:
0.7019893 0.5677402 0.500434	0.500434			7441394 M57710 at	0.37441394 M57710 at redefinition of symbol)
11 Colorectal 0.6896882 0.5667345 0.495918 0.3	0.495918		0.3	7061206 L02785_at	0.37061206 L02785_at DRA Down-regulated in adenoma
					EST: zl74e07.s1 Stratagene colon (#937204) Homo sapiens cDNA
				RC_AA0536	RC_AA0536 clone 510372 3' similar to contains Au repetitive element., mRNA
12 Colorectal 0.6816363 0.5633355 0.491975 0.36	0.491975		0.36	0.36677584 60_at	sequence, (from Genbank)
				L08044_s_at-	
13 Colorectal 0.6661/32 0.5606063 0.488131 0.36401525 2		0.488131 0.3	0.3	64015252	Trefoil factor 3 (intestinal)

FIG. 4A

The design plant plant could be seen that the seen could be seen to be seen t

				# # # # # # # # # # # # # # # # # # #	The state of the s	then Hand and then	ng Arat de 1 i n Barat dati
14	14 Colorectal	0.6661732	0.557618	0.485725	0.3609329 108044	sat	TFF3 Trefoil factor 3 (intestinal)
4.	15 Colorectal	0 6645613	0.5556119	0.483527	0.35857078	U07969_s_a	Intestinal peptide-associated transporter HPT-1 mRNA
18	16 Colorectal	0.6597598		0.481477	0.3561044 X12901 at	X12901 at	VILLIN
1,	17 Colorectal	0.6488326	0.6488326 0.5484788	0.478819	0.3537182		Rhodanese
1,8	8 Colorectal	0.6443836	0.5457429	0.476623	0.351588 t	155998_s_a	Alpha-1 colladen type I gene. 3' end
1	10 Coloractal	0.630657	1	0.4746	0 340E0E8E M77340	7	Transforming growth factor-beta induced gene product (BIGH3)
-	Coloracta	0.00000	0.0410302	0.474	0.04909000	ĕ	MA IOD CASTDOINTESTINAL TIMOD ASSOCIATED DECTEIN
7	20 Colorectal	0.6345016	0.5388692	0.472279	0.34737322 M93036_at		MAJOR GASTROINTES TINAL TOMOR-ASSOCIATED PROTEIN GA733-2 PRECURSOR
2,	21 Colorectal	0.6183873	0.5373365	0.470427	0.34542933 X93036 at		MAT8 protein
2,	22 Colorectal	0.6162866	0.5337368	0.468914	0.34354696 X16354	at	BGP Biliary glycoprotein (alternative products)
2.	23 Colorectal	0.6135939	0.5322881	0.467634	0.34195346 X79882	at	Lrp mRNA
24	4 Colorectal	0.604686	0.5295914	0.466112	0.34027967 X68314	at	GPX2 Glutathione peroxidase 2, gastrointestinal
25	5 Colorectal	0.5409228	0.5289235	0.464264	0.3388225 t	(12876_s_a	KRT18 Keratin 18
26	26 Colorectal	0.5346139	0.5278842	0.463016	0.3370235 L03840	S	at FGFR4 Fibroblast growth factor receptor 4
2.	27 Colorectal	0.5314592	0.5263897	0.461656	0.33576262 J04469 at		Mitochondrial creatine kinase (CKMT) gene
						a.	middle deal of the control of the co
5	28 Colorectal	0.5262153		0.459832	0.33431423 t		Alpha-1,3 fucosyltransferase 6 (FCT3A) mRNA
72	29 Colorectal	0.5178417	0.5230292	0.458503	0.3330468 X73501		at-2 KERATIN, TYPE I CYTOSKELETAL 20
స	30 Colorectal	0.5178417		0.457537	0.33154407 X73501	X73501_at	KERATIN, TYPE I CYTOSKELETAL 20
ઝ	31 Colorectal	0.5177953		0.455465	0.33026433 U51096	U51096_at	Homeobox protein Cdx2 mRNA
3	32 Colorectal	0.5161443	0.5194929	0.453944	0.32879257 L23808_at	L23808_at	MMP12 Matrix metalloproteinase 12 (macrophage elastase)
က်	33 Colorectal	0.5147349	- 1	0.452769	0.32764837 L20826_at		I-plastin mRNA
ř	34 Colorectal	0.5127617	0.5174283	0.452021	0.32639337 X54925 at		MMP1 Matrix metalloproteinase 1 (interstitial collagenase)
	35 Colorectal	0.5402813	0.5169292	0.450713	RC_A 0 32528314 71 at	A2534	EST: zr77g09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 860472 3' mBNA sequence (from Genhank)
) ×	36 Colorectal	0.5056632		0.449718	0.32434413 L10343 at	L10343 at	PI3 Protease inhibitor 3, skin-derived (SKALP)
37	7 Colorectal	0.5009919	1	0.448466	0.3232134	0.3232134 X05232 at	MMP3 Stromelysin
			1			HG2788-	
ñ	38 Colorectal	0.4974572	0.5122448	0.447924	0.32208204 HT2896	HT2896_at	Calcyclin
 	39 Colorectal	0.4731978	0.5109233	0.446611	0.32114545 U78556_at	U78556_at	Cisplatin resistance associated alpha protein (hCRA alpha) mRNA
7	40 Coloractal		0.4665764 0.5403841	0.445483	0 31003556	L41668_rna1	IIDD-Galactoce 4 enimerace (GAI E) gene
T A	41 Colorectal	-	0.4652342 0.5193541	0.445063		1153786 at	EVPI Envonlakin
	י ספוסו כמומו	2T0200T.0	0.00000	0.77	710000100	20000	LVI L LIVO DIGNIII

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th trial that Tarif	PI5 Protease inhibitor 5 (maspin)	RPS3 Ribosomal protein S3	NCA Non-specific cross reacting antigen	HTR7 5-hydroxytryptamine (serotonin) receptor 7 (adenylate cyclase-	IM Improp	INTERFERON-AI PHA INDITIOED 41 6 KD BBOTTEIN	EST: zo26h055. Stratagene colon (#937204) Homo sapiens cDNA	cione podub/ 3, mKNA sequence. (from Genbank)					o sapiens cDNA		Gamma-glutamyl hydrolase (hGH) mRNA	Claudin 4		Osteoblast specific factor 2 (OSF-2os)	EST: zl79c09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510832 31 mRNA segrence (from Genhank)		IPL (IPL) mRNA	RNA	22kDa smooth muscle protein (SM22) mRNA		Nr-E2-related factor 3	Pyridoxal Kinase mKNA	SRI Sorcin	DOC Doba decarboxylase (aromatic L-amino acid decarboxylase)	SFN Stratifin	Epithelial-specific transcription factor FSF-1h (FSF-1) mRNA	Human N-benzoyl-L-tyrosyl-p-amino-benzoic acid hydrolase alpha subunit (PPH alpha) mRNA, complete cds	s at Cytochrome P450 euptamily IIIA (ninbodining controller)	o annotation and amount in a full full full file oxidase), polypeptide o
Sort Tren Trees nearly no			M18728_at	U68488 at	U21128 at	X67325 at	RC_AA1349	8	S71043_rna	1 s at	RC_AA1310	L21998 at	RC_AA1349	0.308260 1155206 of	033200 at	at	D13666_s_a	_	RC_AA1000 26_at	AF001294_a	4.0	0.3047288 U42408_at	M95787_at	RC_AA1325	מושל של	Coscoo at	0.3019815 M32886 at	X57348 s_a			_AA4541 s_at	J04813 s at	
hulf gr. turn tare	0.31810844	0.3172188 J04164	U.3161517 M18728	0.31544325 U68488	0.31469578 1121128	0.31340513 X67325	0.3125313 RE_A	2001		0.31138095 1 s at	0.3107684 47	0.31014428 L21998 at	RC_A	0.308269	0.500503	0.30752197	0.0000	0.30693734 t	RC 0.30608693 26		0.3053618 t	0.3047288	0.30399632 M95787	0 30328473 23	0.3036384 Honene	0.0020001	0.3019815 M32886		0.30097124	0.3003053 U73843 at	0.29989058 13	0.29939732 J04813	
	0.44383		0.442532	0.441531	1	1	0.438598		70070	0.438107	0.437162	0.436568	0 43558	0.434647		0.433883	0.4000	0.433330	0.432558		0.431647	0.431022	0.430292	0.429676	0 429105	0 428444	0.427544		0.427.107	0.426731	0.425976	0.425471	
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0 4642504	0.4639263	0.458070	0.430020	0.4568794	0.449968	0.4476498	0.4458659		0.4447822	7701111	0.442524	0.439528	0.4371672	0.4348819		0.4298149	0.4282036	0.75070	0.4248353	0.404040	0.4240332	0.414/611	0.4033880	0.4092692		0.4080049		0.4005646		0.3961033	0.3958408	0.3938758 0.4906323	
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usan Yunt Kant Kan	RC_AA4043 EST: zv63a12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 38 at clone 758302.31 mRNA sequence (from Genhank)	Not56-like protein		Keratin 8	Phospholipase C. hata 4	Protein tyrosine phosphatase mRNA	EST: ze76a01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	Civile 304872.3, mKNA sequence. (from Genbank) EST: aa91c07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA	clone 838668 3', mRNA sequence. (from Genbank)	GLUL Glutamate-ammonia ligase (glutamine synthase)	EST: zo20g08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587486 3' similar to SW:MDCE_MOUSE P21271 MYOSIN-LIKE	PROTEIN: , mRNA sequence. (from Genbank)	STUGATU STUU CAICIUM-DINGING Protein A1U (annexin II ligand, Calbactin I. light polynentide (n111)	ARP1 Amiloride hinding protain 1 (amino exidence)	OIAS (2'-5') olicoadenviate synthetase	Non consolitio creational and the consolition and the creation and the cre	ITGB4 Integrin beta-4 subunit	Paired-like homeodomain transcription factor 2	EST: yw28e07.r1 Homo sapiens cDNA clone 253572 5'. (from Genhank)	EST: EST83940 Parathyroid gland tumor I Homo sapiens cDNA 3'	IFX.1	EST: zr71a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668824.3° mRNA sequence (from Conhank)	ANX2 Annexin II (lipocortin II)	0.28911367 M34516 r at Omega light chain protein 14 1 (Ig lambda chain related) gene even 3	Homo sapiens mRNA expressed in thyroid pland
thet tun ted tend mad tad tad tad	RC_AA4043	0.298146 Y09022 at	AA443499 f	at	RC_AA2428	0.2963615 L77886 at	RC_AA0244	RC_AA4572 I	35 at	Mo3438_s_a t	RC_AA1325	24 at	M38591 at	U11862_s_a t	0.2933345 X02874 at	RC_AA1007	X53587 at		H89551_s_a	A3720	4 at	5629	D00017 at	M34516 r at	RC_AA2563 65_s_at
ii duri lind is faul hui.	RC_A 0.2987325 38_at			0.29754966	RC_A 0.29705 19_at	0,2963615	0.20500002	0.59599900	0.295498 35 at	0.2950936 t	0.0046000	0.£340£23 34 at	0.29408625 M38591	0.2937528+	0.2933345	RC_AA1	0.29226494 X53587	RC_AA6 0.2918897 79 s at	0.29132295	RC_A 0.29090998 18 at	0.2904227 S81914	0.2899723 43	0.28951192 D00017	0.28911367	RC_AA2 0.28869188 65_s_at
10, 13		0.423703		0.423178	0.422642		0.424063	0.24	0.421373	0.42087	0.420502		0.420144	0.419905	0.419346	0.418853	0.418217	0.417771	0.417505	0.416981	0.416761	0.416175	0.415651	0.415184	0.414942
	0.4900717	0,4894687		0.4893894	0.4882457		0.4864893	1	i	0.4858298	0.4853050		0.4846798	0.4844075	0.483671	0.4823856	0.4818361	0.4804687	0.4795685	0.4783426	0.4776064	0.4771514	0.4769289	0.4762957	0.4760904
	0.3937155	0.3925914		0.3919728	0.390575	0.3899017	0.3869763	0.3860436	0.000012	0.3857464	0.3840961	0001000	0.3831372	0.3798282	0.379074	0.3790067	0.3773377	0.3702305	0.3644778	0.3638102	0.3617361	0.3590579	0.3587444	0.3571036	0.355448
	68 Colorectal	69 Colorectal		70 Colorectal	71 Colorectal	72 Colorectal	73 Colorectal	74 Coloractol	500	75 Colorectal	76 Colorectal		77 Colorectal	78 Colorectal	79 Colorectal	80 Colorectal	81 Colorectal	82 Colorectal	83 Colorectal	84 Colorectal	85 Colorectal	86 Colorectal	87 Colorectal	88 Colorectal	89 Colorectal

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Steph With Wind	Tumor necrosis factor type 1 receptor associated protein (TRAP1) mRNA, partial cds	at COI 142 Collacen time I sinke 3	CD89 gene, expn S1	RPS3 Ribosomat protein S3	Dataceiim Channal Bestrie (OL 714 For)	orassium crianner Protein (GD:Z11585)	Melanoma growth stimulatory activity (MGSA)	M87789_s_a (hybridoma H210) anti-hepatitis A IgG variable region, constant	ASS Arainpermentally-determining regions mRNA	Processin m DNA	Hostophic arteriations	Gind Jacob home in the Otoxin receptor mKNA	A DLIA A CINCIE	ARNS Aplysia ras-related homolog 9	Ass amigen precursor mKNA	DPEP1 Dipeptidase 1 (renal)	EST: zo72c02.s1 Stratagene pancreas (#937208) Homo sapiens	cDNA clone 592418 3' similar to TR:G1199669 G1199669 PROTEIN	KINASE C-BINDING PROTEIN BETA 15.;, mRNA sequence. (from	Genbank)	ERBB3 V-erb-b2 avian erythroblastic leukemia viral oncogene	homolog 3 (alternative products)	20-kDa myosin light chain (MLC-2) mRNA	KIAA0152 gene	Pyruvate dehydrogenase complex (PDHA2) gene		COL3A1 Alpha-1 type 3 collagen		OCE IOAT gene for collagen (alpha-1 type X)	PI CRA Dhomhaliman C hata 4	EST: 740h02 s1 Soares pregnant utorus NikuDi Licens	cDNA clone 504435 3, mRNA sequence. (from Genbank)
ingeriff threes their centil centil their three	U12595_at	C.	a l	X57351_s_a t	HG2239- HT2324 at	(<u>8</u>	1_at	M87789 s a	X01630 at	41351 at	M73489 at	X87342 at	δ, t			ja,			A1595			ਗ਼				X06700_s_a		882_rna			428	
Ha R. Marth Bearly	0.2882023 U12595	0.28780922 274616	0.28752562 X87767	0.287160251	HG2239 0.28667745 HT2324		0.28619328 1_at	0.285816731	0.2852261 X01630 at	0.28488582 41351	0.28456652 M73489	0.2843162 X87342 at	0.28386307 25084	0.28356016 1170725 at	010000000000000000000000000000000000000	0.2831329 J05257				0.282/8688 01 at	700000	0.282416/ M34309	0.28186926 JU2854	0.28154293 D63486_at	0.28122646 M86808 at		0.28081584	0.2805408 1 at	0 28016385 585655 24	0.279888751.41349		0.27941817 49 at
al, 1324; 9	0.41475	0.414083	0.4135	0.412799	0.412449		0.412154	0.411772	0.411117	0.41076	0.410335	0.410025	0.409773	0.408981	0 4000 EE	0.400050			1900000	0.408305	0070	0.400	0.407070	0.40/0/3	0.406902	0.406000	0.406638	0,406117	0.405724	0.405248		0.405215
	0.4758498	0.4754698	0.3494644 0.4751242	0.4731991	0.4731492		0.4731211	0.472999	0	0.4719834	0.4712013	0.4704531				0.4033001			0.4608622	0.4090033	0.4693615	0.105501.0	0.4001.001	0.4003466	0.407.9911	701878107	0.4076407	0.4665029	0.4662139	0.4660988		0.465658
	0.3529292	0.3526995	0.3494644	0.3475012	0.3461418	7.00	0.345887	0.3454008	0.3453316	0.3439322	0.3426999	0.3426407	0.3403187	0.3398675	0.3396676	0.00000			0 3390883		0.3363895	0.335006	0 3345019	0.3330034	0.3330031	0 3337304	0.0001.004	0.332153	0.3313465	0.3309523		0.3309307
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1411-1411-1411-1411-1411-1411-1411-141	EST: zx97c05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 811688 3' similar to SW:RB25_RABIT P46629 RAS-RELATED PROTEIN RAB-25 mRNA sequence (from Garbart)	N-benzoyl-L-tyrosyl-p-amino-benzoic acid hydrolase alpha subunit	(FFIT alplied) IIIKIVA	AND A Making at the same	ALDIZ Aldenyde denydrogenase 2, mitochondrial	Neks Inkiva for protein kinase	Kinase Δ anchor protein	EI 173 Alabo (4 2/4 4) £	EST: af61a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	offord 3, III King Sequence. (Ifom Genbank)	Olfactory Receptor Or17-210		EST: 2/46a03.s1 Soares pregnant uterus NbHPU Homo sapiens	Caldizzarin	Interferon-induced lought original contraction of the contraction of t	EST: yu26c05.r1 Homo sapiens cDNA clone 234920 5'. (from Genhank)	EST: zw26d12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770423.31 mRNA santance (from Garbaria)	OVD3A7 Ottober 1 11 11 11 11 11 11 11 11 11 11 11 11	Cell surface protein HCAR mRNA	Mana light choir sectors 44.4 (1-1-1-1)	Vsonhosphatidic acid acultransferre Ed. (19 lambda chain related) gene, exon 3	Thyroid recentor interactor (TDID10) Thyroid recentor interactor (TDID10)	ANX3 Annexin III (linocartin III)	Solonium bir die	CATHEDSIN K DDECLIDEOD	CALLIET SIN N PRECUROLA
N. 110134 '1014' 10151' '1111'	RC_AA4638 61 at	M82062 at	- 17	- 11	41	X65614 at	0.2771918 X97335 at	U27326_s_a	AA6211	HG4115-	HT4385_at	AA147510_s at	A1506	33 at	s,		A4306	D00408_s_a	at		1			A2906	3.24	5
	RC_A 0.2790749461 at	0.27874827 1482962	0.2784384 M14218	0 27809417 X05409	0 2778419	0.2775136 X65614	0.2771918	0.27693212	RC 0 27653858 34		0.27603555 HT4385 at	0.27578703	RC_A	0.27525836 D38583	0.27491027	0.27458924 H78628 at	RC_A 0.27425927 74 at	0.2739331	0.2735841 U90716	0.27337873 M34516 at	0.27305278 U56418	0.27280134 L40379 at	0.27248895 L20591 at	0 27219298 79 at	0.27192706 X82153	1-2-1-1
	0.405046	0.404425			1		0.402542	0.402366	0.40199		0.401657	0.401187	0.400854	0.400546	0.400246	0.399963	0.399575	0.399164	0.398937	0.39867	0.39844	0.398107	0.397758	0.397164	0.396861	
	0.4649201	0.3265352 0.4645526	0.3253648 0.4636824	0.3246478 0.4634886	0.4632541		0.4625747	0.4622362	0.4621217	Į.	0.4618764	0.4615341	0.4614542	1 [0.4604949	0.460224	0.4601988	0.4598908	0.4597153	0.459702	0.4593249	0.4590579	0.4584834	0.4581681	0.4574646	
	0.3291652	0.3265352	0.3253648	0.3246478	0.3246213	0.3245217	0.3238286	0.3229135	0.322097		0.3202075	0.3202045	0.3201549	0.3193956	0.3180397	0.3174135	0.3153257	0.3151839	0.3145525	0.3144143	0.3142386	0.3121006 0.4590579	0.3117978	0.3106408 0.4581681	0.3104196	
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AD000684_c from Homo sapiens DNA from chromosome 19-cosmid R30879 ds1 at containing USF2, genomic sequence	PCK1 Phosphoenolpyruvate carboxykinase 1 (soluble)	VDR Vitamin D (1,25- dihydroxyvitamin D3) receptor	RARS Arginyl-tRNA synthetase	EST: zp74c05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 625928 3', mRNA sequence (from Genhank)	EST: Zx87d04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810727.31 mRNA semience (from Genhank)	de la constant de la	Tubulin, Beta 2	Homo sapiens KIAA0424 mRNA, partial cds	Clone HSH1 HMG CoA synthase mRNA, partial cds	Laminin S B3 chain (LAMB3) gene		clone 773841 3', mRNA sequence. (from Genbank)	LCAT Lecithin-cholesterol acyltransferase	PYGB Glycogen phosphorylase B (brain form)	ITGB1 Integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2 MSK12)	Home acaism characters 1	Tionilo sapiens cindinosome 19, cosmid R28784	EST: HUMGS0003443, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)	EST: zw19c12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 769750 3' similar to contains element MER22 repetitive element mRNA sequence (from Genhank)	EST: af61h05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	1046553 3', mRNA sequence. (from Genbank)	BENE mRNA, partial cds	EST: zv64c05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 758408 3', mRNA sequence (from Genhank)	EST: zx89h11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 810981 3', mRNA sequence. (from Genbank)	High molecular weight B cell growth factor mRNA sequence	LTBP1 Latent transforming growth factor hata hinding protein 4	בי בי בתכנית תמוסיסיייים איסאיני ומסיסי חבים חוומוווא אוסופוויי
AD000684_c	0.2714976 L05144 at	0.27115154 J03258 at	0.2708481 S80343 at	RC_AA1868 0.27061194 97_at	RC_AA4577 0.2703553 18 at	HG1980-	0.27002838 HT2023_at	0.26973784 W27721 at	0.26945966 X83618_at	U17760_rna 0.26923937 1_at	A4275			U47025_s_a 0.26832888 t	0.26817298 X07979 at	RC_AA3992	9	C00038_s_a 0.26754314 t		0.26732546 90 at	A6211			0.2665894 03_at	44594		0.2661315 L15344 at 0.26588395 134683 at 0.26588395 134683 at 0.26588395 134683	ज ज	1
0.27	0.2	0.27	0.2	0.27	0.2		0.27	0.26	0.26	0.26		0.26	0.26	0.26	0.26	0.26		0.26		0.267		0.26	0.70	0.26		0.2	0.26	0.26	
0.396583	0.396073	0.395992	0.395825	0.395391	0.395019		0.394745	0.394414	0.394342	0.394139		0.393862	0.393468	0.393296	0.392712	0.392651		0.392145		0.391782	77700	0.391414	0.331373	0.39108		0.390989	0.389813		
	1	- 1	0.4562675	0.4562675	0.4560627		0.4555158		0.454/286	0.4546229		- 1	0.4541483	0.4539721	0.4536237	0.4532687		0.4529879		0.4526705	7077	0.4525525	0.4316331	0.4517718	07.007.0	0.4512370	0.4509095	0.4503436	
0.3085437	0.3082213	0.3080792	0.3077637	0.3052971	0.3052922		0.3033279	0.3019452	0.300895	0.2979128	0.9070944	0.2370000	0.2976009	0.2964177	0.2960429	0.2944463		0.2905926		0.2904404	0.2000507		111107.0	0.2893714	29000000	0.2880846 0.4512378	0.2879694 0.4509095	0.2874484	
138 Colorectal	139 Colorectal	140 Colorectal	141 Colorectal	142 Colorectal	143 Colorectal	100	144 Colorectal	145 Colorectal	140 COIOI ectal	147 Colorectal	Coloroctol	140 Colorectal	Colorectal	150 Colorectal	Colorectal	152 Colorectal		153 Colorectal		154 Colorectal	155 Coloractal	156 Colorectal	1000000	Colorectal	158 Colorectal	159 Colorectal	160 Colorectal	161 Colorectal	
138	<u> </u>	4	14	14;	14.	7	146	7 7	14(147	148	£ 5	±	150	151	152		153		154	7.77	156	2	157	158	150	38	161	

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Genetic Markers for Tumors Title: Inventors: Sridhar Ramaswamy, et al. RC_AA0253 EST: ze74h04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA AA090778_a EST: yy0416.seq.F Fetal heart, Lambda ZAP Express Homo sapiens X97675_rna Plakophilin 2a gene extracted from H.sapiens mRNA for plakophilin RC_AA3941 | EST: zt52g05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA PPGB Protective protein for beta-galactosidase (galactosialidosis) EST: 46g7 Human retina cDNA randomly primed sublibrary Homo ETV4 Ets variant gene 4 (E1A enhancer-binding protein, E1AF) H89896_s_a EST: yw29e12.r1 Homo sapiens cDNA clone 253678 5'. (from 0.2644313 T62771_s_at Homo sapiens nucleoplasmin-3 (NPM3) mRNA, complete cds clone 364759 3', mRNA sequence. (from Genbank) clone 726008 3', mRNA sequence. (from Genbank) ITPR3 Inositol 1,4,5-triphosphate receptor, type 3 TPM1 Tropomyosin alpha chain (skeletal muscle) sapiens cDNA, mRNA sequence. (from Genbank) FATTY ACID-BINDING PROTEIN, INTESTINAL TDGF1 Teratocarcinoma-derived growth factor 1 Lysyl oxidase-related protein (WS9-14) mRNA cDNA 5', mRNA sequence. (from Genbank) SDC4 Syndecan 4 (amphiglycan, ryudocan) Clathrin, Light Polypeptide B, Alt. Splice 2 Endogenous retroviral protease mRNA RNA for type VI collagen alpha3 chain HOK-2 mRNA for zinc finger protein RAS-RELATED PROTEIN R-RAS Amplaxin (EMS1) mRNA ACY1 Aminoacylase 1 Serine kinase mRNA MLN137 mRNA XMP mRNA Genbank) 2a and b HT2906_s_a 0.26524404 M22960_at 0.26505816 U18018 at D79206_s_a X14253_s_a 0.26396865 X82125 at 0.2635816 X81420 at 0.26333362 U52100 at 0.26256222 U01062 at 0.26241365 M14949 at 0.2621385|X52022 at 0.26181865 M98343 at 0.26109293 M18079 at 0.26043087 W28414 at 0.26166266 U09564 at 0.26088074 U89942 at 0.2596775 M27826 at 0.26140434 Z24727 at 0.2602868 L07548 at HG2797. 0.26379237|52_at 0.2631192|21 at 0.26419505 0.26473483 0.26288193 0.25948972 0.26068738 0.25991017 0.389084 0.38901 0.388819 0.388603 0.388128 0.38927 0.388014 0.3874 0.387096 0.388407 0.387653 0.386690.38613 0.385698 0.385651 0.385072 0.384312 0.38521 0.383468 0.382959 0.384364 0.383921 0.383729 0.384537 0.383229 0.2868318 0.4493014 0.286018 | 0.4488575 0.2854559 0.4487699 0.4498679 0.2863423 0.4492515 0.2842561 | 0.4486165 0.2842944 0.4487521 0.4482635 0.2760558 0.4445678 0.2838166 0.4480006 0.2825118 0.446785 0.2777302 0.4450202 0.2826245 0.4473684 0.2821878 0.4466844 0.2817878 0.4464111 0.2797018 0.4460374 0.2795155 0.4457014 0.2794765 0.4454948 0.2790382 0.4452392 0.2775453 0.4446172 0.2830422 0.4479057 0.2784429 0.4450501 0.2758695 0.4432321 0.2744746 | 0.4427031 0.2758841 | 0.4436831 0.2873887 0.284068 162|Colorectal 163 Colorectal 167 Colorectal 170 Colorectal 164|Colorectal 165 Colorectal 166|Colorectal 168 Colorectal 169 Colorectal 171|Colorectal 172|Colorectal 173|Colorectal 175 Colorectal 176 Colorectal 177 Colorectal 178 Colorectal 174 Colorectal 179 Colorectal 181 Colorectal 183 Colorectal 185 Colorectal 186 Colorectal 180 Colorectal 182|Colorectal 184|Colorectal

Docket No.:

2825.2020-002

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ताम प्रापा प्रमाण मुख्य	Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid			IMAGE:746031 3', mRNA sequence, (from Genbank)	Selenium-binding protein (hSBP) mRNA	EST: zv18a05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	753968 5', mRNA sequence. (from Genbank)	EST: zo31d08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588495.31 mRNA sequence (from Genhank)	Timor sunoressing subtransferable candidate 3	omo sapiens cDNA	luence. (from Genbank)	NIAAU III gene, partial cds Overbing professor	Activated T-cells I Homo sapiens cDNA 5' end,		Promoting the september of the september	AA074933_a cDNA clone 544693 5' similar to gb:J04794 ALCOHOL DEHYDROGENASE (HUMAN): mRNA seminance (from Genhank)	EST: zw17h06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA		IMAGE:683339 5', mRNA sequence. (from Genbank)	INCENTIFICATION OF THE PROPERTY OF THE PROPERT	G9 dene encoding statistase	JTV-1 (JTV-1) mRNA	Variant urokinase plasminogen activator receptor (uPAR2) mRNA, partial cds	MHC class II DO-alpha mRNA, partial cds	FN1 Fibronectin 1	(clone 35.3) DRAL mRNA
And Acres Seed works and Arely Links Their		U79549_rna	RC AA4820	15_at	0.2587583 U29091 at	AA479990_a	+1	RC_AA1437 63_at	AA056958_a	_AA4044	8/ at	0.25727057 D55696 at	AA298786_a	H46617 at		AA074933_a t	RC_AA4259 06_at	4	1 to 044774	116842 at		U24169_at	X74039 at	M29335 at	X02761_s_a t	
Rant tage if the tage		0 25922918 1	0.23322310	0.25900492 15_at	0.2587583		0.25852776	RC 0.25829273 63	0.25806381	7000770	0.23/89955 8/_at	0.25727057	0.2571191	0.2569419 H46617		0.256775381	0.25657907 06	0.05007400	0.250371321	0.255945 1116842	0.25564706 X78687	0.25546265 U24169 at	0.25539052 X74039	0.25512356 M29335	0.25493538	0.25460264 L42176 at
dad "H		0.382903	0.00200		0.382073		0.382073	0.38191	0.381861	0.284045	0.381413	0.381157	0.380887	0.380592		0.380361	0.38018	0000086	0.379693	0.379252	0.378853	0.378731	0.378718	0.378664	0.378569	0.378164
		0.4426029			0.4423659		0.4422453	0.4420108	0.4420007	0 444814			0.4413927	0.4412214		0.4409944	0.44089	0.4408184	0.4406756	0.4403952	0.4401701	0.4401267	0.4400005	0.4393005	0.4384362	0.4384202
		0.2738329	7200	0.2723998	0.2716996		0.2699324	0.2699285	0.2698754	0.2696778	0.2695739	0.2692404	0.2686886	0.2669644		0.2665602	0.26581	7907890	0.2629061	0.2627252	0.2626974	0.26179	0.2617015	0.2615691	0.2610115	0.2609527
		187 Colorectal		188 Colorectal	189 Colorectal		190 Colorectal	191 Colorectal	192 Colorectal	193 Colorectal	194 Colorectal	195 Colorectal	196 Colorectal	197 Colorectal		198 Colorectal	199 Colorectal	200 Colorectal	201 Colorectal	202 Colorectal	203 Colorectal	204 Colorectal	205 Colorectal	206 Colorectal	207 Colorectal	208 Colorectal
		187		188	189	2	180	191	192	193	194	195	196	197		198	199	200	201	202	203	204	205	206	207	208

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CCT. +007-10 -11 CTT - 11 CTT - 10 CTT - 11 C	gb:M55542 INTERFERON-INDUCED GUANYLATE-BINDING DROTFIN 1 (H) IMANN: (from Goobser)	TO THE TOTAL OF THE CONTRACTOR	H.sapiens DNA for cyp related pseudogene	TST Thiosulfate sulfurtransferase (rhodanese)	Glutamine transaminase K	FTL Ferritin, light polynentide	Homo saniens Chromosome 16 RAC clone CITG87SK-A-67A1	CYC1 Cytochrome c-1	EST: zl70b07.s1 Stratagene colon (#937204) Homo sapiens cDNA		C BETA 4.;, mRNA sequence. (from Genbank)	TNNC2 Troponin G2 (fast skeletal)	HSPD1 Heat shock 60 kD protein 1 (chaperonin)	Ras-Related C3 Bott tilinum Toxin Substrate	KIAA0201 gene		726732 3', mRNA sequence. (from Genbank)	Interferon, alpha-inducible protein 27	EST: yh81g01.r1 Homo sapiens cDNA clone 136176 5' similar to	Skeletal beta-tronomyosin	19FBP4 Insulin-like growth factor-hinding protein 4	F12 Coagulation factor XII (Hageman factor)		SCYA11 Small inducible cytokine A11 (eotaxin)	EST: y1095.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', mRNA sequence. (from Genbank)	RPS11 Rihosomal profein S11	Smoothelin	(clone CC6) NADH-ubiquinone oxidoreductase subunit mRNA, 3' end cds
	P30374 at		1	X59434 at	X82224 at	M11147 at	N94824 at	J04444_at		RC_AA0529		M33772_s_a t	M22382 at	HG1102- 0.2523652 HT1102 at	0.2522348 D86956 at	RC AA3982	76_at	RC_AA1612 92_s_at	0.2515013 032304 24	0.2514318 M12125 at	M62403_s_a t	M17466 at	D49372_s_a		AA090632_a t	L77567 s at	ੜ	L04490_at
	0.25448507 R30374		0.25419658	0.25403702 X59434 at	0.25384232 X82224	0.25355202 M11147	0.25339845 N94824 at	0.25324994 J04444			0.25295016 59 at	0.25274342	0.2525344 M22382	0.2523652	0.2522348		0.25207108 76_at	RC_AA1 0.25187638 92_s_at	0.2515012	0.2514318	0.25130942	0.25105903 M17466 at		0.25075394	0.25066942	0.25029984 L77567	0.2501696 Z49989	0.25012305 L04490 at
	0.377939		0.377698	0.377596	0.377096	0.377075	0.376938	0.376324		7	0.376225	0.375947	0.37592	0.375285	0.375253		0.375132	0.374928	0 374735	0.374661	0.374254	0.373718	707000	0.373431	0.373305	0.373143	0.373037	0.372948
	0 4384187	1	0.4380884	0.4379003	0.2578857 0.4377968	0.4373914	0.4373853	0.4373848			0.43/2188	0.4369767	0.4368653	0.4368289	0.4368103		0.4367228	0.436644	0.4366248	•	0.4362318	0.4345914	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.4345358	0.4343934	0.4343443	0.4338554	0.4334525
	0.2599319		0.2595176	0.2590499	0.2578857	0.2567741	0.2558351	0.2546034		0.0500757	0.2038757	0.2526687	0.2526022	0.2525422	0.2524923		0.2523198	0.2513914	0.2509154	0.2500406	0.2499405	0.2497276	700007070	0.2493821	0.2487971	0.2482375	0.2482352	0.2473214
	209 Colorectal		210 Colorectal	211 Colorectal	212 Colorectal	213 Colorectal	214 Colorectal	215 Colorectal		018 (Colorotal	Colorectal	217 Colorectal	218 Colorectal	219 Colorectal	220 Colorectal		Colorectal	222 Colorectal	223 Colorectal	224 Colorectal		226 Colorectal	100000	ZZ/ Colorectal	228 Colorectal	229 Colorectal	230 Colorectal	231 Colorectal
	209		210	211	212	213	214	215		210	017	217	218	219	220		221	222	223	224	225	226	700	777	228	229	230	231

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	Collagen, type I, alpha 2 Short-chain alcohol dehydrogenase (XH98G2) mRNA	ARSE MRNA	DESMOCOLLIN 2A/BB PRECURSOR	RGP3 mRNA	KRT19 Keratin 19	EST: zw38b09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 772313 3', mRNA sequence. (from Genbank)	Yw15d02.r1 Homo sapiens cDNA clone 252291 5'. (from Genbank)			EST: zm17f04.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 525919 3', mRNA sequence. (from Genbank)	o sapiens cDNA		IUMGSU1400, clone		A4370466 a EST: EST68690 HSCT72 cells il nomo sapiens conve si dinimari. Isequence, (from Genbank)	L37a		KNG gene (kininogen) extracted from Human kininogen gene	synthase, H+ transporting, mitochondrial F1 complex,	delta subunit	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	Fibroblast activation protein mRNA	Lower Chapter A	הפידי יוס ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי ליייי	EST: ztb3g11.s1 Soares ovary tumor NDHOT Homo sapiens cDNA clone 726116 3', mRNA sequence. (from Genbank)	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR	at COL15A1 Collagen, type XV, alpha 1	EST: zl51f03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505469 3', mRNA sequence. (from Genbank)	
	s at	X83573 at	U51711 at	U27655 at	Y00503 at	RC_AA4045	04_at	0.2482578 H87671 at	RC_AA4632	34_at	RC_AA0745 0.24770266 14_at	RC_AA4027	20_at			AA370406_a	L06499 at	M11437 cds	2_at		X63422_at	0.24649552 X63422 at-2 subunit	0.24622984 U09278 at	RC_AA2435	02 al	KC_AA4017 63_at	X17093 at		RC_AA1564 50_at	
-	0.24978833 J03464 0.24959934 U73514	0.24930625256714 at	0.24900725 U51711	0.24886379 U27655	0.24866241 Y00503		0.24847391 04	0.2482578	And the second s	0.24800336	RC_A 0,24770266 14_at		0.24768117 20_at	0110110	0.24/465/9	0.247171061	0.24704532 L06499 at		0.24696982 2_at		0.24669023 X63422	0.24649552	0.24622984	RC_A	0.24001204	RC 0.24585667 63	0.24566157 X17093	0.24541639 L25286 s	RC_A 0.2451524 50_at	
-	0.372917	0.372345	0.372097	0.371909	0.371716		0.37156	0.371416		0.371012	0.370947		0.370675	00000	0.3/0532	0.370171	0.370054		0.369792		0.369634	0.369634	0.36938	0.360047	0.303041	0.368688	0.368341	0.368288	0.368126	
1	0.4333727	0.4332613	0.4329534	0.432789	0.43276		0.4325721	0.4324356		0.4319491	0,4318435		0.4316835	70770	0.4314881	0.4313634			0.430956	0	0.4309435	0.430421	10	0 4204008		0.4294153	0.4292812	0.4289072	0.4283096	7
		0.2454265	0,2435387	0.2432521	0.2432249		0.2417218	0.2417041		0.2415092	0.2408507		0.2404307	7	0.2398451	0.2390578	0.2384494		0.237877		0.23/81/1	0.2378171	0.237445	0.0367846	0.2001.040	0.236753	0.236711	0.2356256	0.2355853	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
	232 Colorectal 233 Colorectal	234 Colorectal	236 Colorectal	237 Colorectal	238 Colorectal		239 Colorectal	240 Colorectal		241 Colorectal	242 Colorectal		243 Colorectal		244 Colorectal	245 Colorectal	246 Colorectal		247 Colorectal		248 Colorectal	Colorectal	250 Colorectal	054 Colorontol	כחומו בכומו	252 Colorectal	253 Colorectal	254 Colorectal	255 Colorectal	
	232	234	236	237	238		239	240		241	242		243		744	245	246		247	3	248	249	250	25.4	3	252	253	254	255	

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257 Colorectal 258 Colorectal 259 Colorectal

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. RC_AA4914 EST: ab04a05.s1 Stratagene fetal retina 937202 Homo sapiens cDNA sequence is in conflict with the conceptual translation gene extracted EST: zu36d09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zx88d07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA RC_AA1578 EST: zo35h03.s1 Stratagene colon (#937204) Homo sapiens cDNA AA454908_s EST: zx79c12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zk83h03.s1 Soares pregnant uterus NbHPU Homo sapiens EST: zu11f02.s1 Soares testis NHT Homo sapiens cDNA clone X51755_cds |from Human lambda-immunoglobulin constant region complex Ig light-chain, partial Ke-Oz- polypeptide; Author-given protein Homo sapiens mRNA for putative Sqv-7-like protein, partial cDNA clone 489461 3', mRNA sequence, (from Genbank) Homo sapiens mRNA for KIAA0517 protein, partial cds clone 809974 5', mRNA sequence. (from Genbank) clone 810829 3', mRNA sequence. (from Genbank) clone 740081 3', mRNA sequence. (from Genbank) clone 588917 3', mRNA sequence. (from Genbank) clone 839792 3', mRNA sequence. (from Genbank) Canicular multispecific organic anion transporter Human poliovirus receptor mRNA, clone H20A Human BAC clone GS025M02 from 7q21-q22 731547 3', mRNA sequence. (from Genbank) PPBP Connective tissue activation peptide III D21S2056E, novel nuclear protein 1 Acyl-CoA thioester hydrolase mRNA COL6A2 Collagen, type VI, alpha 2 TUBG Tubulin, gamma polypeptide COL4A2 Collagen, type IV, alpha 2 CC chemokine LARC precursor GLB1 Beta-D-galactosidase IDO Indole 2,3-dioxygenase Unknown product KIAA0175 gene (germline) AA431505_a RC_AA4588 RC AA0545 RC_AA4790 0.243444 M61764 at RC_AA4649 RC AA4701 RC AA4122 0.24429834 M34423 at RC_AA4771 0.24302162 X05610 at RC AA0105 0.24482329 U66674 at 0.24457671 D79997_at 0.24378608 X15882 at 0.24192263 M34455 at 0.24173522 U64197 at 0.24157457 D28124 at 0.24119541 U91316 at 0.24092536 M54995 at 0.24400778 | 06_s_at 0.24273828 84 s at 0.24392831 44 s at 0.24237236|5_s_at 0.24289443 14_at 0.24322605|99 at 0.24250843 35 at 0.2422004 61 at 0.24206237|65 at 0.24143389|45_at 0.2408065|30_at 0.24356449 0.24499446 0.368043 0.367443 0.367328 0.367017 0.366612 0.36626 0.366087 0.3659860.365818 0.367738 0.367488 0.3655690.368027 0.366193 0.365768 0.365314 0.366507 0.365586 0.3652990.364932 0.364844 0.364784 0.364533 0.364342 0.2344479 | 0.4276524 0.4282645 0.235389 0.4282106 0.234363 0.4270255 0.2351394 0.4280374 0.2346506 0.4277001 263 Colorectal | 0.2343158 | 0.4270182 0.2313208 | 0.4262463 0.2312584 0.4261007 0.2353334 0.4281947 0.2325791 0.4266124 264 Colorectal | 0.2340646 | 0.4269951 0.2328659 0.4269734 0.426753 0.2308645 | 0.4260578 0.2292832 0.4258433 0.2292013 0.4257856 0.424666

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266 Colorectal

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0.2291508 0.4255351

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276 Colorectal 277 Colorectal 278 Colorectal 0.2250794

279 Colorectal

Phys. (2019, 227) 1920, 1920, 1925, 1911, 1921,

						Inve	entor	s: \$	Srid	har	Ra	am	asv	vamy	, et	al.						
Cystatin B gene	Na.K-ATPase beta-1 subjuit mRNA	RC_AA4212 Homo sapiens putative tumor suppressor protein (101F6) mRNA, 68_at complete cds	815A9.1 gene (myosin heavy chain) extracted from Horno saniens	chromosome 16 BAC clone CIT987SK-815A9 complete sequence	OF LK Cystic tibrosis conductance regulator Actin denolymentaing factor thuman fetal basis and 4 4 from	Genethonin 1	FII Gene	CYP4A11 Cytochrome P450. Subfamily IVA Indynentide 11	EST: zp88e03.s1 Stratagene HeLa cell s3 937216 Homo sapiens	cDNA clone 627292 3' similar to contains Alu repetitive element;, mRNA segmence (from Canhant)	C2 Complement component C2	Mac-2 hinding protain mDNA	EIF2A Eukaryotic translation initiation factor 2A	CKB Creatine kinasa B	Albert Antitute of the state of	CTNNA1 Catenin (cadherin-associated profein) apply 1 (102/b)	Ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA	EST: 15b2 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genhank)	EST: zx10e03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 786076 3. mRNA sequence (from Ganhank)	Himan hTRIP (hTRIP) mRNA complete ad-	EST. 2l76c05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510536.31 mRNA segmence (from Genhank)	Ribosomal protein L14
U46692_rna 1_at	U16799_s_a t	RC_AA4212 68_at	548_r	1	<u></u>	RC_AA4525 98 s at	U80184 rna 1 at	at	V V V V V V V V V V V V V V V V V V V	4 8 4		T	at l	M16364_s_a	t				10	_AA1864 s_at	A0558	A5048
0.24061918 1_at	0.24049804	RC_A 0.24029635 68_at		0.240143 nat at	0.23991685 S65738	RC_AA4 0.23977596 98 s at	0.2396546	0.23938963 L04751		0.2392877 95 at	0.23915909 L09708 at	0.2389286 L13210 at	0.23878038 J02645	0.2385777	HG3517-00 HT3744	0.23813273 U03100_at	0.23799877 U53445_at	0.23774703 W25933 at	RC 0.23764469 63	RC 0.2374841127	RC_A 0.23731422 09 at	0.23715094 14 at
0.364282	0.364256	0.364061		0.363926	0.363704	0.363612	0.363478	0.363226	-	0.363004	0.362807	0.362739	0.362534	0.362369	0.362228	0.362136	0.361876	0.361476	0.361382	0.361363	0.36121	0.361095
0.4244825	0.4242902	0.2237412 0.4242748		0.4241056		0.4240344	0.4238209	0.4238209		0.4237679	0.4236443	0.4234047	0.4232847	0.4230354	0.4229702	0.4229702	0.4229226	0.4227956	0.4227762	0.4226796	0.4225038	0.4223527
0.2244888	0.2244395	0.2237412	0000	0.2237204	0.2229676	0.2229479	0.2224907	0.2217537		0.2212446	0.2212011	0.2201314	0.2199767	0.2197534	0.2195442	0.2191761	0.2174458	0.2171963	0.2170434	0.2166066	0.216346	0.2160157
280 Colorectal	281 Colorectal	282 Colorectal	1000	284 Colorectal	285 Colorectal	286 Colorectal	287 Colorectal	288 Colorectal		289 Colorectal	290 Colorectal	291 Colorectal	292 Colorectal	293 Colorectal	294 Colorectal	295 Colorectal	296 Colorectal	297 Colorectal	298 Colorectal	299 Colorectal	300 Colorectal	301 Colorectal
280	281	282	200	284	285	286	287	288		289	290	291	292	293	294	295	296	297	298	299 (300	301 (

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AA2623 EST: zr44g03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone f at 666292 3', mRNA sequence, (from Genbank)	Desmin gons	ECE1 Endothelin converting enzyme 1	DD96 mRNA	CAST Calpastatin	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	EST: zr15d05.s1 Stratagene NT2 neuronal precursor 937230 Homo	Septens CLIVA Gorle 603463 3, mRNA sequence. (from Genbank) TFF1 Trefoil factor 1 (breast cancer, estrogen-inducible sequence		Homo sapiens GW112 protein (GW112) mRNA, complete cds	NGAL Gene	Forkhead protein FREAC-1 mRNA	Oncodene Amil-Evi-1 Eusion Activated				EST: zh86b04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 428143 3', mRNA seguence, (from Genhank)	(Authorities and Authorities a	Nucleoside Diphosphate Kinase Nm23-H2s	Occiudin	LIMK-2	Transcription factor RTEF-1 (RTEF1) mRNA	at-2 TEA domain family member 4	EST: zh51h04.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	NEO1 Neogenin (chicken) homolog 1
	n 33	Z35307 at	U21049 at	D16217 at	M97936 at	AA2	X52003 at	AA372630_s	Jan 1 166359 at	111			W38597 i a	1	AA295819_s _at	RC_AA0019 36_at					U63824_at	U63824_at-2	M/78726 at	U61262_at
348 0.23696794 51	M 0.23679978	0.23663089 Z35307	0.23642176 U21049 at	0.23622829 D16217	0.2360938 M97936	RC 0.23500826.62	0.23592868 X52003 at	10000000	0.23553297 J66359	0.23532106 X99133	0.23521934 U13219	HG4058- 0.23504303 HT4328	0.22470650	0.2347 9030	0.23470141	RC_A 0.23450056 36_at	HG1153	0.23423012 (111135	0.23401211	0.23385955 D45906	0.2338088 U63824	0.23372023 U63824	0.03361337 10/78706 94	0.23349696 U61262
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0.4220851	0.4220488		0.4217475	0.2154369 0.4213895	0.4213895	0.4211144		0.4205355	0.4205039	0.4203111	0.4202541	0.4201149	0.4200318	0.150021.0	0.419534	0.4193819	0.4186250	0.4184691	0.4777269	0.41/1/200	0.41/504	0.4174936	0.4173119	0.4172798
0.215741	0.2156857	0.2156719	0.2155447	0.2154369	0.2138341	0.2137431	0.2128677	0.2427374	0.2123357	0.2112828	0.2110833	0.2107744	0 2107521	1 10 10 11 11	0.2106079	0.2093179	0.2082233	0 2074357	0.2073005	0.2013003	0.20/ 1615	0.2071615	0.2067716	0.2065829 0.4172798
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RC_AA1133 EST: zn70g06.s1 Stratagene HeLa cell s3 937216 Homo sapiens 87_at cDNA clone 563578 3', mRNA sequence. (from Genbank)	Lysophospholipase homolog (HU-K5) mRNA	at Activin A recentor type II-like 1	THBS2 Thrombospondin 2		UPA gene		(clone PK2.) CDC2-related protein kinase (DISSI BE) "DNA	Human zing-finder domain-containing protein mBNA martial also	CLTA Clathrin light chain A	AA422029_a EST: zv26g08.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t 754814 5', mRNA sequence, (from Genhank)	Integrin alpha 6 (or alpha E) protein gene extracted from Human	MATE IN BURGUII AIDIR O	TAP1 Transnorter 1 ABC (ATP hinding cascatto)	AA129547_a EST: zn83f01.r1 Stratagene lung carcinoma 937218 Homo sapiens	cDNA clone 564793 5', mRNA sequence. (from Genbank)	EST: HUMGS0003737, Human Gene Signature, 3'-directed cDNA sequence mRNA sequence (from Control)	BDKR82 Bradykinin recentor R2	EST: zb20c11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 302612.5', mRNA sequence. (from Genbank)	EST: zw34b09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	EST: af54e12.s1 Soares total fetus Nh2HF8 ow Home canions CDNA	clone 1035502 3', mRNA sequence, (from Genbank)	EST: zv34e11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	Glone 755564 3' similar to SW:PTN2_RAT P35233 PROTEIN-	Genbank)		OIAS (2'-5') oligoadenylate synthetase		sequence. (from Genbank)
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0.4172628	- 1	0.4164088	0.4161472		0.4159612	0.4159195			0.4151186	0.414631	0.4145514				0.4142000	0.4140218	0.4138213	0.4137722	0.4136169		0.4133649			0.4131035	0.4497873	0.4127589	0.4126949	21.77.1.50
0.2064035	0.2002332	0.2062282	0.2060922	1	0.205696	0.2052573	0.2050409	0.2049733	0.2048363	0.2039772	0.2038375	0.2036814	0.2032533	0.2034472	0.203 1472	0.2026946	0.2024833	0.2022269	0.202178		0.201821			0.2011614	0.2006984	0.2002416	0 1999146	122
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Expressed oseudo TCTA mRNA at f(1:3) translocation site	EEF1A1 Translation elongation factor 1-alpha-1	at-2 Human Bci-2 hinding component 3 (bbc3) mRNA partial ode	BG-2 binding component 3 (bbc3) mRNA partial cds	Mr 110 000 antinen	Protessome ethinite 112	Aretolactors cunthan hamples with	Acetolackate symmese momentaly mixing 64 KD ALITOANTIGEN D1		IMAGE:685447 3', mRNA sequence, (from Genbank)	1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE at PHOSPHODIESTERASE BETA 3		Ecotropic viral integration site 1		Sm-like protein CaSm (CaSm) mRNA	NF-AT3 mRNA	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR	RPL8 Ribosomal protein L8	Eukaryotic translation initiation factor (eIF3) mRNA	Kallikrein mRNA, clone clone phKK25			Decorin, Alt. Splice 1	EST: zr79b01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681865 31 mRNA certificate (from Corbon)	M-PHASE INDUCER PHOSPHATASE 2	EST: zt97b10.r1 Soares testis NHT Homo sapiens cDNA clone	730267 5', mRNA sequence. (from Genbank)	piens cDNA clone	mRNA sequence, (from Genbank)	C1S Complement component 1. s subcomponent	Cathepsin B	EST: aa61c10.s1 NCl_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825426 3', mRNA segrence, from Genhank)	a SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA	
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0.1891975	0.1890445	0.1888832	0.1888832	0.1876353	0.1876054	0.1874838	0.1871072		0.1870685	0.186834		0.1868124	0 1864537	0.1861585	0.1867976	0.103/3/0	0.1856037	0.1855529	0.1845051			0.1841088	0.1839668	0.1839458		0.1827556		0.1826154	0.1824051	0.1815284	0.181393	0.1812437	
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DNA-binding protein (HRC1) mRNA	r at Mucin 3, Intestinal (Gb:M55405)	Proteasome (prosome macropain) 26S subunit non-ATPassa 13	EST: zx70a12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	COAGULATION FACTOR X PRECIESOR	Keratin 8	EST: zn18b04.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547759 3', mRNA sequence. (from Genbank)	KIAA0334 gene	Paraoxonase (PON2) mRNA	EST: zu81h12.s1 Soares testis NHT Homo sapiens cDNA clone	Translational initiation factor 2 heta subunit (AE-2-heta) mRNA	EST: zr71c02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	668834 3' similar to TR:G969170 G969170 PX19. ;, mRNA sequence	(HOLLI Gettibalik) KIAA0124 nene narfial ods	EST: Human fetal brain cDNA 3'-end GEN-081G02, mRNA seguence	(from Genbank)	2-19 gene (2-19 protein) extracted from H.sapiens G6PD gene for glucose-6-phosphate dehydrogenase	EST: zx80d02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 810051 5' similar to TR:G1020091 G1020091 NEUROPSIN.	AA465016_a ; contains element LTR3 repetitive element ;, mRNA sequence. (from	Genoamy Beta subunit of enithalial amilorida-sansitiva sodium channal	EST: Human HL60 3'directed Mbol cDNA, HUMGS01145, clone pm2260, mRNA sequence (from Genhank)	EST: zx3zg10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	cione roozzo 3, mrvva sequence. (rrom Genbank) Thymosin beta-4 mRNA	EST: zt66c01.s1 Soares testis NHT Homo sapiens cDNA clone 727296 3', mRNA sequence. (from Genbank)
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0.22276407 M91083_at	HG2147 0.22268288 HT2217	RC 0.22253454 91	RC_A	0.22232442 L29433	Z838 0.22216293 1 at	RC_A 0.22211528 18 at	0.22198282	0.22189309 L48513 at	RC_A	0.2215906 M29536		RC_AA2	0.22132495 D50914 at		0.22113867	0.22104083 2_			0 22090986	0.22074215 X87159	0.22059147	0000000000	0.2203273 M17733	0.22023967 21
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0.180716	0.1804325	0.179763	0.1796245		0.1792444	0.1786292	0.1782558	0.1778101	0.1756461	0.1755425		0,1755385	0.1754513		0.1754297	0.1752464			0.1746087	0.174411	0.1741242	0.1739448	0.1738675	0.1738624
399 Colorectal	400 Colorectal	401 Colorectal	Colorectal	403 Colorectal	404 Colorectal	405 Colorectal	406 Colorectal	407 Colorectal	408 Colorectal	409 Colorectal		410 Colorectal	411 Colorectal		412 Colorectal	413 Colorectal			414 Colorectal	415 Colorectal	416 Colorectal	417 Colorectal	418 Colorectal	419 Colorectal
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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. EST: zx16e06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: za85a06.r1 Soares fetal lung NbHL19W Homo sapiens cDNA EST: HUMGS0005758, Human Gene Signature, 3'-directed cDNA U41766_s_a | Metalloprotease/disintegrin/cysteine-rich protein precursor (MDC9) RC_AA0355 EST: zk26b02.s1 Soares pregnant uterus NbHPU Homo sapiens MMP2 Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, EST: aa64g12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone RC_AA6100 EST: af08e11.s1 Soares testis NHT Homo sapiens cDNA clone Monocyte chemoattractant protein-4 precursor (MCP-4) mRNA S100A3 S100 calcium-binding protein A3 (formerly S100E) cDNA clone 471627 3', mRNA sequence. (from Genbank) Transforming growth factor beta 1 induced transcript 1 IMAGE:825766 31, mRNA sequence. (from Genbank) clone 299314 5', mRNA sequence. (from Genbank) clone 786658 3', mRNA sequence. (from Genbank) RCH1 RAG (recombination activating gene) cohort 1031084 3', mRNA sequence. (from Genbank) sequence, mRNA sequence. (from Genbank) MULTIDRUG RESISTANCE PROTEIN 1 Proteasome activator hPA28 subunit beta Guanine Nucleotide-Binding Protein Hsr1 0.21804747 L02326_f_at (clone Hu lambda-17) lambda-like gene FBN1 Fibrillin 1 (Marfan syndrome) RNS1 Ribonuclease A (pancreatic) CDH3 Cadherin 3 (P-cadherin) ITGB5 Integrin beta-5 subunit G1/S-SPECIFIC CYCLIN E KIAA0007 gene, partial cds **TUBULIN ALPHA-4 CHAIN** 72kD type IV collagenase) KIAA0750 gene product Oncomodulin gene Garp gene mRNA mRNA C00125 s a RC_AA4518 RC AA5050 AA157623_s X53002_s_a D87716_s_a 0.21784674 Z18948 at 0.21914238 W05585_at RC_AA2332 0.2197131 M14758 at 0.21904136 X63629 at 0.2183302 M74093 at 0.21882729 M55593_at ä 0.21979126 L13923 at 0.21848814 L20348 at 0.21743883 HT3404 at ä क् 0.21725959 D45248 at 0.21716623 U28386 at 0.21764944 X06956 at 0.2193254 D26129 0.21955204 Z24680 0.21877955 U46767 ₩ 0.21963376 95 at 0.21898192 70 at 0.21985555 14 at 0.21731475 57 at aţ 0.22017857 77 0.22006811 0.21860664 0.2181762 0.21777372 0.21767299 0.344774 0.344748 0.344613 0.344399 0.34413 0.344624 0.344613 0.344024 0.343953 0.3439030.343732 0.344266 0.342304 0.344226 0.3433680.342043 0.343864 0.343707 0.343571 0.342879 0.342845 0.342653 0.34271 0,342387 0.1690355 0.3999129 0.342197 0.342891 0.4025816 0.1737058 0.4025284 0.1736943 0.402457 0.1734535 0.4022192 0.1733749 0.4020973 445 Colorectal 0.1688801 0.3999087 0.1708696 0.4012243 0.1729153 0.4019776 0.1721121 0.4018173 429 Colorectal | 0.1718734 | 0.4016974 0.1715397 | 0.4016271 0.1714253 | 0.4015857 0.1694984 0.4001872 0.1690883 0.4000302 0.1725793 0.4019096 0.1724256 0.4018521 432 Colorectal | 0.1710495 | 0.4014494 0.1699521 0.4007216 0.1695 0.4002795 0.1691347 0.4001326 0.1699515 0.4006932 0.1695879 0.4003103 0.1699524 0.4007933 0.4009031 0.400523 0.173791 0.1703653 0.169787 427 Colorectal 440 Colorectal 441 Colorectal 420 Colorectal 421 Colorectal 426 Colorectal 428 Colorectal 423 Colorectal 424 Colorectal 425 Colorectal 422 Colorectal 430 Colorectal 431 Colorectal 433 Colorectal 435 Colorectal 444 Colorectal 434 Colorectal 436 Colorectal 437 Colorectal 443 Colorectal 438 Colorectal 439 Colorectal 442 Colorectal

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	TGFBR2 Transforming growth factor heta recentor II (70, 80,0)	(10-00AD)	Landsteiner-Wiener Blood Groum Chamadain (1)	the A B and a state of the control o	RC_A4256 Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA	splicing ractors, Prp1/Zer1 and Prp6 Mitochondrial intermediate peptidase precursor (MIPEP) mRNA	I		one	A clone 288662 5'. (from		Tubulin, Alpha 1 Isoform 44	iens cDNA clone	re, 3'-directed cDNA	sequerice, IIIKINA sequence. (from Genbank)	EST: zp03e05.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595328 31 mRNA sequence (from Gonback)	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 2	STM-7 protein	EST: aa64a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825682 31 mRNA sequence (from Contract)	EST: 2v08e10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	TGB5 Integrin beta-5 subunit	0.21480893 L03411 s at RD Radin blood group	RC_AA1351 EST: zo27a05.s1 Stratagene colon (#937204) Homo sapiens cDNA 85_at clone 588080 3', mRNA sequence. (from Genbank)
RC_AA1499	D50683 at	11 1	HT4224_s_a	D49824_s_a	RC_AA4256	27 at	0.21637894 U80034_at RC_AA0353	66 at	RC_AA2363 56 at	N79354 at	HG2259-	HT2348_s_a t	RC_AA6095 92_at	C.00476 at		RC_AA1739 81_at	M55543_at	X92493_s_a t	A5048	RC_AA4365 60_at	J05633_at	L03411 s at	RC_AA1351 85_at
RC_A	0.21691293 D50683		0.21675077	0.21865724	RC A	0.2.100101	0.21637894	0.21628368 66 at	RC_A 0.21623269 56 at	0.21608981 N79354			0.21577172 92	0.21577172 C00476		RC_A 0.21566679 81_at	0.21561334 M55543 at	0.21540578 t	0.21533175 03 at	RC_A 0.21517071 60 at	0.21506318 J05633	0.21480893	RC_A 0.21468474 85_at
0.341902	0.341		0.341626	0.341542	0 341		0.341478	0.341415	0.341415	0.341386		0.341352	0.341283	0.341063		0.341022	0.340981	0.340873	0.340803	0.340778	0.340543	0.340353	0.340172
0.3997103	1 1		0.3996956	0.3995984	1	1	1	0.3994775	0.3994277	0.3993781		0.3993452	0.399217	0.3991573		0.399136	0.3991324	0.399104	0.3990471	0.3990317	0.3987303	0.3987299	0.3984724
0.1688689	0.1688496		0.1685865	0.1683068	0.1681806	0 4870435	0.101.0	0.1678417	0.1676434	0.1673252		0.1672328	0.1672166	0.1671251		0.1667122	0.1665861	0.1665606	0.166446	0.165736	0.1655869	0.1655231	0.1653327
446 Colorectal	447 Colorectal		448 Colorectal	449 Colorectal	450 Colorectal	454 Coloractel		452 Colorectal	453 Colorectal	454 Colorectal		455 Colorectal	456 Colorectal	457 Colorectal		458 Colorectal	Colorectal	460 Colorectal	461 Colorectal	462 Colorectal	463 Colorectal	464 Colorectal	465 Colorectal
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દુવારી મહાસે વૈદ્યાર	_AA4191 EST: zv34h05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA at clone 755577 3¹, mRNA sequence. (from Genbank)		0.21445012 S71018 at-2 Peptidylprolyl isomerase C (cyclophilin C)	Cyclophilin C [human, kidney, mRNA, 883 nt]	Ran GTPase activating protein 1	of cds for alternative solicing DC42 g		ure, 3'-directed cDNA		Fibronectin, Alt. Splice 1	ovary tumor NbHOT Homo sapiens cDNA	9	apiens cDNA			PBIgene	EST: zw86b07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 783829 3', mRNA sequence. (from Genbank)	Human mRNA for KIAA0007 gene, partial cds	Fatty acid amide hydrolase mRNA	0.21245596 K01160_s_at HLA-DQA1 MHC class II DQ alpha	EST: HUMRTPGEAL Homo sapiens cDNA. (from Genbank)	Cellular retinoic acid-binding protein 1
Thirt Then their enell unet that theel fully	RC_AA4191 39_at	X71874_cds 1_at	S71018 at-2	0.2143/135 S71018 at	68 s at	L11369_at	L33930 s at	C00225_s_a t	HG3044-	HT3742_s_a	A2357	L21954 at	RC_AA4565 95_at	X17644_s_a t	D89501 at-2	D89501 at	44436	354	at	K01160_s_at	M91493_at	A4030
tini tini it dest tini	RC_A 0.21463652 39_at	X718 0.21449578 1_at	0.21445012	0.2143/135	0.21426827 68 s at	0.21414681 L11369	0.21399806	0.213931261		0.21368803	RC_A 0.21362731 07_at	0.21351211 L21954 at	RC_A 0.21338874 95_at	0.21317948 t	0.21299042	0.21293436 D89501	RC_A 0.21288554 67_at	RC_D60 0.21277869 s_at	0.21261954	0.21245596	0.21236816 M91493_at	RC_A 0.21234865 41_at
II. Hail	0.340161	0.340157	0.34013	0.338842	0.33993	0.339658	0.339517	0.33943		0.339319	0.339238	0.339172	0.33907	0.339057	0.339043	0.338872	0.338842	0.338644	0.338479	0.338403	0.338365	0.338334
	0.3984437	0.3982009	0.3980459	0.3978031	0.3979631	0.3977973	0.3977175	0.397591		0.3975688		0.3973875	0.3973582	0.3972327	0.397137	0.397121	0.3969455	0.3967438	0.3900425	0.3965244	0.396479	0.3963925
	0.1651904	0,1648333	0.1646377	7.70010	0.1645432	0.1643057	0.1637872	0.163628		0.1635248	0.1631892	0.1630999	0.1629482	0.1628553	0.1628099	0.1628099	0.1626895	0.162363	0.1023031	0.1619627	0.1616623	0.1616189
	466 Colorectal	467 Colorectal	468 Colorectal	2000	470 Colorectal	471 Colorectal	472 Colorectal	473 Colorectal		474 Colorectal	475 Colorectal	476 Colorectal	477 Colorectal	478 Colorectal	479 Colorectal	480 Colorectal	481 Colorectal	482 Colorectal	Too colorectal	484 Colorectal	485 Colorectal	486 Colorectal

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Paniane CDMA clone	dsteiner-Wiener blood	epetitive element;, mKNA	sapiens cDNA clone	<u>κ</u>)	, complete cds		sette)	Inve	nto	ors: S	rid	har Rar ≌	nas	Wa	amy, et	al				*8 9w Homo sapiens cDN/			atelets, synovial fluid)	ZAP Express Homo	Genbank)	enomatosis 1)	Insaminase
FOT: WITE AND A COOK NIME NIME SA Homo sanians COMA Chone	669219 3' similar to gb:L27670 Human Landsteiner-Wiener blood	group glycoprotein (HUMAN);contains Alu repetitive element;, mKNA sequence. (from Genbank)	EST: zr51f08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	666951 3', mRNA sequence. (from Genbank)	Homo sapiens mRNA for zinc finger protein, complete cds	Placental bikunin mRNA	TAP2 Transporter 2, ABC (ATP binding cassette)	Hypothetical protein 384D8 6 gene extracted from Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence	D21S2056E, novel nuclear protein 1	EST; zk70b10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488155 3' similar to contains element MER9 repetitive	element;, mRNA sequence. (from Genbank)	EST: zm95f07.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone 545701 3', mRNA sequence. (from Genbank)	AA481201_a EST: aa34c12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:815158 5, mKNA sequence. (from Gendank)	EST: ae62a09.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 951448 3', mRNA sequence. (from Genbank)	BMP1 Bone morphogenetic profein 1	ACTH-R gene for adrenocorticotropic hormone receptor	0.21059452 L22524_s_at MATRILYSIN PRECURSOR	Myosin light chain kinase (MLCK) mRNA	RC_AA4516 EST: zx44b03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDN/76 at clone 789293 3¹, mRNA sequence. (from Genbank)	CD39-like 2	Tazarotene-induced gene 2 (TIG2) mRNA	PLA2G2A Phospholipase A2, group IIA (platelets, synovial fluid)	AA091231_a EST: cchn2158.seq.F Fetal heart, Lambda ZAP Express Homo	sapiens cDNA 5', mRNA sequence. (from Genbank)	CCND1 Cyclin D1 (PRAD1; parathyroid adenomatosis	GFP Glutamine-fructose-6-phosphate transaminase
rri: "berr frat" trede ands "c	<u>n 6</u>	A2364	A2362		584	at	at	317_rna	at	RC_AA0464 0		_AA0789 at	AA481201_a		AA6097	at,	ä	L22524_s_at	U48959 at	RC_AA4516 76 at	A4783	at	0.21019143 M22430 at	AA091231_a		T	0.20990054 M90516_at
it of dust dust. It		RC_A 0.21209438 81_at		0.21208075 80_at	RC_AA2 0.21196768 82 s at	0.21173109 U78095	0.21172099 M74447	0.21166928 6 at	0.2115748 U79775		0.21132918 06_at	RC 0.21119437 32		0.211110121	RC 0.21103315 95	0.21087967 U50330	0.21070218 X65633	0.21059452	0.21055259 U48959 at	RC_A 0.21049681 76 at	0.21045355 00 at	0.21033625 U77594	0.21019143		0.21007404	0.21000372 X59798_at	0.20990054
span, harb - 21		0.33828		0.338205	0.338097	0.338003	0.337912	0.33787	0.337795		0.337721	0.337613	7	0.3373	0.3373	0.337048	0.33704	0.336887	0.33687	0.336793	0.336636	0.336509	0.336328		0.336	0.336171	0.336089
		0.3963835	2000	0.3963129	0.3962475	0.3959201	0.3958512	0.3958136			0.3956529	0.3954982		0.3954701	0.3954353	0.3953815	0,395285	0.3951381	0.3950984	0.3950417		0.3948976	0.3946397		0.1556963 0.3945324	0.15532 0.3944851	0.1552322 0.3944281
		0.1615999	0.00	0.1606803	0.1602888	0.1602171	0.1601474	0.1595165	0.1591935		0.1590418	0.1589532	1	0.15849	0.1575591	0.1569468	0.1565222	0.1564706	0.1564513	0.1561238	0.1559671	0.1557691	0.1557269		0.1556963	0.15532	0.1552322
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		187	5	488	489	490	491	492	493		494	495		496	497	498	499	500	501	502	503	504	505		506	50,	508

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EST: Homo sapiens thymus mRNA (randomly primed, normalized), single-pass sequence, mRNA sequence. (from Genbank)			UDP-galactose translocator	a Protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A heta)	(2) mRNA	EST: zu13c03.s1 Soares testis NHT Homo sapiens cDNA clone 731716 3. mRNA sequence (from Genhank)	sapiens cDNA clone	A FC RECEPTOR I"A	phoenhatasa	, nuclear gene encoding	EST: zu70f09.s1 Soares testis NHT Homo sapiens cDNA clone 743369 3', mRNA sequence, (from Genbank)	EST: zn83a11.s1 Stratagene lung carcinoma 937218 Homo sapiens contract co	ovarian cancer cell line OC6, mRNA	COLbA1 Collagen, type VI, alpha 1	Zinc finger protein 200 EST: HUMGS0003774, Human Gene Signature, 3'-directed, CONA	0.20818146 C01811 f at sequence, mRNA sequence. (from Genbank)	COX7A2 Cytochrome c oxidase VIIa subunit (liver specific)	KIAA0064 gene	EST: zr74b07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669109 31. mRNA sequence. (from Genhank)	G2/MITOTIC-SPECIFIC CYCLIN B1
0.2098014 L44538_at	AA251078_a	RC_AA0749 7 19_at	0.20944932 D84454 at	AA094752_t	0.20931253 M32405 at	RC_AA4170 179 at	RC_AA2337 90 at	0.20900838 M63835 at	D15049 at	0.2088442 U75370 at	RC_AA4005 28_at	RC_AA1222 17_at	S	AA338573_i	at	C01811_f_at	X15822_at	D31764 at	RC_AA2340 66 at	M25753 at
0.209801	0.20963876 t	İ	0.20944932	0.2093829	0.20931253	RC 0.20914608 79	0.2090498 90 at	0.20900838	0.20896049 D15049	0.2088442	RC_A 0.20866127 28_at	RC_A 0.20855671 17_at	0.20852254 S75256	AA3385	0.20830275	0.20818146	0.20797463 X15822_at	0.20788004 D31764 at	0.20771392 66	0.20758401 M25753
0.335977	0.335733		0.335471		0.335234	0.335224	0.335085	0.334907	0.334854	0.334761	0.334744	 0.334698	0.334573	0.334422	774400.0	0.334397	0.334314	0.33414	0.334034	0.333964
0.3943015	0.3942341	f .	0.0340334		0.3939991	0.3939194	0.3939163	0.393889	0.3938167	0.3935947	0.3935785	 0.3933713	0.3933333	ſ	0.2002.0	0.3931952		0.3930866		0.3927834
0.1549872	0.1547511	0.1547084	0.104400	0.1542577	0.1541217	0.1536185	0.1535545	0.1534945	0.1533766	0.1533382	0.153082	0.1524428	0.1517651	0.1510072		0.1508668		0.1503324		0.1498392
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20	21	57	5	51	2	51	51	51.	24	518	52(52,	522	524	1 2	526	527	528	529	530

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Inventors: Sridhar Ramaswamy, et al. RC_AA4859 CDNA clone 843335 3' similar to SW:SUCA_RAT P13086 SUCCINYL-RC_AA0226 EST: ze73a01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA IGHA1 gene extracted from Human Ig germline H-chain G-E-A region RC_AA0183 EST: ze41d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone RC_AA4546 | EST: zx99f06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone AA071381_a EST: zm61d03.r1 Stratagene fibroblast (#937212) Homo sapiens EST: ab40h12.s1 Stratagene HeLa cell s3 937216 Homo sapiens AA406433_a EST: zv12d10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR Mitogen-activated protein kinase-activated protein kinase 5 cDNA clone 530117 5', mRNA sequence. (from Genbank) UMPS gene extracted from Human UMP synthase mRNA Chromosome 17q12-21 mRNA, clone pOV-2, partial cds Mitogen-responsive phosphoprotein (DOC-2) mRNA clone 364584 3', mRNA sequence. (from Genbank) COA LIGASE;, mRNA sequence. (from Genbank) TPM1 Tropomyosin alpha chain (skeletal muscle) 811907 3', mRNA sequence. (from Genbank) 361559 3', mRNA sequence. (from Genbank) T-COMPLEX PROTEIN 1, GAMMA SUBUNIT 753427 5', mRNA sequence. (from Genbank) Homo sapiens mRNA for p27, complete cds IGL@ Immunoglobulin lambda light chain Uridine nucleotide receptor (UNR) gene Beta2-syntrophin (SNT B2) mRNA 33 kDa transcriptional co-activator COL5A2 Collagen, type V, alpha Pyruvate kinase, liver and RBC RNA polymerase I subunit A: gamma-3 5' flank SIL mRNA M19267 s_a AF008442 a D13243 s a 0.20730981 U53446 at X57809_s_a 0.20698786 U40572 at RC AA1957 J03626_ma1 J00220_cds 0.20672369 M74558 at 0.2062354 U18919 at 0.20553958 M11718 at RC AA4777 0.20566429 L34600 at 0.20562492 X74801 at 0.20541492 U40223_at RC AA2367 0.2050854 M30496 at 0.2074444|54 at 0.2072322|32 at 0.20688641 46 at 0.20652114 20 at 0.20618701 65 at 0.20598646 s_at 0.20522827 01_at 0.20515011 47 at 0.2053823|5 at 0.20715122 0.20663773 0.20699231 0.2067851 0.20578396 0.20604913 0.333825 0.333861 0.333719 0.333703 0.333437 0.333260.333076 0.333035 0.332989 0.3326960.333437 0.1459308 | 0.3915806 | 0.332399 | 0.332269 0.332891 0.332697 0.332577 0.332145 0.332079 0.332131 0.332068 0.331841 0.331798 0.33162 0.331466 0.1464579 0.3918662 0.3927706 0.1491703 0.3926815 0.39265890.1487316 | 0.3924795 0.1465549 0.3919869 0.3924395 0.1469579 0.3922158 0.1465781 0.3921879 0.1473992 0.3923646 0.1472546 0.3923127 0.1464099 0.3918206 0.392371 0.1459415 0.3918171 0.1454744 0.3912747 0.1444047 0.3908004 0.1456732 0.3914018 0.1453867 0.3911521 0.1452846 0.3910876 0.39098 0.1449419 0.3909658 0.1447022 0.3908173 0.1445668 0.3908009 0.1491762 0.1491638 0.1486853 0.148371 0.1449539 535 Colorectal 536 Colorectal 531 Colorectal 537 Colorectal 538 Colorectal 532 Colorectal 534 Colorectal 539 Colorectal 540 Colorectal 543 Colorectal 533 Colorectal 541 Colorectal 554 Colorectal 542 Colorectal 544 Colorectal 545 Colorectal 546 Colorectal 553 Colorectal 549 Colorectal Colorectal 552|Colorectal 547 Colorectal 548 Colorectal 550 Colorectal 551

2825.2020-002

Title: Genetic Markers for Tumors

Docket No.:

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PTPN12 Protein tyrosine phosphatase, non-receptor type 12	C1R Complement component C1r	EST: zv47b09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 756761 5', mRNA sequence. (from Genbank)	EST: zo94e09.r1 Stratagene ovarian cancer (#937219) Homo sapiens	cDNA clone 594568 5', mRNA sequence. (from Genbank)	EST; zw55b04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 773935 3', mRNA sequence. (from Genbank)	EST: zw52e11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 773708 3' similar to contains Alu repetitive element;, mRNA	sequence, (from Genbank)			Tumor Necrosis Factor Receptor 2 Associated Protein Trap3	Mucin 6, Gastric (Gb:L07517)	EST: 3724h08 s.1 Stratagana NT2 neuronal practicsor 937230 Homo	saniens cDNA clone 664383 3' mRNA seguence. (from Genbank)	FST: 778n10.s1 Spares NhHMPu S1 Homo sapiens cDNA clone	669570 3' similar to contains Alu repetitive element: mRNA	sequence. (from Genbank)	EST: af61g01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	1046544 3', mRNA sequence. (from Genbank)	ERK6 mRNA for extracellular signal regulated kinase	FST: zh27n04 r1 Soares parathyroid tumor NbHPA Homo sapiens	cDNA clone 304854 5', mRNA sequence. (from Genbank)	EST: zs23b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:686011 5' similar to SW:YHH6_YEAST P32793	HYPOTHETICAL 41.8 KD PROTEIN IN SPO13-ARG4 INTERGENIC	REGION.;, mRNA sequence. (from Genbank)	COX6B gene (COXG) extracted from Human DNA from overlapping	ACCOST 10 C CHROTHOSONIE 18 COSTINGS NO 1530, 1 2040 1, GITA 150 1010 COLUMNING	COAND AIR UPINA, USINIIN SEQUENCE	KPLPU Kibosomai protein, large, PU	Estrogen receptor-related protein (hERRa1) mRNA, 3' end, partial cds
M03425 at	Į.	S.	at	AA165144 i	at	RC AA4366			RC_AA4339	30_at	HG4683-	HT5108_s_a	+	HG880- HT880_at	DC A A2430	58 at	3	BC. AA2349		RC AA6211	59_at	X79483_at	W38778 s	at			AA262132_a	1	A COO044 E	45,000,113_C	, G	M17885 at	L38487_at
6 18 18 18 18 18 18 18 18 18 18 18 18 18	0.20303420 M14058 at		0.20479114		0.20469745		0.20456348 08 at			0.20444244 30_at			0.20435798 t	HG880 0.20420091 HT880		0.20406649 58 at	0.0000000000000000000000000000000000000		0.20393468 25	The state of the s	0.20380616 59_at	0.20371859 X79483		0,20368525 at				0.203607021		330340000	0.20345855 US I	0.20338286 M17885	0.20327981 138487
0 324203	0.331163		0.331074		0.330982		0.330963			0.330919			0.330634	0.330462		0 330301	20000		0.330168		0.330084	0.33005		0.330029				0.329971		7 20004	0.329914	0.329662	0.329598
NO08006 0	0.3900004		0.3907539		0.3907445		0.3905691			0.3904927			0.3904657	0.3904283		0 3000456	,		0.3899879		0.3899682	0.3899612		0.3898947				0.3898051			- 1	0.3895923	0.3895293
702007		1	0.1441881		0.1438796	1	0.1433866			0.1433587			0.1430477	0.1429431		0 1428845	0.1420040		0 1425521		0.1424765	0.1423671		0.1423272				0.1421333		0 4 4 4 0 4 10	0.14.191.72	0.1417995	0.1416053
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Inventors: Sridhar Ramaswamy, et al. C1QB Complement component 1, q subcomponent, beta polypeptide SLC18A3 Solute carrier family 18 (vesicular acetylcholine), member 3 HYPOTHETICAL 23.1 KD PROTEIN IN SHP1-SEC17 INTERGENIC EST: zf65e11.r1 Soares retina N2b4HR Homo sapiens cDNA clone EST: zo36a01.s1 Stratagene endothelial cell 937223 Homo sapiens RC_AA4266 EST: zv47f11.s1 Soares ovary turnor NbHOT Homo sapiens cDNA AA447876 a EST: aa20c09.r1 Soares NhHMPu S1 Homo sapiens cDNA clone EBV/C3d receptor {alternatively spliced, exons 8a,9,10} [human, cDNA clone 588936 3' similar to SW:YBF7_YEAST P34222 Homo sapiens mRNA for cytochrome b5, partial cds clone 756813 3', mRNA sequence. (from Genbank) Guanine nucleotide regulatory protein (tim1) mRNA REGION: ,, mRNA sequence. (from Genbank) 381836 5', mRNA sequence. (from Genbank) RNA polymerase II subunit (hsRPB8) mRNA Homo sapiens clone 24711 mRNA sequence 813808 5', mRNA sequence. (from Genbank) PSEN1 Presenilin 1 (Alzheimer disease 3) U1 small nuclear RNP-specific C protein 0.20129351 S62696_s_atl Jurkat T cells, mRNA Partial, 151 ntl Oncogene MII-Af4, Fusion Activated Cell growth regulator CGR11 mRNA RXRA Retinoid X receptor, alpha SPARC SPARC/osteonectin Protein tyrosine phosphatase 0.20181869 X52773 at-2 Retinoid X receptor, alpha 0.20177579 X52773 at RXRA Retinoid X receptor, GRO3 GRO3 oncogene CYC1 Cytochrome c-1 Poliovirus Receptor CD9 CD9 antigen Homeo box B5 AA059327_i HT5207_s_a ₩ RC_AA1431 0.20151506|HT3598 at RC_AA4318 0,20134012|U09210_at 0.2012092 J03040_at M92299_s_a X53800 s a 0.20156671 U37689 at 0.20212127 M38690 at 0.2020956 U66468 at 0.20261255 Z48541 at 0.20243344 M22877 at 0.20301951 U40380_at RC AA1890 0.20278817 U02082 at 0.20220411 X12517 at 0.20110364|K03430_ HG4757-HG3415-0.2019909 90 s at 0.20216668 73_at 0,20262466 16 at 0.20315456 15_at ä 0.2014449 0.20167392 0.20286448|t 0.20236476 0.20276329 office death the super per such 0.327248 0.327516 0.327313 0.1372264 0.3875924 0.327518 0.327874 0.327734 0.327664 0.328314 0.32807 0.327915 0.327844 0.1385709 0.3882337 0.328149 0.327987 0.328688 0.328376 0.328271 0.329065 0.329138 0.328977 0.328856 0.329482 0.329568 0.329534 0.329446 595 Colorectal | 0.1361887 | 0.3872636 0.136795 0.3875116 0.1377286 0.3878684 0.1367271 0.3874195 0.1389986 0.3885009 0.1375565 0.3877516 0.1374446 0.3877117 589 Colorectal | 0.1375699 | 0.3877516 0.1391638 0.3886307 0.1388823 0.3883795 0.1380976 0.3880465 0.1380976 0.3879883 0.1396057 0.3886772 0.138408 0.3880641 0.1397436 0.3888428 0.388648 0.1390463 0.3886001 0.1412662 0.3891311 0.1399544 0.3889351 575 Colorectal | 0.1405472 | 0.3890792 0.3894798 0.3892001 0.1415465 0.139491 0.1413702 588 Colorectal 592 Colorectal 594 Colorectal 580 Colorectal 581 Colorectal 591 Colorectal 593 Colorectal 590 Colorectal 586 Colorectal 587 Colorectal 582|Colorectal 585 Colorectal 574 Colorectal 576 Colorectal 583 Colorectal 584 Colorectal 572 Colorectal 573 Colorectal 577 Colorectal 578 Colorectal 579 Colorectal

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	at Nek2 mRNA for protein kinase	GGCX Gamma-glutamyl carboxylase	X104 mRNA	RYK RYK receptor-like tyrosine kinase	EST: zr82h02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	682227 3', mRNA sequence. (from Genbank)	EST: ze47c08.s1 Soares retina N2b4HR Homo sapiens cDNA clone	362126 3', mRNA sequence. (from Genbank)	FUT4 Fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-	specific)	HEXB Hexosaminidase B (beta polypeptide)	EST: zv81c03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA iclone 760036 3', mRNA sequence, (from Genbank)		Mucin 4, Tracheobronchial	Placenta copper monamine oxidase mRNA	EST: zo57h03.s1 Stratagene pancreas (#937208) Homo sapiens	cDNA clone 591029 3', mRNA sequence. (from Genbank)	10. 6 - 10. 10. 10. 10. 10. 10. 10. 10. 10. 10.	KIAAU/ 40 gerre product	Integrin beta 4 binding protein	ADORA2B Adenosine A2b receptor		Human 28S ribosomal RNA gene, complete cds. (from Genbank)		AFFX-M27830_M_at (endogenous control)	0.19954881 J03934 s at NMOR1 NAD(P)H:menadione oxidoreductase	RC_AA1349 EST: zo23g05.s1 Stratagene colon (#937204) Homo sapiens cDNA 65 i_at clone 587768 3', mRNA sequence. (from Genbank)	0.19939151 04483 s. at RPS21 Ribosomal profein S21	Homo sapiens SRp46 splicing factor retropseudogene mRNA		Annexin II (lipocortin II) pseudogene 2
	729066_s_at				RC_AA2566	58_at	RC_AA0010	49_at		M58597_at	M23294_at	RC_AA4241 48 at	HG2157-	HT2227 at	U39447_at	RC_AA1590	25_at	AA447244_a	-	RC_AA4282 43 at	X68487_at	AFFX-	M27830_M_at-2	AFFX-	M27830_M_ at	J03934 s at	RC_AA1349 65_i_at	104483 c at	0.19930212 N78005 at	L33799_at	M62895_s_a t
turis territ il muri contr	0.20103195 Z29066_	0,20093626 L17128_at	0.20082115 L27476	0.20075868 S59184_at		0.20071375	RC_AA0010	0.20064518 49_at		0.20058395 M58597	0.20053466 M23294	RC_A 0.2004496.48.at		0.20043641 HT2227	0.2002967 U39447		0.20024462 25_at	00,00000	0.20009403	RC_A 0.1999966 43 at	0.19978234 X68487		M27 0.1997248 at-2		M: 0.19956233 at	0.19954881	RC_AA 0.19947852 65_i_at	0 1003015	0.19930212	0.19923906 L33799	0.1991721
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	0,3872297	0.3871917	0.3871591	0.3869832		0.3869177		0.3867928		0.3867714	0.3867035	0.3864796		0.3863635	0.3863466		0.3862258		0.3861477	0.3861477	0.3859375		0.3858976		0.3858492	0.3858044	0.38577	0 3856008		- 1	0.3854617
	0.1361352	0.1357074	0.1355016	0.1351314		0.1346302		0.1344563		0.1343301	0.1342465	0 1341348		0.134009	0.1335087		0.1332906		0.133234	0.1328404	0.1328117		0.1325887		0.1325887	0.1325647	0.1325387	0.1399667	0.1321966	0.1320532	0.1320363
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် က				U25182 at	RC_AA4762 35_at		- 1	J02947 s a	X01038	RC_AA4002	X85740 at	Z11502 at	X58298_s_a t		76 s at	U16997_at	//1/3/13_s_				801		- 11	11
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A. A. A. A. A.	0.1318774 0.3854134 0.325455 0.198986141 H73519_s a HG3342- 0.1316323 0.3854134 0.325355 0.19897164 U66661 at GABA-A receptor epsilon subunit mRNA (GABA-A receptor epsilon subunit mRN	0.1318774 0.3854134 0.325455 0.19898614 HG3342- HT3519_s a HT3122 Connection factor TFIIE bela subunit, 34 kD a 0.1310938 0.3851432 0.32572 0.19884351 D86960 at KIMAQ205 General transcription factor TFIIE bela subunit, 34 kD a HT310938 0.3851432 0.325175 0.19884351 D86960 at KIMAQ205 General transcription factor TFIIE bela subunit, 34 kD a HT310938 0.3851432 0.325175 0.19884351 D86960 at KIMAQ205 General transcription factor TFIIE bela subunit, 34 kD a HT310938 0.3851432 0.324847 0.1984489 35_at clone 7713173' mRNA sequence. 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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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KIAAAAA		Crystallit, beta 63 (GB:X15145)		sapiens cDNA clone 664024 3' mRNA segmence (from Genhank)	EST: zv47h07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	Shk interacting protein 2-28 mbNA			PEKFR1 6-phoenhofmoto 3 theory (from Genbank)	Platelet activation factor acotylawicalog 10.	Growth-arrest-snecific profein (gas) mPMA	Transcription factor hGATA-6 mRNA		Deoxynucleotidyltransferase, terminal	Proetate differentiation factor - Paris	FI P.1 mRNA sources	FST - 7655000 rd Contra relia Mol. 4115 11	at 381818 5', mRNA sequence. (from Genhank)		Homo sapiens clone 24706 mRNA sequence	SDH1 Succinate dehydrogenase, iron sulphur (Ip) subunit	LDHA Lactate dehydrogenase A	KIAA0755 gans product	Indian hedgehog protein (IHH) mRMA 5' ond		EST: zr76e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	669336 3', mRNA sequence. (from Genbank)	MAAUZU6 gene, partial cds	Homo sapiens clone 192 Rer1 mRNA complete cds	EST: zf64c05.s1 Soares retina N2b4HR Homo sapiens cDNA clone	of 1 of 5, III NIVA Sequence. (Ifom Genbank)
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0.19687009	HG2191	0.19663636		0.19653714 19_at	RC_A 0.1964962840_at	0.1963967 U85611		RC_A 0.19628575 11_at	0.19620813 X52638	0.19610842 D63391	0.19604763 L13720 at	0.19599566 U66075		0.1959323 95_at	0.19583826	0.19570024 M88458 at		0.19567592		0.19560139 20	0.19553293 U17886 at	0.13041030	0.19537848 35	0.19524361 L38517 at	0.19524361		0.19508958 93 at	0.13000410	0.19493294 42	0.1948496 46	
0.323345				0.323274	0.323257			0.323184	0.323146	0.323142	0.323086	0.322973		0.322889	0.322885	0.322823		0.32273			0.322451		0.322195	0.322123	0.322082	0.500000 O	0.322012	0.024000	0.322033	0.321918	
0.383938	0.3838695	1		0.3836988	0.3836536	0.383612		0.3835005	1 1			0.3832378		0.3831516		0.3830174		0.3829249	0000000	0.3620062	0.3826842		0.3823456	0.3821932	0.3821478	0 3824107	0.3821174		0.38205	0.3818007	
0.1278501	0.1277185		1	0.12/5945	0.1274344	0.1272982		0.1271576	0.1271194	0.1270278	0.1269114	0.126/1/3	0.4066405	0.1200405	0.1263899	0.1261906		0.1261373	0 1260684	0.1260647	0.1256548			0.1251066	0.1250249	0.1249676	1		0.124412	0.1243377	
643 Colorectal 0.1278501	644 Colorectal	5 Colorectal		o40 COIDIECIAI	647 Colorectal	648 Colorectal		649 Colorectal	650 Colorectal	651 Colorectal	652 Colorectal	oss cololectal	654 Coloractal	COOLECIAI	655 Colorectal	656 Colorectal		657 Colorectal	658 Colorectal	1	į		661 Colorectal	662 Colorectal	663 Colorectal	664 Colorectal	+	+	666 Colorectal	667 Colorectal	
64.	64	64	979	2	647	64{		646	650	657	700	200	657	3	655	929	1	657	658	629	099		661	799	663	664	665		999	299	

The principal parties of the principal parties

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

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6681	668 Colorectal	0,1241185 0.3817327	0.3817327	0.321866	0.19469456 M73077 at	l	Glucocorticoid receptor repression factor 1 (GRF-1) mRNA
699	669 Colorectal	0.1240252	0.3816356	0.321767	0.19466443 U96094	#	Sarcolipin (SLN) mRNA
					TO THE PARTY OF TH		EST: zs86h10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
					X	√279633_a	AA279633_a IMAGE:704419 5' similar to contains element L1 repetitive element ;,
029	670 Colorectal	0.1239886	0.3816297	0.32164	0.1945989 t		mRNA sequence. (from Genbank)
671	671 Colorectal	0.1237255	0.3814003	0.321519	0.1944212 X14787	at	THBS1 Thrombospondin 1
672	672 Colorectal	0.1237255		0.321428	0.19439913 X14787	at-2	Thrombospondin 1
							Mitochondrial ATP synthase subunit 9, P3 gene copy, mRNA, nuclear
673	673 Colorectal	0.1237121	0.3813404	0.321418	0.19432822 U09813_at		gene encoding mitochondrial protein
674	674 Colorectal	0.1236289	0.3812598	0.321297	0.19428834 X77584	77584_at	TXN Thioredoxin
					N. W.	RC AA4421	
675	675 Colorectal	0.1234703	0.3810924	0.321227	0.19422735 25_at	5 at	KIAA0331 gene product
					X	RC_AA4258	EST: zw47g11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
929	676 Colorectal	0.123212	0.381041	0.321201	0.1940369 52_s_at	2 s at	clone 773252 3', mRNA sequence. (from Genbank)
229	677 Colorectal	0.1231618	0.3808966	0.321196	0.19395724 U43519	43519 at	DRP2 Dystrophin related protein 2
					A	AA131127_a	
678	678 Colorectal	0.1230573	0.3808346	0.321145	0.19385812 1		Cathepsin Z
629	679 Colorectal	0.1229442		0.321119	0.19382109 X92814	92814 at	Rat HREV107-like protein
089	680 Colorectal	0.1228716		0.321081	0.19368309 D38293	38293_at	Clathrin-like protein
681	681 Colorectal	0.1227563	0.3807509	0.320973	0.19358245 D43950	43950_at	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT
682	682 Colorectal	0.1225971	0.3806008	0.320966	0.1934891 D25274	25274_at	Randomly sequenced mRNA
683	683 Colorectal	0.1224722	0.3805043	0.320837	0.19335964 D26018	26018_at	KIAA0039 gene, partial cds
					ח	U27328 s a	Fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis
684	684 Colorectal	0.1223172	0.1223172 0.3804649	0.320789	0.1932318 t		plood group included)
					T.	RC_AA1470	EST: zo32a02.s1 Stratagene colon (#937204) Homo sapiens cDNA
685	685 Colorectal	0.1222639	0.3804564	0.320783	0.19322662 67	7_at	clone 588554 3', mRNA sequence. (from Genbank)
						M10277_s_a	
989	686 Colorectal	0.1220887	0.3803847	0.320777	0.1931/591		ACTB Actin, beta
				1	<u> </u>	RC_AA2570	EST; zr82c03,s1 Soares NnHMPu S1 Homo sapiens cuivA cione
687	687 Colorectal	0.1220792	- 1	0.320685	0.19308423 /4 at	4 at	682180 3, mKNA sequence. (Iroin Genbank)
688	688 Colorectal	0.1218589	0.3803211	0.320593	0.19302863 U95006_at	195006_at	D9 splice variant A mRNA
						AA094507_s	
689	689 Colorectal	0.1217905	0.3802693	0.320566	0.1930049	at	cDNA 5', mRNA sequence. (from Genbank)
		!					EST: zu49d12.s1 Soares ovary tumor NbHO1 Homo sapiens CDINA
					Ľ.	RC_AA4028	clone 741335 3' similar to contains Alu repetitive element, mikiva
069	690 Colorectal		0.121765 0.3801889	0.320555	0.19295281 00_at	0 at	sequence. (from Genbank)
691	691 Colorectal	0.1215827	0.1215827 0.3801688	0.320296		(92720_at	Phosphoenolpyruvate carboxykinase
692	Colorectal	692 Colorectal 0.1215787 0.380007	0.3800073	0.320113	0.19273862 M83751 at	/83751 at	Arginine-rich protein (ARP) gene

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AA173597_a EST: zp03c08.r1 Stratagene ovarian cancer (#937219) Homo sapiens	Guanine Nucleotide-Binding Protein Ral, Ras-Oncogene Related Enteric smooth muscle gamma-actin gene, 5' flank and		EST: zt79h07.s1 Soares testis NHT Homo sapiens cDNA clone	Homeo box c1 protein, mRNA	Epidermal growth factor receptor kinase substrate (Eps8) mRNA	KIAA0011 gene	CARS Cysteinyl-tRNA synthetase	Gem GTPase (rem) mon A	Desmonlarin I	EST: Human fetal brain cDNA 3'-end GEN-098C12, mRNA sequence.	EST: zk95b03.s1 Soares pregnant uterus NbHPU Homo sapiens	Grand Handler Sequence. (from Genbank)	AA380393_a EST: EST93352 Supt cells Homo sapiens cDNA 5' end, mRNA	X66401_cds LMP2 gene extracted from H.sapiens genes TAP1, TAP2, LMP2, 1 at LMP7 and DOB	Human Chromosome 16 BAC close Cittootory A 20100	EST: 2x74g11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	EST: zf20c08.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 377486 31, mRNA sequence (from Genhank)	EST: zx08f10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785899 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;, mRNA sequence. (from Genbank)
	HG1103- 0.19256769 HT1103 at 0.19248337 D00654 at	RC_AA1674 36 i at	RC_AA4357 69 s at	M16937 at	U12535_at	D13636 at	0 1918137 1184720 at	U10550 at	HG174- HT174 at	RC_C14898 at	AA1267	A2058	AA380393_a	X66401_cds 1_at	A1521	3471_s	_AA0558 at	
0.19265793		RC_AA 0.19233952 36_i_at	0.19229622 69 s at	0.19213337 M16937	0.19205002 U12535	0.1918/795 D13636 at	0 1918137	0.19169855 U10550	HG174- 0.19165988 HT174 at	0.19158694	0.19140579 19	RC_A 0 10120631 03 at	0.191270261	X664 0.1911793 1 at	RC_A 0.1911104603 at	0.19102597		RC 0.19093734 75
0.320062	0.319914	0.319713	0.319691		0.319609	0.319526			0.319098	0.319069	0.319056	0.318937	0.318931	0.318815	0.318644	0.318574	0.318574	0.318568
0.3799817	0.1213798 0.3799744 0.1212289 0.3799523	0.3799256			0.3798241		0.3796654	0.1204366 0.3795269	0.3794884	0.3793192	0.3793083	0.3792779	0.3792536	0.3791769	0.3791715	0.3790575	0.3789529	0.3789345
0.1215052	0.1213798	0.1210308	0.1209356	0.1209061	0.1208698	0.1206173	0.1204419	0.1204366	0.1203954	0.1201526	0.1200641	0.1198904	0.119448	0.1188506	0.1183064	0.118229	0.1179214	0.1178902 0.3789345
693 Colorectal	694 Colorectal 695 Colorectal	696 Colorectal	697 Colorectal	698 Colorectal	700 Colorectal	701 Colorectal	702 Colorectal	703 Colorectal	704 Colorectal	705 Colorectal	706 Colorectal	707 Colorectal	708 Colorectal	709 Colorectal	710 Colorectal	711 Colorectal	712 Colorectal	713 Colorectal

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EST: zx38a01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788712 3', mRNA sequence. (from Genbank)		Interferon-related develonmental radii dator 1		MaTi MN mBNA for 254/69N motors	Social 401			Mac25	Polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)			EST: yv38f12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA	nroline 4-					DNA clone	FOCES Exercised 5, IIIRNA Sequence. (from Genbank)	EST: 2/3/ht/0 st Constant of IgGs, flow affinity flat, receptor for (CD/16)	cone 755587.3" mRNA sections (from Contrart)	INP10 Interferon (gamma)-included cell line, profeso 10 from	MST1R Protein-tyrosine kinase RON	GOT2 Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate	aminotransferase 2) Phanylalkylamino kinding anothin	Transfermed brokens	Latent Wemprane Protein Lmp1	EST: ZIZUNU8.S1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502527 3', mRNA sequence, (from Genhank)	EST: zk74f05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488577 3', mRNA sequence. (from Genbank)
RC_AA4499 42_at	RC_AA4173 373 at	RC_AA4056	RC_AA4057	X66839 at			11 .	HT987_at	D81608_at	Y08639_at	X76534_at	N72380 s a		W49521 at	1 1	RC_AA1567	92 at	KC_AA2360 18_at	104162 at		17 at	X02530 at	0.18925394 X70040 at	000001	737986 at		11144 dl	אל אל אל אל 73_at	A0472
RC_A 0.19087711 42_at	RC 0.19075918 73	0.19057879 12 at	0.19052759.44 at	0.19046406 X66839	0.19038299 U07550	0.19029583 X54941	The state of the s	0.19015858 HT987	0.19011314 D81608	0.1900737 Y08639	0.18990482 X76534	0.18984148†		0.18976343 W49521	0.18965365 X13334	0	0.18956053 92	18949509 18	0.18942805,104162		0.18937059 17 at	0.18931441 X02530	0.18925394	0.40007444	0.18901491 737986	HG742-	0.10030430	0.18892474 73_at	RC 0.18888468 90
0.318468	0.318365	0.318296	0.318253	0.3182	1_	L			0.3178		0.317715	0.317655		0.317634	0.317588	7,7	0.3175	0.317498	0.317325		0.317125	0.317088	0.316991	0.346020	0.316806	0 34676		0.316721	0.316529
0.378897	0.1174486 0.3788644	0.3788196	0.3788065	1	0.3784709	0.378439		- 1	0.378394	- 1	0.3/81449	0.3780906			0.3779147	0.977094	0.377031	0.377796	0.3777811				0.37777167	0.3777467		0 3774440	71	0.3773945	0.377328
0.1175263	0.1174486	0.1174355	0.1174113	0.1173908	0.1173887	0.1171897	1	0.11/116	0.1170865	0.1168432	0.1165629	0.1162928		0.1161021	0.1159714	0 11/0368	0.1143300	0.1147768	0.114763		0.11451	0.1144905	0.1141271	0.1139887	0.1137097	0 1136393		0.113539	0.1134186
714 Colorectal	715 Colorectal	716 Colorectal	717 Colorectal	718 Colorectal	719 Colorectal	720 Colorectal	-	721 Colorectal	722 Colorectal	724 Colorectal	724 COIOI ectal	725 Colorectal		/zb Colorectal	727 Colorectal	728 Colorectal		729 Colorectal	730 Colorectal		731 Colorectal	732 Colorectal	733 Colorectal	734 Colorectal	735 Colorectal	736 Colorectal		737 Colorectal	738 Colorectal
7	71	77	7	7.1	7	7.7	7	7)	7	7 5	71	72	1	7)	2	72	1	72	73		73	33	25	73,	73	736		73.	738

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. 111 101	Phosphotyrosine independent ligand p62 for the Lck SH2 domain mRNA	26S PROTEASE REGULATORY SUBUNIT 7		cds			my CE. (1145 5, IIIXAA Sequence. (Ifom Genbank)	SNRPB Small nuclear ribonucleoprotein polypeptides B and B1	tein (NCC27) mRNA	COL1A1 Collagen, type I, alpha 1	GIPR Gastric inhibitory nolymentide recentor	EST: Human aorta cDNA 5'-end GEN-304G05, mRNA sequence.		GARS Given that surfaces		EST: zi09g09.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 430336 3', mRNA sequence. (from Genbank)		1 factor	itheli m (#937231) Homo	sapiens cDNA clone 531836 3', mRNA sequence. (from Genhank)		-	754012 3', mRNA sequence. (from Genbank)	KIAA0213 gene, partial cds	ECIVARYOTIC INTITATION FACTOR 4A-LIKE NUK-34 FST: FST83074 Homo canians contact and circular to Mana.	at Genbank)	RPS6KA2 Ribosomal protein S6 kinase, 90kD, polypeptide 2	Cytochrome c oxidase subjunit VIII (COX8) mRNA	
	0.18871331 U46751 at	0.1886412 D11094_at	RC_AA4357	0.18851288 20_f_at	0.18840776 M22760 at	RC_AA2925 0.18837102 33_at	X17567 c 2	007 t	0.18818274 U93205_at	0.18809533 Z74615 at	X81832_s_a 67_t	D62600_s_a	0.187810381.27080.24	0.18766183 U09587 at		RC_AA0106 0.18762258 19_at	RC_AA2331 02 70 at	0.18737254 M92934 at	RC_AA1160	0.1873025 36_at	RC_AA3218 38 33_at	RC_AA4789	22 67 at	0.16704036 D86968 at	20 DZ 1033 at	0.18690695 T35341 s at	0.18681534 L07597_at	J04823_rna1 D4_at	
11111									أ			0.18788427	0.187810	0.187661		0.187622	RC_A 0.18740402 70 at	0.187372		0.18730	RC 0.1872338 33		0.18718122 67	0.107030	201.0	0.186906	0.186815	0.18676004	
	0.316489	0.316455		\perp	0.316278	0.316247	1			0.316004	0.315769	0.315752				0.315621	0.315578	0.315546		0.315458	0.315199	1	0.315182	0.315107		0.315103	0.314993	0.314982	
	0.3772997	0.1128246 0.3772854			0.3772103	0.3770899			f	0.3769757	0.3769163	0.1116565 0.3769163	0.3768666	0.376859		0.376736	0.3766674	0.3766201		0.3766073	0.3765291	0.70	0.3/64139			0.3762199	0.3760927	0.11045 0.3760301	
	0.1132421	0.1128246	77070	0.112/841	0.112/803	0.1126677		0.1120379	0.1120189	0.1117037	0.1116607	0.1116565	0.1115345	0.1113154		0.1111667	0.1110516	0.1110429		0.1110066	0.1108751	0 4407570	0.1107559	0.110665		0.1105232	0.1105111	0.11045	
	739 Colorectal	740 Colorectal	100000	741 Colorectal	742 Colorectal	743 Colorectal		744 Colorectal	745 Colorectal	COIOI COIGI	747 Colorectal	748 Colorectal	749 Colorectal	750 Colorectal		751 Colorectal	752 Colorectal	753 Colorectal	-	/54 Colorectal	755 Colorectal	758 (00/00/04)	757 Colorectal	758 Colorectal		759 Colorectal	/60 Colorectal	761 Colorectal	
	735	740	1	147	147	743		744	7/8	7	747	748	749	750		751	752	753	L	45	755	756	757	758		759	30	761	

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	EST: zf07h12.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 376295 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element; mRNA sequence. (from Genbank)	EST: zr75h04.s1 Soares NhHMPu S1 Horno sapiens cDNA clone 669271 3', mRNA sequence. (from Genbank)	CYP27 Cytochrome P450, subfamily XXVII (steroid 27-hydroxylase, cerebrotendinous xanthomatosis)	Selenoprotein P	FH Fumarate hydratase	EST: zs12g10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:685026 3', mRNA sequence, (from Genbank)	TCF1 Transcription factor 1, hepatic; LF-B1, hepatic nuclear factor (HNF1). albumin proximal factor	EST; zw62c11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 774644 3' similar to TR:G207250 G207250 RAT GROWTH	AND TRANSFORMATION-DEPENDENT;, mRNA sequence. (from	Genbank)	KIAA0103 gene		Neuronal PAS domain protein 2		Homeo box B1		HOXB1 Homeo box B1	AA195893_a EST: zp97e03.r1 Stratagene muscle 937209 Homo sapiens cDNA	clone 628156 5', mRNA sequence. (from Genbank)	Z25821_ma Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme	A isomerase)		Major Histocompatibility Complex, Class I, C (Gb:X58536)	Mediator of receptor-induced toxicity		Ciaudin 3	EST. 2800006.51 NOT COAR GOD HOURS sapiets COINA CIONE MARCE: 703767 31 mRNA comience (from Genhank)	Afavia-telandiactasia group D-associated protein mRNA	EST: 2443406 s 1 Soares total fetus Nh2HER 9w Homo saniens cDNA	clone 789227 3', mRNA sequence. (from Genbank)
1	A0395	A2364	at			A2523		at			A4417		D14659 at	RC_AA4559	67_at	X16666_s_a		X16666_s_a		AA195893_a		Z25821_rna	1 s_at	HG658-	HT658_f_at	X84709_at	RC_AA4821	26 at	NC_MAZ 103	1 2/203 at	PC AA4502	33 at
	RC_A 0.1866799 76_at	RC_A 0.1866324 60_at	0.18651803 X59812	0.18645349 Z11793 at	0.18636103 U59309 at		0.18633045 95_at	0.18620825 M57732				0.18616688 98_at	0.18606272 D14659 at		0.18603663 67_at		0.18593888 t-2		0.18587461		0.18580322		0.185724511		0.18563227 HT658_f	0.18554266 X84709	00,0120,0	0.18540493 Zb at	0.18532212 02 at	0.185271012/203 at	0.1002/13	0.18518591 33_at
	0.314861	0.314826	0.31479	0.31479	0.314749		0.314526	0.31446				0.314306	0.314255		0.314135		0.314118		0.314106		0.314064		0.314014		0.313833	0.313822	7000	0.31361	0 313510	0.010010		0.313458
	0.3760109	0.3759728			0.3757923	1	0.3757726	0.3757363	ł			0.3756432	0.3754573		0.3754449		0.3754011		0.3751272	1	0.3750993		0.3750481		0.3749245	0.3747783		0.3/4/63/	0.3777591	- 1		0.3745598
	0.1102982	0.1101836	0.1101059	0.1096608	0.1095469		0.1094853	0 1094749				0.1094025	0.1086783		0.1085378		0.1083784		0.1083784		0.1082166		0.1082015		0.1081496	0.1080974	0000	0.1080925	0.4080370	0.100001.0	0.1000002	0.1079596
	762 Colorectal	763 Colorectal	764 Colorectal	765 Colorectal	766 Colorectal		767 Colorectal	768 Colorectal				769 Colorectal	770 Colorectal		771 Colorectal		772 Colorectal		773 Colorectal		774 Colorectal		775 Colorectal		776 Colorectal	777 Colorectal		//8 Colorectal	770 Coloractal	780 Coloroctal	COIOLECIAI	781 Colorectal
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EST: zw03c10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 768210 3. mRNA sequence. (from Genbank)	AA489716_a 823656 5' similar to contains element MER22 repetitive element ;;	Dystrophin (dp140) mRNA, 5' end	Clone 23548 mRNA sequence	0.1848114/S69272 s at Cytoplasmic antiproteinase	RC_AA5984 Homo sapiens clone 486790 diphosphoinositol polyphosphate	phosphorydrolase mklvA, complete cds ECT: 30/8405 c1 NICL CGAD CCB1 Home conjunction along	IMAGE:824169 3', mRNA sequence. (from Genbank)	(chromosome 3p25) membrane protein mRNA	Homo sapiens mRNA for zinc finger protein, complete cds		Banilator of C protain cinnaling E	11 beta-hydroxysteroid dehydrogenase type II mRNA		EST: zw32f12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 771023 3' similar to contains Alu repetitive element; contains	element OFR repetitive element;, mRNA sequence. (from Genbank)	AA036794_a cDNA clone 471912 5' similar to WP:T20B12.3 CE01409;, mRNA sequence. (from Genbank)		HOXB5 Homeo box B5 (2.1 protein)	ETFA Electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	EST: zs94do7.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:705133 3. mRNA sequence (from Genhank)	H105e3 mRNA	at GCN5-like 1	5-aminoimidazole-4-carboxamide-1-beta-D-ribonucleoti de transformylase/inosinicase	0.18366866 D82348 at-2 ribon ucleotide transformylase/inosinicase, complete cds
2_AA4248	AA489716_a	L35854 at	11	S69272 s at	RC_AA5984	A4908		L09260 at	D45213_at	J03460_s_at	AA081209_a	U26726_at		A4279	78_at	AA036794_a t	X03794_s_a	+	J04058_at	RC_AA2812 45 at	U47105 at	လ	aţ	D82348_at-2
3386 0.18515852 81	0.18505086	0.184967181135854	0.18489441 U79277	0.1848114	0.40476999	0.104/0222 44 al	0.18471572 85_at	0.18461254 1.09260	0.18451354 D45213 at	0.18444666 J03460_s	0 18432246	0.18428504 U26726			0.18425202 78_at	0.18417485		0.18413731	0.18404259 304058	0.18397607 45 at	0.18394175 U47105	0.18386884 S82447	0.18372026 D82348	0.18366866
0.313386	0.313304	1	1	0.313172	73087	0.01000	0.313037	0.313037	0.312959	0.312854	0.312743	0.312695			0.31266	0.312572	1	0.312513	0.312471	0.312384	0.31236	0.312333	0.312306	0.312253
0.3744406	0.3744339	0.3742585	0.3742047	0.3741384	0.3740643	0,004,10,0	0.3740326	0.3740277	0.3739299	0.3739	0.3736877			1	0.373621	0.3735119		0.3734322	0.3732599	0.3731474	0.3730889	0.3730461	0.3730134	0.3729946
0.1078156	0.1076643		0.1073138	0.107282	0.4074564	1001.00	0.1071265	0.1069943	0.1069878	0.1068639	0.1064241				0.1058599	0.1056269	L	0.10558	0.1055759	0.1055733	0.1054405	0.1052258	0.1050332	0.1050332
782 Colorectal	783 Colorectal	784 Colorectal	785 Colorectal	786 Colorectal	787 Coloractal	2000	788 Colorectal	789 Colorectal	790 Colorectal	791 Colorectal	792 Colorectal	793 Colorectal		-	794 Colorectal	795 Colorectal	-	/yo Colorectal	797 Colorectal	798 Colorectal	799 Colorectal	800 Colorectal	801 Colorectal	802 Colorectal
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the Benth thank	EST: zx66c02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796418 3', mRNA seguence (from Ganbank)	PLN Phospholamban	Crystallin, Beta B3 (Gb:X15144)	Homo caniane clono 94770 unite	DDH1 Dihydrodiol dehydrogenase	EST: 2l43h11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 5047413', mRNA segmence. (from Ganhank)		-, -				0	Interferon regulatory factor 3		DNA clone	enbank) sapiens cDNA clone	recess, mind sequence, (from cenbank)	VON WILLEBRAND FACTOR PRECURSOR	TEL ALOCT IE NOCLEAR PACTOR 4	(clone 14VS) metallothionein-IG (MT1G) gene	LIVE OF TRIASE MIKINA	KIAA0187 gene	AA329542_a EST: EST33182 Embryo, 12 week II Homo sapiens cDNA 5' end, t mRNA sequence. (from Genbank)
Antis Kour duste south worth th	RC_AA4599 1 60_s at	0.18349603 M63603 at	HGZ190- 0.183438 HT2260_at	RC_AA1714 4 88 at		RC_AA1514 9 35_at	0.18319568 D45371 at	RC_AA2837 3 74 at	HG4716- 0.1830483 HT5158 at	AA402298_s		A2339	1 at	AA247685_a t	RC_AA4890	A4245	/10321_s_a	87870 at	J03910_rna1	ta	s s	D80009 at	AA329542_a E
t IL the the				RC_A 0.1834114 88_at	0	RC 0.18327339 35	0.1831956	RC_A 0.18316203 74 at	0.183048;	0.18294445		RC_A 0.1828722 57_at	0.18280217	0.18273248	0.1827102 91 at	RC_A 0.18257977 17 at	N 400400400	0.1824167 X87870	0.4899940	0.182257031 33804	0.1821856	0.18209319	0.18198761
il test the	0.312239		0.312186		0.312153	0.312098	0.312098	0.312058	0.311945	0.311896		0.311779	0.311453	0.311318	0.311197	0.31111	0.344079	0.311008	0.310788	0.310763	0.310696	0.310641	0.310531
		0.3728766	0.3728493		0.3727079	0.3725623	0.3724439	0.372392	0.3723761	0.3723377		0	0.372103	0.3719171	0.3717969	0.3717966	0.3716924	0.3716767	0.3716735	0.3716703	0.3715265	0.3714274	0.371401
	0.1047495	0.104/429	0.1046492	0.1045248	0.1043271	0.1041077	0.103823	0.1037316	0.1036369	0.1034785		0.1034678	0.1033997	0.103123	0.103017	0.1028238	0.1026596 0.3716924	0.1023984	0.1022189	0.1020303	0.1019609 0.3715265	0.1016902	0.1016138
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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. AA418214_a 767749 5' similar to TR:G633926 G633926 APK1 ANTIGEN. ;, mRNA EST: aa90n11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA EST: zw47g05.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA Non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds AA461426_r | EST: zx63h02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: zv70f08.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA N89563_s_a | EST: HFBEST-40 Human fetal brain QBoqin2 Homo sapiens cDNA, Beta-galactoside alpha2,6-sialyltransferase (SIAT1) mRNA, exon W EST: zu44g09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA AA442428_a HYPOTHETICAL 60.5 KD PROTEIN IN PDB1-ABD1 INTERGENIC EST: aa20d05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone clone 773240 5' similar to SW:ALG5_YEAST P40350 DOLICHYL-RC_AA4569 clone 838629 3' similar to contains Alu repetitive element;, mRNA EST: zv08f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zv97f07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA4286 EST: zw69c02.s1 Soares testis NHT Homo sapiens cDNA clone AA425251_a|PHOSPHATE BETA-GLUCOSYLTRANSFERASE;, mRNA Putative serine/threonine protein kinase PRK (prk) mRNA clone 759015 5' similar to SW:YB72_YEAST P38137 clone 740896 3', mRNA sequence. (from Genbank) clone 796179 5', mRNA sequence. (from Genbank) MYH9 Myosin, heavy polypeptide 9, non-muscle PSG6 Pregnancy-specific beta-1 glycoprotein 6 REGION.;, mRNA sequence. (from Genbank) 753057 3', mRNA sequence. (from Genbank) 813801 3', mRNA sequence. (from Genbank) 781442 3', mRNA sequence. (from Genbank) SCAD gene, exon 1 and joining features mRNA sequence. (from Genbank) Activin beta-A subunit (exon 2) KIAA0199 gene, partial cds sequence. (from Genbank) sequence. (from Genbank) sequence. (from Genbank) CALPAIN 1, LARGE X57579_s_a RC_AA4364 RC_AA4477 RC AA4777 Z80345_rna 0.18142752 M31013 at 0.18177584 U67849 at 0.181525 D83782 at 0.18125597 X04366 at 0.1809571 U56998 at ਜ਼ 0.18071891|D86479 at 0.18072318 X17098 0.18179104 1_s_at 0.18161505|29_at 0.18131231 77 at 0.18108182 81 at 0.18103768 22_at 0.18106878 03 at aţ 0.18137753 0.18188469 0.181682 0.18103768 0.18090901 0.1807964 0.310315 0.309696 0.310429 0.310431 0.30984 0.309749 0.309709 0.309578 0.310299 0.310279 0.310255 0.310156 0.0993158 0.3699015 0.309516 0.310261 0.310231 0.309907 0.309522 0.30951 0.1015221 0.3711679 0.371024 0.1010276 0.3706148 0.0999086 0.3702316 0.1015356 0.3712717 0.1015099 0.3710451 0.1010108 0.3704874 0.1008865 0.3704431 0.1005393 0.370402 0.1004137 0.3703068 0.1001854 0.3702498 0.0998011 0.3701576 0.099793 0.3701058 840 Colorectal | 0.0994662 | 0.3700781 0.36998 0.1013914 0.3709471 0.1011125 0.3708007 0.0993145 0.3698788 0.1014571 0.0993424 833 Colorectal 838 Colorectal 839 Colorectal 843 Colorectal 830 Colorectal 831 Colorectal 834 Colorectal 825 Colorectal 828 Colorectal 829 Colorectal 832 Colorectal 837 Colorectal 841 Colorectal 842 Colorectal 326 Colorectal 327 Colorectal 335 Colorectal 836 Colorectal

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HG491- 4 HT491 at	0.18051022 41_at	RC_AA4525 4 38 at	118391 s_a	185289 at	Ø	124485_s_a	at	at	0.17996137 U65579 at	3996	ซี	A6085 8 at	AA287289 a E	ω	A0106	77	:	
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0.30944	0.309379	0.309305	0.30928		0.30923	0.309186	0.308989	0.30892	0.308848	0.308817		0.308801	0.308689	0.308553	0.308426	0.308416	0.308004	0.307925
0.0992493 0.3696489	0.3695954	0.3695771	0.3695127	0.0982712 0.3694668	0.3694266	0.3693816	0.3693463	0.3692421	0.3691822	0.3691728		0.3690573	0.3686484	0.3686215	0.3685397	0.3685113	0.3684908	0.3082811
0.0992493	0.0990316	0.0986173	0.0983304	0.0982712	0.098265	0.0981109	0.098003	0.0979339	0.0974983	0.0974748	•	0.0968551	0.0964766	0.0964245	0.0960668	0.0960401	0.0959868	
844 Colorectal	845 Colorectal	846 Colorectal	847 Colorectal	848 Colorectal	849 Colorectal	850 Colorectal	851 Colorectal	852 Colorectal	853 Colorectal	854 Colorectal 855 Colorectal		856 Colorectal 857 Colorectal	858 Colorectal	859 Colorectal (860 Colorectal	861 Colorectal (862 Colorectal (863 Colorectal C	\dashv
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Anis anis sens	Dynamin (DNM) mRNA	A Donicotion and A Contraction A Contraction of the	INS 1 months	KIAAAAAA CACAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Refinoir acid-resonantia and the second seco	MCP Membrane cofactor protein (CD46, trophoblast-lymphocyte	cross-reactive antigen) KIAA0180 gene nartisl প্ৰ	Himon mDNIA for VIA Action	AA478674_a EST: zv19f08.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	` —		EST: zw59c03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA		ARSB Anjeufeteen B	piens cDNA clone	rom Genbank)		EST: zs25e01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686232 3' similar to WP:R05G6.4 CE07417;; mRNA sequence (from Genhank)		S NbHPU Homo sapiens	EST: csg1676.seq.F Human fetal heart, Lambda ZAP Express Homo	EST: zv24f04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	EST: zs87f02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	KIAA0035 gene, partial cds	AA078862_s EST: zm92d02.r1 Stratagene ovarian cancer (#937219) Homo	sapiens culva clone 545379 5', mRNA sequence. (from Genbank) ELONGATION FACTOR TU, MITOCHONDRIAL PRECURSOR
Unif their Their made reall	0.17928061 L36983_at	31 07493 at		0.17905654 D86957 at	U50383 at	0 17886594 X59406 at	0.17874716 D80002 at	D80002 at-2	AA478674_a	0.178526551129195 24	M55621 at	A4300	5 f	M32373 at	RC_AA4373 23 at	RC_AA6088		_AA2622 at		A1279	A248169_a	A4063	AA2797	äţ	4A078862_s E	
		0.17913303 07493		0		0.17886592	0.17874716	0.1786732		1	0.1783631 M55621	RC_A 0.17836049 74 at	0.17826907	0.17823921 M32373	RC_A 0.17805123 at	RC_A 0 17802346 50 -st	0.110040	RC 0.17794147 61	0.17781886 U90915_at	RC_A 0.1777522 46_at	0.177661051	0.17762522 20 at	0.17757253 87	0.17743365 D21262	0 17741808	0.17734616 S75463 at
L	0.307918	0.307852		0.307734		0:307	0	0.307336	0.307336	L		0.30722	0.30714	0.307072	0.306854	0.306816		0.306712	0.306548	0.306247	0.306184	0.306132	0.306122	0.306098	0.306016	0.305938
0 36802		0.3681307	0.3681182	0.3680734	0.3680191	0.3679965	1 1	0.3678478	0.3677385		0.3676104	0.3675207	0.0947793 0.3674794	0.3672888	0.3672148	0.3672111		0.3671756	0.3671325	0.3670834	0.3670663	0.3670338	0.3668634	0.3665892	0.366504	0.3664064
0.0958927	2000000	0.0957509	0.0956532	0.0956037	0.095559	0.0953243	0.0951026	0.0951026	0.0950603	0.0950569	0.0950386	0.0949239	0.0947793	0.0946479	0.0944786	0.0944084		0.0943732	0.094198	0.0941319	0.0940872	0.0938772		0.0931873	0.0927504	0.0921649
865 Colorectal		866 Colorectal	867 Colorectal	868 Colorectal	869 Colorectal	870 Colorectal	871 Colorectal	872 Colorectal	873 Colorectal	874 Colorectal	875 Colorectal	876 Colorectal	877 Colorectal	878 Colorectal	879 Colorectal	880 Colorectal		881 Colorectal	COLOT ECTAI	883 Colorectal	Colorectal	885 Colorectal		887 Colorectal		889 Colorectal (
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830	890 Colorectal	0.0919764	0.3661593	0.305894	0.17725754 X53331 at		MGP Matrix protein gla
891	891 Colorectal	0.091899	0.3661587	0.305843	0.17721215 U45285_at		Specific 116-kDa vacuolar proton pump subunit (OC-116KDa) mRNA
					1	A090842_a	AA090842_a EST: yy0444.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
892	892 Colorectal	0.0918772	0.3661394	0.305724	0.177093941		cDNA 5', mRNA sequence. (from Genbank)
					ت	DC 000027	EST: zv60c04.s1 Soares testis NHT Homo sapiens cDNA clone
893	893 Colorectal	0.0917985	0.3661088	0.305633	0.17704633 63_at	7744	SPECIFIC CYCLIN B2.; mRNA sequence. (from Genbank)
894	894 Colorectal	0.0916026	0.0916026 0.3660908	0.305611	0.17696834 D30755	J30755_at	VIM Vimentin
895	895 Colorectal	0.0916026	0.3659485	0.305539	0.17690636)30755 at-2	0.17690636 D30755 at-2 Human mRNA for KIAA0113 gene, partial cds
			(]	Homo sapiens cDNA
						4A478131_a	AA478131_a clone 740658 5' similar to TR:G433963 G433963 P18H-REV 107.;,
896	896 Colorectal	0.0915553	0.3658933	0.305526	0.17685972		T
						RC_AA3977	piens cDNA clone
897	Colorectal	0.0915244	0.3658475	0.305441	0.17679666 79	79_at	
							Kidney mRNA for putative membrane protein with histidine rich charge
868	898 Colorectal	0.0911797	0.3658407	0.305382	0.17671314 D82060 at	D82060_at	clusters
						RC_D51235	
868	899 Colorectal	0.0910688	0.3658318	0.305334	0.17667067	f_at	Tumor rejection antigen (gp96) 1
						AA343629_a	
906	900 Colorectal	0.0907928	· ·	0.30528	0.17658818	-	spo e
901	901 Colorectal	0.0907866		0.305222	0.17648873 L.10413	L10413_at	ase, CAAX box, alpha
902	902 Colorectal	0.0907267	0.3655602	0.305185	0.17641185 V01514	V01514_at	AFP Alpha-fetoprotein
						RC_AA4421	EST: zw56h03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
903	903 Colorectal	0.0905193	0.3654815	0.305185	0.17637348 44_at	44_at	clone 774101 3', mRNA sequence. (from Genbank)
904	904 Colorectal	0.0904557	0.365401	0.305034	0.17626467 M95178 at	M95178_at	ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM
						RC_AA2365	EST: zs39e02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
908	905 Colorectal	0.0904479		0.304976	0.17623897 59_at	59_at	687578 3', mRNA sequence. (from Genbank)
906	906 Colorectal	0.090388	0.3653446	0.304942	0.17616539 U70212_at	U70212 at	Single-minded (Drosophila) homolog 1
						RC_AA4901	EST: ab05f07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
907	907 Colorectal	0.0903135		0,304911	0.17611153 42	42_at	clone 839941 3', mRNA sequence. (from Genbank)
306	908 Colorectal	0.0901215	0.3652385	0.304868	0.17608988 X70649	X70649_at	CI.1042 mRNA of DEAD box protein family
			1				EST: yl56g01.r1 Homo sapiens cDNA clone 162288 5'. (from
300	909 Colorectal	0.0899683	0.3651849	0.304849	0.1759395	0.1759395 H25982_at	Genbank)
						X51362_s_a	
910	910 Colorectal	0.0899229	0.3651123	0.304843	0.175914231	ţ	DRD2 Dopamine D2 receptor
94	011 Colorectal	0.0898177	0.3650917	0.3047		C00180 f at	0.1758407 C00180 f at Synaptic alycoprotein SC2
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Homo sapiens chromosome 9 P1 clone 11650	Phospholipase C, beta 3 (phosphatidylinositol-specific)	33 kDa transcriptional co-activator	EST: yw36d01.r1 Homo sapiens cDNA clone 254305 5'. (from Genbank)	Thyroid autoantigen (truncated actin-binding profein) mRNA		Glutamine cyclotransferase	KIAA0233 gene	0.17527397 S62028 s. at RCV1 Recoverin	M38193_rna Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine 1_s_at esterase 1)	EST: zx89g02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810962 3' similar to SW:MV10_MOUSE P23249 PUTATIVE GTP-BINDING PROTEIN MOV10.;, mRNA sequence. (from Genbank)		AEEX_CroX & of (minorallomount profits)	A PER VIOLE TO THE CHIPS OF THE CHIPS)	NGEB Nerve growth factor beta		EST: 2542906.51 Soares NhHMPu S1 Homo sapiens cDNA clone	MAC30 mRNA, 3' end	CDC16Hs mRNA	EST: zf63e06.s1 Soares retina N2b4HR Homo sapiens cDNA clone 381634 31 mRNA secuence (from Ganhank)	DNA-DIRECTED RNA POLYMERASE II 144 KD POI YPEPTINE	Clone 23961 mRNA sequence	0.1742654 U79295_at-2 Human clone 23961 mRNA sequence
RC_AA1792 98_at	Z37544_rna 1_s_at	RC_AA2365 16_at	0.17563848 N81162_at	0.17551358 M62994_at	0.1754635 D61871 r at	a	D87071_at	S62028_s_at	M38193_rna 1_s_at	RC_AA4594 02 s at	H81448_s_a t	AFFX-CreX-5 at-2	AFFX-CreX-	X52599 at	AA053096_a	358		at .	A0590	at	at	U79295_at-2
RC_A 0.175794 98 at	0.17571668	0.17566574 16_	0.17563848	0.17551358	0.1754635	0.17542724 X71125	0.17539804 D87071 at	0.17527397	M3819. 0.17524418 1_s_at	RC_AA4 0.1751563 02 s at	0.17509894	0.17493787	AFF)	0.1747826 X52599	0.17471111	0.17463842 03 f at	0.17458098 L19183 at	0.17449743 U18291	RC_A 0.17445114 14 at	0.17441405 Z27113	0.174368 U79295	0.1742654
0.304618	0.304544	0.304365		0.304219	0.304209	0.304189	0.304127	0.304073	0.303965	0.303907	0.303854	0.303745	0.303736	0.303637	0.303548	0.303543	0.303457	0.303353	0.303279	0.303247	0.303244	0.303191
0.3649236	0.3646752	0.3646393	1	0.3645176	0.3644964	0.3644176	0.364372	0.3642209	0.3641273	0.3640126	0.3638175	0.36377	0.3637284	0.0885625 0.3636926	0.3636769	0.0884516 0.3636729	0.3636514	0.3636181	0.3635748		0.3635193	0.3634415
0.089772	0.0895391	0.0894386	0.0893178	0.0892828	0.0891553	0.0891149	0.0890112	0.0889243	0.0889151	0.0888401	0.0887433	0.0886368	0.0886368	0.0885625	0.0885268	0.0884516	0.0882725 0.3636514	0.0881408	0.0880567	0.0880195	0.0880064	0.0880064
912 Colorectal	913 Colorectal	914 Colorectal	915 Colorectal	916 Colorectal	917 Colorectal	918 Colorectal	919 Colorectal	920 Colorectal	921 Colorectal	922 Colorectal	923 Colorectal	924 Colorectal	925 Colorectal	926 Colorectal	927 Colorectal		-	aon colorectal		932 Colorectal	933 Colorectal	934 Colorectal
912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927 (928 (929 (320	931 (932(933(934 (

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The state of the s	AF007875_a Dolichol monophosphate mannose synthase (UPM1) mKNA, parma	cos EST: zr58h06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	667643 3', mRNA sequence. (from Genbank)	GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR	(CF:V00371)	Heat Shock Protein, 70 Kda (Sp. 1003 11)	ILDUA Aludiase A		GRO3 oncogene	CRP1 Collagen-binding protein 1	CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR	FST: 7147a06 s1 Soares NhHMPu S1 Homo sapiens cDNA clone	666514 3', mRNA sequence. (from Genbank)	RPL31 Ribosomal protein L31	EST: zt61d08.s1 Soares testis NHT Homo sapiens cDNA clone	726831 3', mRNA sequence. (from Genbank)	EST: zo19e03.s1 Stratagene colon (#937204) Homo sapiens CUINA	clone 587356 3', mRNA sequence. (from Genbank)	EST: zo01d11.s1 Stratagene colon (#937204) Homo sapiens CUINA	clone 566421 3' similar to contains Alu repetitive element, contains	element MER22 repetitive element;, mRNA sequence. (from	Genbank)	mental complete sequence	Homo sapiens cione 040 director of the Nhouse of the DNA	[EST]: zw86c12.s1 Soares total retus muzini o swittering subsidered and the subsidered subsidered and the subsidered subs	Clone (83002 3 similar to W. Cosserie Court of the Court	PROTEIN L11; mkina sequence, (non sembann)	Human ets domain protein ERF mRNA, complete cds		Chromosome 1 specific transcript KIAA0491	COMP Cartilage oligomeric matrix protein	EST: zv28g12.s1 Soares ovary tumor norto 1 norto saptens corva-	EST; hbc3204 Homo sapiens cDNA clone hbc3204 5'end. (from	(Genbank)
right of the garden appropriate of the first	F007875_a D	RC AA2921 E					ä	M36821_s_a	_	D83174_s_a	ñ	338		10 21	3		A1328				RC_AA1488			वा		A4430	83_at	RC_AA2849 76 at	RC AA4651	1	L32137_at	RC_AA4221	5	0.17296158 T48536 at
No. of the second secon	A	0.1742237 t	0.17417912 28 at	0.17413254 J03909_at	<u></u>	0.17399655 HT2995_at	0.17396699 X12447		0.173883451	1 0 1738300	0.113676A2 MA2Q277	0.17307042	0.1736560656 at	0 1736013 X15940 at		0.1735786 46 at		0.17352936 74 at		7470		0.17339826 59 s at		0.17332432			0.17325146 83_at	RC_A 0.17319033 76 at		0.17314506	0.173065 L32137	RC A	0.17.0001.0	
To a second		0.303137	0.303102	0.303034		0.303016	0.302755		0.302719	77000	0.3027 14	0.302001	0.302587	0 302511	0.302.01	0.302477		0.302364				0.302362		0.302272			0.302128	0.30205		0.30205	0.302022		0.30180	0.301954
	1	0.3633758	0.363332	0.3632222		0.36322	0.3629631		0.3629171		0.3029123	0.3028/11	0.098888 0.38308	0.002020	0.3020222	9627950	0.0021 020	0.3627847				0.3626874		0.3625827			0.3625132	1	1	0.3624357	0.3624297		0.3624032	0.362243
		0.0879879 0	0.0879218	0.0878082	1 .		0.0877215 (0.087407	Į.	ł	0.08/166	0.00888	0.00000	0.0866092 0.362622	0.088558	0.00000	0.0862218				0.0857385		0.0856766			0.0855655	0.0854834		0.0852693	0.0852481		0.0849922	0070780
		935 Colorectal 0	936 Colorectal C		+-	938 Colorectal (-	-	940 Colorectal	├	\dashv	942 Colorectal	- I che	+	944 Colorectal	latoprolo t	945 COIDI ECIAI	latorato	340 COIDI ECIAI			947 Colorectal		948 Colorectal			949 Colorectal	050 Colorectal	OOIO COIG	951 Colorectal	952 Colorectal		953 Colorectal	1
	-	935 C) 936 0	037 6	2	938 C	939 C		940		941	942 (343	944	2,0	940	2,0	340			047	5	948			949	050	300	951	952	}	953	

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors The party of the p

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. EST: ag28h05.s1 Jia bone marrow stroma Homo sapiens cDNA clone RC_AA1289 | EST: zn90a05.s1 Stratagene lung carcinoma 937218 Homo sapiens AA093834_a EST: c11190.seq.F Fetal heart, Lambda ZAP Express Homo sapiens EST: H. sapiens putatively transcribed partial sequence; UK-HGMP RC_AA4028 EST: zu54a01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: ae37b10.s1 Gessler Wilms tumor Homo sapiens cDNA clone Homo sapiens pt-wd mRNA for WD-40 repeat protein, complete cds EST: HUMGS0003713, Human Gene Signature, 3'-directed cDNA EST: zv39e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: aa32c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 0.17255814 38 at 730937 3', mRNA sequence. (from Genbarik)
RC_AA1478 EST: zl50b04.s1 Soares pregnant uterus NbHPU Homo sapiens EST: zu05b09.s1 Soares testis NHT Homo sapiens cDNA clone sequence ID AAAYRK; single read, mRNA sequence. (from EST: yo37b10.r1 Homo sapiens cDNA clone 180091 5. (from AA410925_a|ENHANCER PROTEIN 1 (HUMAN);, mRNA sequence. (from cDNA clone 565424 3', mRNA sequence. (from Genbank) cDNA clone 505327 3', mRNA sequence. (from Genbank) clone 756044 5' similar to gb:M99435 TRANSDUCIN-LIKE IMAGE:814956 3', mRNA sequence. (from Genbank) clone 741768 3', mRNA sequence. (from Genbank) Homo sapiens mRNA for nucleolar protein hNop56 897979 3', mRNA sequence. (from Genbank) 1090905 3', mRNA sequence. (from Genbank) sequence, mRNA sequence. (from Genbank) cDNA 5', mRNA sequence. (from Genbank) Chloride channel (putative) 2163bp NADP+-dependent malic enzyme Spliceosomal Protein Sap 62 Metallopanstimulin 1 Reticulocalbin ORF mRNA Genbank) Genbank) Genbank) 0.17286918 27_at RC_AA5988 RC_AA4165 RC_AA5999 0.17278965|Z19899 at 0.17243756|X79440_at 0.17233664 C01765_at 0.17210557 HT3391_at RC_AA4588 0.17216685|R84594 at 0.17205548 D42073_at 0.1720057 HT3194_at 0.17180516 M68864 at 0.17230633 Z30644_at 0.17222661 Y12065 at HG3214-HG3033-0.17271367|72_at 0.17264414|49_at 0.17260127|02 at 0.17172186|54 at 0.17170094 86_at 0.17244168 0.17162894 0.301933 0.301779 0.301841 0.301708 0.301585 0.301649 0.301514 0.301325 0.301471 0.301333 0.301159 0.301092 0.30106 0.301297 0.30099 0.300959 0.300821 0.300808 0.300927 0.300777 0.3622086 0.3622 0.0848168 0.3621617 0.0847012 0.3621331 0.0846797 0.3620108 0.0844689 0.3619776 0.0844638 0.3619716 0.0842947 0.3619229 0.0834329 0.3618044 0.0837558 0.3618484 0.361668 966 Colorectal | 0.0833202 | 0.3616422 0.0833189 0.3616004 0.083063 0.3614467 968 Colorectal 0.0832619 0.3615744 969 Colorectal 0.0832096 0.3614558 971 Colorectal 0.0830454 0.3612629 0.0830167 0.3612629 974|Colorectal | 0.0826057| 0.3611782| 0.0829826 0.3612551 0.0849143 0.0849125 0.0833271 964 Colorectal (955 Colorectal 956 Colorectal 957 Colorectal 959 Colorectal 960 Colorectal 958 Colorectal 963 Colorectal 967 Colorectal 961 Colorectal 962 Colorectal 973 Colorectal 970 Colorectal 972 Colorectal

Docket No.:

2825.2020-002

માં માનવી સમારે માત્ર માત્ય માત્ર માત્ય માત્ર મ

							In	vento	ors	: Sri	dh	ar R	ama	SW	am	у,	et a	l.													
EST: af85c04 s1 Spares testis NHT Homo sapiens cDNA clone	1048806 3' similar to SW:YK61_YEAST P36160 HYPOTHETICAL	39.6 KD PROTEIN IN MIDT-NUP133 INTENSENTO NECTORS :: mmRNA sequence. (from Genbank)	EST: zv20e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	754200 3', mRNA sequence. (from Genbank)	Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds		EST: zh83a05.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 427856 31, mRNA sequence. (from Genbank)	EST: zu83d08.s1 Soares testis NHT Homo sapiens cDNA clone 744591 3', mRNA sequence. (from Genbank)	The state of the s	0.17125268 D84239_at-2 lgG Fc binding protein	IgG re binaing protein	EST: zx68g01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 796656 3' similar to TR:G577189 G57/189 SiMiLAR 10 DEAD BOX RNA HELICASES. ;; mRNA sequence. (from Genbank)		0.17090756 M54994_f_at Carboxyl ester lipase (bile salt-stimulated lipase)	SA mRNA for SA gene product	EST: yi04d08.r1 Homo sapiens cDNA clone 138255 5' similar to contains Alurenetitive element: (from Genbank)	CCT: ECT76503 Pineal cland II Homo sabiens cDNA 5' end, mRNA	sequence. (from Genbank)	EST: zk46h09.s1 Soares pregnant uterus NbHPU Homo sapiens	cDNA clone 485921 3', mRNA sequence. (from Genbank)	SSRP1 High mobility group box	EST: zt01b06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:711827 3', mRNA sequence. (from Genbank)	EST: zv54f03.s1 Soares testis NHT Homo sapiens cDNA clone	757469 3', mRNA sequence. (from Genbank)	SDC1 Syndecan 1	EST: zv44e06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 756514 3', mRNA sequence, (from Gendalik)	EST: HUMR I PGEG Homo sapiens culva. (Horli Gerbain)	cDNA clone HY18-3 3', mRNA sequence. (from Genbank)
1		A6213	A4787		A1329 at		A0019	A6212		D84239_at-2	0.17122382 D84239_at		A4614		M54994 f at	0.17090331 D16350 at	0 17084618 D56678 at	1130010 at		11	3 65 at	3 M86737_at	RC_AA2808	9 65_at	RC_AA4372	5 58_at	0.17046368 Z48199_at	RC_AA4364	3 20 at	0.17034793 M91222 at	KC_AAUU7 9 60 at
He thust tents if		RC_A 0.17153001 40 at		0.17137393 94 at	RC_AA1 0 17134686 69 s at		RC_A 0.17134237 08 at	RC_A 0 17131984 77 at		0.17125268	0.17122382		RC_A 0.17103413 76 at		0.17090756	0.1709033	0 1708/618	0.17004010	0.17077523		0.1707098 65 at	0.17066623 M86737	A La Company of the C	0.17061129 65_at		0.17054886 58 at	0.1704636			0.1703479	0.17030239 60
		0.300759		0.300675	0.300651	2000	0 300548	0 300528	22000	0.300427	0.300341		0.300314		0.300258	0.300247	600000	0.300223	0 300179		0.300112	0.300108		0.300046		0.299982	0.299923			0.299777	0.299688
		0.3611596	200	0.3611034	0 3640455	201000	0.3600324	0.3608286	0.200020	0.3607682	0.3607292		0 3606988		0.360518	0.360422	0000000	0.300300	0.3603115	1	0.3602785			0.3601831		0.3601299	0,3599102		0.3597956	0.3597343	0 0803047 0 3596878
		0.0828014		0.0825341			0.00007E4				0.0820697		0.0820426		0.082042	0.0819521	1000100	0.0818907	0.0815508	2000	0.0815452	0.0812312		0.0810845		0.0809646	0.0807475		0.0806754	0.0803246	0.0803047
			8/3 COIOLECIAI	078 Colorectal (+	att colorecial			a/a colorecial	980 Colorectal	981 Colorectal		082 Coloractal		983 Colorectal	984 Colorectal		Colorectal	086 Coloractal	COLOI COLOI	987 Colorectal	988 Colorectal		989 Colorectal		990 Colorectal	991 Colorectal		992 Colorectal	993 Colorectal	00.4
		71	3/3/	078	3(0)	3//6	7	970	18/8	086	981 (080	202	983	984		C26	080	200	987	988	3	686		066	991		992	993	200

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

0.29966 0.17026065 U02680 at Protein tyrosine kinase mRNA	RC_AA0756 EST: zm88e09.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 545032.3' mRNA serving of from Contactive	0.1700276 W27770 at sapiens cDNA, mRNA sequence. (from Genbank) 0.16996102 X61970 at PROTEASOME ZETA CLIAIN	HG2743- HT2846_s_a t Caldesmon 1, Alf. Splice 4, Non-Muscle	0.299448 0.16984347 Z96810_at and chloride-dependent glycine transporter 1 (GLYT-1) like Force
.29966 0.1702606	0.299503 0.17017648 66_at	0.299492 0.170027 0.299491 0.1699610	0.299452 0.169886341	99448 0.1698434
		1 1	0.0791645 0.3593253 0.2	
0.0802925	0.0802769	0.0796214	0.0791645	0.0791311
995 Colorectal 0.0802925 0.3596844	996 Colorectal 0.0802769 0.359664	997 Colorectal 0.0796214 0.3593957 998 Colorectal 0.0793234 0.3593702	999 Colorectal	1000 Colorectal 0.0791311 0.3592957
55	36	56	66	100

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=	1 Leukemia		2.1245492 0.4423031	0.398474	_	0.3168242[120688 at GDB-discociation inhibitor material and many many many many many many many many
	2 Leukemia	1.7983353	3 0.4104766	0.37298		mDNA from the figure of the first (Ly-5DI) mKNA
	3 Leukemia	1.770247	0.3996912			
	4 Leukernia	1.7262069	1 1		0.2794635	U43901_ma 37 kD laminin receptor precursor/p40 ribosome associated protein
	5 Leukemia	1,626872	0	/	0	Ribosomal Profein S13
J	o ceukeima	1.5929008	0.381187	0.343753		Growth factor independence-1 (Cf. 1) m DNA
	7 Leukemia	1.5842817	0.3790399	0.339392	0.26589945	X04347_s_a Liver mRNA fragment DNA binding protein UPI homologue (C-terminus)
	8 Leukemia	1.5754955	0.3753435	0.336293	0.26270148 D87735_at	CAG-isl 7 {trinucleotide repeat-containing sequence} [human, pancreas, mRNA Partial, 701 ntl
_	9 Leukemia	1.5749655	1.5749655 0.3715162	0.333566		Glia maturation factor, gamma
1	Cancella	1.3740241	1.37 40247 0.3701863	0.330908	0.25715446 U14970 at	RPS5 Ribosomal profein S5
<u> </u>	11 Leukemia	1.5661684	1.5661684 0.3673442	0.329057	HG4319- 0.25483343 HT4589_at	Ribosomal Protein L5
7141	12 Leukemia 13 Leukemia	1.5449955	1.5449955 0.3640238 1.5306438 0.3631739	0.326474	0.252562 Z49148 s at	0.252562 Z49148 s. at Enhancer of rudimentary homolog mRNA
					HG1428-	KIAA0131 gene, partial cds
۳ (14 Leukemia	1.5063082	0.3615369	0.323043	0.24852082 t	Globin. Befa
اب	15 Leukemia	1.4976654	1.4976654 0.3610132	0.321369	0.24683218HT613 at	Bihosomal Destain 040
			The state of the s		1	Nibosoffiai Protein 612

FIG. 5A

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9	diam'r.	4 4075446	0 350675	0 240647	0 24555060 4 04	1 of 0	Do CO and for ribasamal profess S8
10	10 Leukelilla	1.49/3440	0.702020	0.313017	0.24333060	7	ADO DEDOCMAL DEOTERA CLEA
=	1/ Leukemia	1.4901200	0.330/2/9	0.317831	0.24399223 0.2591	9	403 RIBUSUMAL PIXO I EIN SI 3A
188	18 Leukemia	1.4926745	0.3580288	0.317018	0.24269743 L19527	L19527_at	RPL27 Ribosomal protein L27
						HG4542-	
191	19 Leukemia	1.4878429	0.3560807	0.31536	0.24142163 HT4947	ā	Ribosomal Protein L10
707	20 Leukemia	1.4762723 0.3536887	0.3536887	0.314561	0.23992863 X55954	ä	RPL17 Ribosomal protein L17
211	21 Leukemia	1.4723858 0.3529107	0.3529107	0.313701	0.23885897 X60489 at		Elongation factor-1-beta
22	22 Leukemia	1.466343	0,3522405	0.312553	0.23763658 L22009	1	HIRIND H MRNA
						rna	The second secon
23 [23 Leukemia	1.4643947	0.3514966	0.311742	0.23648864	1 s at	PTMA gene extracted from Human profrymosin alpha mRNA
						X89399 s a	The same of the sa
24	24 Leukemia	1.4440879	0.3501856	0.310584	0.23545831	1	Ins(1,3,4,5)P4-binding protein
						M61827_rna	
25	25 Leukemia	1.4405453	0.3491933	0.309734	0.23415814	s at	Leukosialin (CD43) gene
						HG3549-	
26	26 Leukemia	1.4365484	0.3488895	0.308725	0.23311779 HT3751	at	Wilm'S Tumor-Related Protein
27 1	27 Leukemia	1.4194885 0.3472533	0.3472533	0.308086	0.23221248 M24194 at	M24194 at	Alpha-tubulin mRNA
28	28 Leukemia	1.4186814	0.3468086	0.306922	0.23130439 L49380	L49380 at	Transcription factor ZFM1 isoform B3 mRNA, complete cds
29 1	29 Leukemia	1.4112004	0.3455588	0.306108	0.23045073 D14530	at	40S RIBOSOMAL PROTEIN S23
30 [30 Leukemia	1.4087023	1.4087023 0.3441794	0.305179	0.22946984 X55715	X55715 at	RPS3 Ribosomal protein S3
31	31 Leukemia	1.4042301	0.3435043	0.304458	0.22863418 X78136 at	X78136 at	HnRNP-E2 mRNA
						D87017 cds	D87017 cds C7 segment gene extracted from Human (lambda) DNA for
32 1	32 Leukemia	1.4035159	0.3429812	0.303716	0.227764063	3_at	immunoglobin light chain
331	33 Leukemia	1.4016054	0.3421459	0.302837	0.22693126 U64105_at		Guanine nucleotide exchange factor p115-RhoGEF mRNA, partial cds
		,	•			A4103	EST: zv16e02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
341	34 Leukemia	1.3964151	0.3416564	0.301841	0.22612083 38_at	38_at	753818 3', mRNA sequence. (from Genbank)
						M77232_ma	
351	35 Leukemia	1.3906124	0.3411185	0.301009	0.22543746 1	1_at	Ribosomal protein S6 gene and flanking regions
					<u>-</u>		Heterogeneous nuclear ribonucleoprotein D (hnRNP D), partial cds,
198	36 Leukemia	1.3863678		0.300395	0.22468512 M94630_at		clone cDx4
37.1	-eukemia	1.3846071	0.3409466	0.299665	0.22423486 U39318_at		AF-4 mRNA
							RbP gene (renin-binding protein) extracted from Human Xq28
							genomic DNA in the region of the L1CAM locus containing the genes
							for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin
							receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related
							protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1),
	•	0000	7007070	0		112_ma	and interleukin-1 receptor-associated kinase (IRAK) genes, and
381	38 Leukernia	1.3846068	0.3401984	0.298582	0.22343864 5_at	5 at	Xq28lu2 gene

Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

Accession Acce	Ribosomal protein S24 Esterase D, 5'UTR (sequence from the 5'cap to the start codon) 40S RIBOSOMAL PROTEIN S19 RPL6 Ribosomal protein L6 WAS Wiskott-Aldrich syndrome (ecezema-thrombocytopenia) Ras-Related Protein Rap1b Ribosomal Protein Rap1b Ribosomal Protein S4, X-Linked Adult tooth pulp of third molar fibroblast mRNA for MSX-2 Transcription Factor Btf3b Orphan G protein-coupled receptor (CEPR) gene ZNF134 Zinc finger protein 134 (clone pHZ-15) Transformer-2 alpha (htra-2 alpha) mRNA HISTONE H3.3
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Docket	t No.:	2825.2020-002
Title:	Geneti	ic Markers for Tumors
Invento	ors: Sri	dhar Ramaswamy, et al.

122	122 Leukemia	1.2453121	1 0.310659	0.269195	0.19137341 X13482	X13482 at	112 SMALL NI ICLEAP BIRONI ICLEOPROTEIN AL
123	123 Leukemia	1.2451864	4 0.3103134			11	M4 protein mRNA
124	124 Leukemia	1.2445465	5 0.31006	0.268479		B i	HMG2 High-mobility group (nonhistone chromosomal) protein 2
125	125 Leukemia	1.2416011	0.309915	0.268381	0.19047858 D13748	D13748_at	EIF4A1 Eukaryotic translation initiation factor 4A (elF-4A) isoform 1
126	126 Leukemia	1.2412574	0.309801	0.268106	0.19029194 [138980	U38980 at	PMS8 mRNA (yeast mismatch repair gene PMS1 homologue), partial
127	127 Leukemia	1.2404771		L.		[]	YMP mRNA
128	128 Leukemia	1.239503	3 0.3094296	0.267647			RPS25 Ribosomal profein S25
129	129 Leukemia	1.2388306	0.3093489	0.267582			AQP2 Aquaporin 2 (collecting duct)
130	130 Leukemia	1.2368712	0.3091966	0.267336	0.18940248 249107	ဟ	at Galectin
131	131 Leukemia	1.2361124	0.3090251	0.267149	HG3636-0,18916345 HT3846	HG3636- HT3846 at	Managin House, Debendant of Managin House
132	132 Leukemia	1.234553	0.3089393		0.18897024 D14661		KIAA0105 gene
133	133 Leukemia	1.2333759	0.3089393	0.266628	0.18873556	U45448_s_a t	P2x1 receptor mRNA
134	134 Leukemia	1.2330676	0.3086549	0.266501	0.18856694.1	U49869_ma	Historiette
1351	135 Leukemia	1.2300403	1 1	0.266424	0.18825643 Z23064 at	Z23064 at	HNRPG Heterodeneous nuclear ribonus contratais C
36	136 Leukemia	1.2289646	0.3084368	0.266405	0.18810901 D64142 at	D64142 at	Histone H1x
137[137 Leukemia	1.2281015	0.3083881	0.265953	0.1877856	X15729_s_a	DAS DROTEIN
38	138 Leukemia	1.227778	i 1	0.265902	0.18754287 M94046	te	Zinc finder protein (MAZ) m DNA
36	139 Leukemia	1.2270217	0	0.265615	0.18737027 U02493	at	54 kDa protein mRNA
4 5 1 1	140 Leukemia	1.2268015		0.265308	0.18716872 M84711		RPS3A Ribosomal protein S3A
42	141 Leukellila 142 Leukemia	1 2250143	0.3072902	0.265289	0.1869955 M64925		MPP1 Membrane protein, palmitoylated 1 (55kD)
43	143 Leukemia	1,2257375		0.264834	0.18672927 D63482_at		KIAA0148 gene
44 L	144 Leukemia	1,2243629		0.204665	0.1000288 L20316 at	at e	GCGR Glucagon receptor
45 L	145 Leukemia	1.2234674		0.264574	0.18613164 X00354	ָל װּ	KAF I V-raf-1 murine leukemia viral oncogene homolog 1
46 L	146 Leukemia	1.2231642	1 1	0.264219	0.18589729 U10323	at a	at Niclear factor NE45 m DNA
4/ [14/ Leukemia	1.221944	0.3063171	0.264126	0.185669 U01038	व	PLK mRNA
							Alpha-globin 1 gene extracted from Human DNA sequence from
48	148 Leukemia	1 22046	0 3081257	0 30630	7	721_cds	chromosome 16, spanning 2Mb of 16p13.3 Contains alpha and zeta
49	149 leukemia	12170087	0.3061651	708607.0	0.185436862 at		globin genes and ESTs
1	5	1000	1.000000.0	0.203113	U.18518446 L38941	ä	RPL37 Ribosomal protein L37

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	HG3527- HT3721 f at Luteinizing Hormone Refa Subunit		rna		ä	at	to	ی ای	s a	U30827_s_a	Splicing factor SRp40-1 (SRp40) mRNA 0854 at IRPS16 Ribesomal protein S16	, to	, a	INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN 633 at PRECLIRSOR	a te			, a			0.18147752 U57341 r_at Neurofilament triplet L protein mRNA, partial crts	0.18126565 Y08765 s at ZFM1 profein alternatively enlined and handlest	013_at GLUTAMINYL-TRNA SYNTHETASE
WHITE ALL THE STATE OF THE STAT	HG3527 0.18505192 HT3721	0.1847654 U40343	X75756 0.18455225 1_s_at	0.18449408 X83368_at	0.184342711145974	0.18408845 X78338	HG273- 0 1839925 HT273 s	0.18379508 U12465	0.18357657 t		0.1831046 M60854 at	0.18297808 HT4606	0.18280509 HT662	0.18265115 L07633	HG2463- 0.1824216 HT2559 at	0.18232065 D28	0.1821297 X16135 at	0.18200736 X92396	HG4606 0.1818137 HT5011	0.18170589 U07132 at	0.18147752 U57	0.18126565 Y08	0.18116085 X76013 at 0.18110165 U77718 at
	0.263688	0.263523	0.263206	0.262911	0.262766	0.262685	0.26255	0.262463	0.262444	0.969494	0.262124	0.261628	0.261532	0.261374	0.261311	0.261227	0.261225	0.251093	0.260629	0.260627	0.260431	0.260324	0.260214
		0.3054116	0.3052923	0.3052791	0.3051662	0.3044576	0.3044128	0.3043453	0.3042996	0.3041582	0.3037405	0.3033187	0.3032731	0.3031735	0.3029563	0.3028952	0.302875	0.0020034	0.3024052	0.3022202	0.3022002	_	
,	1.2162648	1.2150172	1.2147936	1.2147683	1.2133484	1.2129612	1.2126172	1.2123963 0.3043453	1.2120221	1.211662		1.2101176	1.209184	1.2083427	1.2083071		1.2069051	_	1.2061185 (1.2057818	1.2052876 0	1.2034352 0.3020802 1.2028148 0.3019385
	150 Leukemia	151 Leukemia	152 Leukemia	153 Leukemia	154 Leukemia	155 Leukemia	156 Leukemia	157 Leukemia	158 Leukemia	159 Leukemia	160 Leukemia	161 Leukemia	162 Leukemia	163 Leukemia	164 Leukemia		167 Leukemia		168 Leukemia 1		170 Leukemia 1		173 Leukemia 1
	150	151	152	153	154	155	1561	157	1581	159	1601	161 L	162 L	163 L	164 L	165 L	100 F		168 L.	2	170 LE	171 Le	172 LE

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Ribosomal protein L28 mRNA		Ribosomal Protein L26	HnRNP C2 protein mRNA	ARH12 Aplysia ras-related homolog 12	DNA sequence from intron 22 of the factor VIII gene, Xq28. Contains	the end of a 9.5kb repeated region, int22h-1, involved in many cases	of haemophilia	TIALL TIAL evictoric granule-associated RNA-binding protein-like 1	Unknown protein mRNA, partial cds	Adenine phosphoribosyltransferase (aprt) gene extracted from Human	APRT gene for adenine phosphoribosyltransferase	Oncoprotein 18 (Op18) gene	0.1795011 Y10807 s. at Suppressor for yeast mutant	Novel member of serine-arginine domain protein, SKrp129	NASP Nuclear autoantigenic sperm protein (histone-binding)	Profilin mRNA	P62 mRNA	KIAA0220 gene, partial cds	0.1784388 Z19554_s_at VIM Vimentin	ZNF43 Zinc finger protein 43 (HTF6)	DNA-BINDING PROTEIN A		NC2 alpha subunit	AND or cide for cide	Sickle cell beta-globili IIIKINA	LKP DEAD/A (ASP-Glu-Ala-Asp/Als) box polybepiede 3 (1317) indicase A)	Alpha NAC mRNA	PDE4A Phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-	at homolog phosphodiesterase E2)	Heat shock transcription factor 4
at	HG384-	4T384_at	116342_at	.25080 at			(86012_at	M96954_s_a	195040 at	1 1	00	M31303_rna 1_at	ਗ	ĺ	1	J03191_at	M88108 at	D86974_at	Z19554_s_at	X59244 f at	M24069_at	X96506_s_a	ب	M25079_s_a]	L13848 at	X80909 at		S75213_s_a	0.17716108 D87673_at
0.1808775 U14969		0.18075792 HT384	0.18056273 M16342	0.18045427 L25080			0.1803269 X86012_at	1 40045820	0 17999448 195040 at		0.17989491 1_at	M31: 0.1797336 1_at	0.1795011	0.17928208 Y11251 at	0.17911504 M97856 at	0.17894888 J03191 at	0.17877895 M88108 at	0.17851272 D86974_at	0.1784388	0.17820542	0.17802805 M24069_at		0.17782216	7477777	10100///10	0.17759909 L13848	0.17741168 X80909		0.17733383 S75213_s	0.17716108
0.259953		0.259672	0.259541	0.259325			0.259146	0.000440	0.233119	2000000	0.258699	0.258696	0.2586	0.258512	0.258254	0.258052	0.25766	0.257539	0.257515	0.257308	0.257169		0.257051	0.00	0.256846	0.2566	0.256475		0.25634	0.256007
0.3018221		0.3017252	0.3012116	0.3011774			0.3010232	000000	0.3000674	10000	0.3003981	0.3003066	0.3000982	0,3000552	0.2999695	0.2989811	0.2989804	0.2989127	0.2988568	0.2987545	0.2984847		0.298375	0.000	0.2982459	0.2982394			1.1818244 0.2980894	1.1804932 0.2980198
1,2026554		1,2002693	1.1982379	1 1980317			1.1972903	07000	1.191249	1.1903513	1.1963266	1.1950643	1.1944383	1.193796	1.1923729	1.1921172	1.1904725	1.189373	1.1891887	1.1890529	1.1887918		1.1865348	101111111111111111111111111111111111111	1.1855581	1.1850606	1.1843607		1.1818244	1.1804932
174 leukemia		175 eukemia	176 eukemia	Pulkemia	5		178 Leukemia		179 Leukernia	100 Leukellila	181 Leukemia	182 Leukemia	183 Leukemia	184 Leukemia	185 Leukemia	186 Leukemia	Leukemia	188 Leukernia	189 Leukemia	190 Leukemia	Leukemia		192 Leukemia		193 Leukemia	194 I eukemia	Leukemia		196 Leukemia	197 Leukemia
174		175	176	177			178		8/1	2	181	182	183	184	185	186	187	188	189	196	191		192	3	19.	194	195		196	6

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198 Leukemia	a 1.1794626	0.2979992	0.255954	0.17698868	Z68280_cds	sequence from cosmid L25A3, Huntington's Disease Region, chromosome 4p16.3 contains Human tetracycline transporter-like protein and erythrocyte adducin alpha subunit, multiple ESTs and a parteting Control of the cont
199 Leukemia	a 1.1791159		0.255882		x95404 at	CFL1 Cofflin 1 (non-muscle)
200 Leukemia	1.179037	0.2977709	0.25568	AC002 0.17666484 ds3 at	\C002115_c ls3_at	AC002115_c chromosome 19 cosmids R31396, F25451, and R31076 containing ds3 at COX6B and UPKA genomic sequence
201 Leukemia	a 1.1767216	0.2977417	0.255529	0.1765575 1 at	X56997_rna 1_at	UDA52 gene coding for ubjanitin 52 aming gold for the
202 Leukemia	1.1761341	0.2976536	0.255337	0.17640434 1 at	351_rna	Peptidylprolyl isomerase gene extracted from Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
203 Leukemia	1.1748629	0.2975881	0.255318	0.1762864 U48405	J48405 at	G protein counted recentor OGR1 gans
204 Leukemia	1.1744432	0.2975271	0.255305	HG2873 0.17621805 HT3017		Ribosomal Protein L30 Homolog
205 Leukemia	1.1728004	0.297279	0.255236	0.17605063 t	AF008937_a	Svnfaxin-16C mRNA
206 Leukemia	1.1719639	0.2970226	0.254878	0.1758481 HT1602	, ta	Ifranhin
207 Leukemia	-	0.2969898	0.254833	0.17570893 X64044 at		SPLICING FACTOR 1/24F 65 KD SUBLINIT
208 Leukemia	1.1708757	0.2969872	0.254613	0.17564848 U42412		5'-AMP-activated profein kinasa gamma-1 sukunit menya
209 Leukemia	1.169984	0.296758	0.254525	0.17551471 t	M34338_s_a	SRM Spermiding confluence
210 Leukemia	-	0.2967441	0.25445	0.17527379 X07948 at		TNP1 Transition protein 1 (TP1)
Z11 Leukemia	1.1698916	0.2966667	0.254308	0.17519422 L49173 f at		OCP2 gene, partial cds
212 Leukemia	1.1694614	0.2963972	0.254047	HG3364 0.17505342 HT3541	, to	Rihosomal Protein 1 37
213 Leukemia	1.1687437	0.2962276	0.253936	0.17484337 M64992	at	PSIMA2 Proteasome component C2
214 Leukemia	1.1685/25	0.2961727	0.253817	0.1747057 U79262	at.	DHPS Deoxyhypusine synthase
- 10 Leunellia	1.1001/09	0.2961308	0.253788	0.17453593 M21812	ä	MYL2 Myosin, light polypeptide 2, regulatory, cardiac, slow
216 Leukemia	1.1674801	0.2956751	0.253683	H H- 0.17440426 t	HG2868- HT3012_s_a t	Xe7, Pseudoautosomal Gene, Alt. Splice 2
217 Leukemia	1.166249	0.2956078	0.253556	0.17428826 M	90356 f at E	0.17428826 M90356 f at BTF3 protein homologue gene
218 Leukemia	1.1653548	0.2955859	0.253489	O 17409502 t)2386 s_a l	C02386_s_a EST: HUMGS0010652, Human Gene Signature, 3'-directed cDNA
219 Leukemia	1.1652404 0.2955517	0.2955517	0.253221	0.17398985 Yng216	t	Sequence, mrnA sequence. (from Genbank) Profess Kingan, Profess
220 Leukemia	1.164727	0.2955114	0 25300	0 47070404 VEGSSS	<u>.</u>	Totali Nildoe, Dyikz

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to want thank the tength taken thank to the tends made thank thank thank thank thank	X52730_rna Phenylethanolamine n-methyltransferase gene extracted from Human gene for phenylethanolamine N-methylase (DNIMT) (100.000)	0.16957933 L32831 s at PROBABLE G PROTEIN-COUPLED RECEPTOR GPR3	i i	at at	0.16901068 Z47038 s at horden 14 (MAD4 A)	M36430_s_a GNB1 Guanine nucleotide binding protein (G protein), beta	ø,	0.1685722 U38268 at Cytochrome b pseudogene, partial cds	22376_cds	to	at			416_rna		J70439_s_a	Z69915 at mRNA (close ICBE-Fort Jone)	्व			.12711 s at TKT Transfered	(Wernicke-Korsakoff syndrome)
	X527 0.16970333 1_at				0.1690106	0.1689065	0.16879904	0.16862282	0 18944EE2 2	0.16832282 X90761	0.1682302 D87437	0.16806996 X84740	0.16778138 X69550 at	0 167771602 4	0.16763291 K01383 at	0 16755875	0.16746695 Z69915	0.16731027 M11353	0.16702329 247727	0.16685395 X98411 at 0.16671152 U62962 at	0.16659564 L	
	0.248939	0.248889	0.248649	0.248564	0.248132	0.248045	0.248027	0.247711	0.247667	0.247481	0.247445	0.247327	0.247178	0.247145	0.247101	0.247063	0.246941	0.246783	0.246608	0.246482	0.246168	
	0.2917726	0.2916955 0.2916355	0.2914688	0.2914579	0.2913019	0.2912244	0.2911485	0.2908772	0.2908703	0.2906564	0.2905/94	_	0.2902518	0.2899953	LI		0.289834 (1. 1.	0.2894479 0	0.2893198 0	
	1.1441656	1.1434027	1.1432002	1.1431863	1.1425124	1.1424148	1.1423041 0.2911485 1.1422026 0.290852	1.140583		1.1394109 (. 1	1.1369768 0		1.1358911 0	1	1.1348822		1.1329956 0.		1.1322204 0.3	
	252 Leukemia	253 Leukemia 254 Leukemia	255 Leukemia	256 Leukemia 257 Leukemia	258 Leukemia	259 Leukemia	260 Leukemia 261 Leukemia	262 Leukemia		265 Leukemia 265 Leukemia	-	1	268 Leukemia 1		Z/U Leukemia 1		273 Leukemia 1	+-1	275 Leukemia 1.	++	278 Leukemia 1.	
	252	253	255	256	258	259	260	262	263	265	799Z	267 L	7 897	269 L	7/0 5	271 Lt	273 Le	274 Le	275 Le	277 Le	278 Le	

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		İ			_ma	Smb protein gene extracted from Harrian general sman neared
279 Le	279 Leukemia	1.1309122	0.289316	0.246081	1 s at	ribonucleoproteins and announce
280 Le	280 Leukemia	1.1302959	0.2892097	0.246048	0.16643462 Z49878_at	Guanidinoacetate N-methyltransterase
281 Le	281 Leukemia	1.129755	0.2891943	0.245944	0.16633128 X56932 at	LCAT Lecithin-cholesterol acyltransferase
282 Le	282 Leukemia	1.129514	0.2891271	0.245777	0.16616645 X74795_at	CDC46 HOMOLOG
283 6	283 Leukemia	1 1291142	0.2890729	0.245471	0.1660515 X69150_at	Ribosomal protein S18
284 l e	284 l eukemia	1.128326	1	0.245425	0.16587387 M91592 at	ZNF76 Zinc finger protein 76
2851 6	285 Leukemia	1.1265644	10	0.24531	0.16584118 U86409_at	Hyaluronan synthase 3 (HAS3) gene, partial cds
286 Le	286 Leukemia	1.1255598		0.24509	0.16578884 M58285_at	Membrane-associated protein (HEM-1) mRNA
287 Le	287 Leukemia	1.125383	1.125383 0.2887524	0.245046	0.16564767 Z69720_at	MPG N-methylpurine-DNA glycosylase
288 Le	288 Leukemia	1,1252847	0.2887193	0.244955	0.16557367 M34276_at	Plasminogen mRNA
					RC_AA6099	EST; af09h02.s1 Soares testis NHT Homo sapiens cDNA clone
289 Le	289 Leukemia	1.1246662	1.1246662 0.2885988	0.244946	0.16534217 77_at	1031187 3', mRNA sequence. (from Genbank)
290 Le	290 Leukemia	1.1225882	1.1225882 0.2885784	0.244732	0.16520637 U58682 at	RPS28 Ribosomal protein S28
291 Le	291 Leukemia	1.12252	1.12252 0.2885706	0.244406	0.16510895 C06269_at	EST: similar to none, mRNA sequence. (from Genbank)
292 Le	292 Leukemia	1.1220155	0.2881413	0.244355	0.16498981 X79536_at	HNRPA1 Heterogeneous nuclear ribonucleoprotein A1
					×	Controlly colored a shift or least a state of the state o
293 Le	293 Leukemia	1.1216736	0.2881277	0.244247	0.16487932 1_at	Rod cG-PDE G gene 10r 3, 5-cyclic nucleorine prospriouresterase
294 Le	294 Leukemia	1,1208966	0.288098	0.244105	0.1647394 U34038 at	Proteinase-activated receptor-2 mRNA
295 Le	295 Leukemia	1.1203524	0.2880561	0.244053	0.16465314 Z48042 at	mRNA encoding GPI-anchored protein p137
296 Le	296 Leukemia	1.1181958	0.2880113	0.243974	0.16453451 M37583_at	H2AZ H2AZ histone
297 Le	297 Leukemia	1.118027	0.2876341	0.243849	0.16442089 U80073_at	Tip associating protein (TAP) mRNA
298 Le	298 Leukemia	1.1172501	<u> </u>	0.243731	0.16428559 M25269_at	ELK1 ELK1, member of ETS oncogene family
299 Le	299 Leukernia	1.1160593	0.2872661	0.243696	0.16425402 X57959_at	RPL17 Ribosomal protein L7
300 Le	300 Leukernia	1.1154639	0.2872085	0.24362	0.1641192 X82434 at	EMD Emerin (Emery-Dreifuss muscular dystrophy)
301 Le	Leukemia	1.1154184	0.2870454	0.243597	0.16401269 X56741_at	RAS-RELATED PROTEIN RAB-8
3021.6	300 Loukemia	1 115225	0.2869661	0.243358	0 163858591134301 r a	at Nonmuscle myosin heavy chain IIB gene, promoter region and exon 1
700	5110000		,			
303 Le	303 Leukemia	1.1151443	0.2868831	0.243254	0.16379945 HT2219 at	Mucin (Gb:M57417)
304 Le	304 Leukemia	1.1151345		0.243167	0.16370875 M63483 at	MATRIN 3
					HG3319-	
1	•	i			HT3496_s_	D 7 L T
305 1	305 Leukemia	1.1150829	0.2868093	0.243110	0.1030U0Z411	COI 16A1 Alpha-1 fore XVI collagen
207 1.0	207 Leakernia	1 11/10/35	1_			Ribosomal protein 27a mRNA
30816	308 Leukemia	1.1143427				Immunophilin homolog ARA9 mRNA
309 Le	309 Leukemia	1.1130372		_	11	Geranylgeranyl transferase II
31016	310 Leukemia	1 1129369			0.16314812 U66618 at	SWI/SNF complex 60 KDa subunit (BAF60b) mRNA
7 2 1 1	A1117411174		!		37	

0.16304502 Y08766 s at	0.16300045 U15552 at	0.16284847 X16663_at	0.16271928 M93651 at	0.16261557 L00635_at	.2129 0.16255267 U70671 at Ataxin-2 related protein mRNA, partial cds	0.16251051 D16105_at	.2026 0.16236947 M17886_at RPLP1 Ribosomal protein, large, P1	0.16231644	X56681_s_a	0.16226187 t	0.16211317	0 16199352	0.16191407 X54637 at	HG2566-	0.16181475	11189 0.16174133 U31930_at DUT DUTP pyrophosphatase	YWHAZ Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase	0.10100017 W00400 at	0.1615375 M97287_at	0.1614906 M29581_at	10689 0.1613819 J02621 s at Non-histone chromosomal protein HMG-14 mRNA	0.16126516 X65488_a	10506 0.16118191 U60325_at POLG DNA polymerase gamma	Smn gene (survival motor neuron protein SMN) extracted from	 U80017_ma	0.16106379 3_at	10344 0.16101246 U14187 at Receptor tyrosine kinase ligand LERK-3 (EPLG3) mRNA	0.16095036 U75679_at	0.16085316 M93718_at	0.16074711 X73113 at	AB002356_s	0.16063266 at	0.1605167 U40714 at	23998 0.1603849 D84557_at P105MCM mRNA
0.242532	0.242456	0.242401	0.242191	0.242167	0.242129	0.242026	0.242026	0.241824		0.241823	0.241479	0 241475	0.241386		0.241294	0.241189	0.240994	1.0001	0.24097	0.240704	0.240689	0.240563	0.240506			0.240408	0.240344	0.240279	0.240263	0.240138		0.240079	0.240079	0.23998
0.2860316	0.2859941	0.2859084	0.2858837	0.2857677	0.2857232	0.2856785	0.2856439	0.2855242		0.285508	0.2855046	0.2854269	0.2854197		0.2853949	0.2852632	0.2851508	0.4.001.000	0.2850826	0.2850741	0.2849745	0.2848574	0.2847856			0.2846162	0.2845467	0.2843184	0.2842417	0.2842359				0.2840951
	1.1099217	1.109396	1.1093055	1.1090453	1.1078787	1.1077245	1.1053149	1.1050891		1.1044514	1.1036431	1 103209	1	[1.1022385	1	1 1013687	1.101000	1.1007587	1.100501	1.0995275	1.0994701	1.0991381			- 1			1.0961341	1.0950685				1.0935458
311 Leukemia	312 Leukemia	313 Leukemia	314 Leukemia	315 Leukemia	316 Leukemia	317 Leukemia	318 Leukemia	319 Leukemia		320 Leukemia	321 Leukemia	322 I Pukemia	323 Leukemia		324 Leukemia	325 Leukemia	326 Leukemia	Leavening	327 Leukemia	328 Leukemia	329 Leukemia	330 Leukemia	331 Leukemia			332 Leukemia	333 Leukemia	334 Leukemia	335 Leukemia	336 Leukemia		337 Leukemia	338 Leukemia	339 Leukemia
311	312	313	314	315	316	317	318	319		320	321	322	323		324	325	326	020	327	328	329	330	331			332	333	334	335	336		337	338	339

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0.16028678 U15008 at SnRNP core protein Sm D2 mRNA	IG1322- IT5143_s_a	0.16009448 U03634 at P47 LBC oncogene mRNA		X70944_s_a Splicing factor prolline/glutamine rich (polypyrimidine tract-binding 0.15983514 t-2	000460_a		,at	म			₹ †	j ;	0.15895419 D23660 at RPI 4 Ribsemal gradain 14	; te	L17131_ma1 at	HG210- 0.15879697 HT210 s at Galactokinase 2	5	s_at	₩,	at_	0.1583713 U17894_at Alpha(1,2)fucosyltransferase	X66142_s_a t	J06155_s_a	0.15811275 Y00433 at GPX1 Glitathing peroxidase 4	, to	, to	at			0.13/318/4 045982_at G protein-coupled receptor GPR-9-6 gene
	H H 0.160173731			Ĺ												0.1587		0.1585	0.1585,	0.1584;	0.158;	0.1582572	0.158247961	0.15811	0.15802	0.15797	0.15787	0.1577	0.15/63	U.13/31
0.239966	0.239957	0.23968	0.23958	0.239435		0.239184	0.239166	0.239049	0.238994	0.238896	0.238820	0.238803	0.23865	0.238625	0.238568	0.23841		0.238393	0.238265	0.238105	0.237934	0.2378	0.237714	0.23764	0.237594	0.237576	0.237377	0.237317	0.23/194	0.431040
0.2839587	0.2837795	0.283724	0.2837193	0.2834316		0.2832874	0.28328/4	0.2832694	0.2829181	0.2020033	0.282674	0.2825215	0.2824906	0.2823955	0.282215	0.2822067		0.2821873	0.2821048	0.2820638	0.2819287	0.2817653	0.2816694	0.2816178	0.2815631	0.2815472	0.2814679	0.2813997	0.2013400	7,40 10200
1.0925126	1.0912216	1.090349	1.0900426	1.0900426				- 1	1.0880/35	1.				1.0868239	1.0866914	1.086631	1				1.0800000	1.0855914 (1.084546					1.0815961 (1
340 Leukemia	341 Leukemia	342 Leukemia	343 Leukemia	344 Leukemia	-	345 Leukemia	+	+	349 Leukernia	+-	+-	\vdash	┼-	354 Leukemia	355 Leukemia	356 Leukemia		-	+	\dashv	ooo renkelilla	361 Leukemia	362 Leukemia				\dashv	367 Leukemia 1	+-	-
340	341	342	343 1	344 1	7	3451	2401	340	3491	350 L	351L	352L	353 L	354 L	355 L	356 L		357 L	350 L	3601	2000	361 L	362 L	363 L	364 L	365 Li	366 Li	367 L	3691	1 2 2 2

gert, gerts, gerts, jamen gener gjerts, gerts, 0.15741014 D50918 at-2 Human mRNA for KIAA0128 gene, partial cds 0.1573883 D50918 at KIAA0128 gene, partial cds 0.15736118 M95678 at PLCB2 Phospholipase C, beta 2 0.15736118 M95678 at PLVEPT Human immunodeficiency virus type I enhancer-binding	protein 1 SWI/SNF complex 155 KDa subunit (BAF155) mRNA Thyrotroph embryonic factor (TEF) mRNA Mitochondrial trifunctional protein beta subunit mRNA, partial cds	KIAA0272 gene, partial cds LAMB2 Laminin, beta 2 (laminin S) EST: ze06b01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 358153 5' similar to PIK:A40555 A40555 Criminatorial protein kinase major membrane substrate;, mRNA sequence. (from Genbank) Genbank) DLST Dihydrolipoamide S-succinyltransferase (E2 component of 2-	oxo-glutarate complex) ZNF132 Zinc finger protein 132 (clone pHZ-12)	KIAA0101 gene	Mucin 3, Intestinal (Gb:M55405) FFS Feline sarcoma (Snyder-Theilen) viral (v-fes)/Fujinami avian	sarcoma (PRCII) viral (v-fps) oncogene homolog	FUT5 Fucosyltransferase 5 (alpha (1,3) fucosyltransferase)	Cyclophilin-like protein CyP-60 mRNA		CD53 CD53 antigen	HMGI-C	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR	GRB2 Growth factor receptor-bound protein 2 KIAA0164 gene	Serine Hydroxymethyltransferase, Cytosolic, Alt. Splice 3 PROC Protein C (inactivator of coagulation factors Va and VIIIa)
0.15741014 D50918 at-2 H 0.15736118 M95678 at E X51435 s.a	0.15715927 t 0.15707237 U66615 at 0.15702824 U44059 at	ज ज	0.15662755 W95348_at	0.15656048 t	0.15637726 D14657 at	0.15636076 HT2217_at	0.15619878 X52192 at	0.15618/61 L15409 at		M60784 s a	0.15589432 t 0.15576376 M37033_at	X92518_s_8 0.15568334 t	0.15565534 D16562 at	0.15561327 t 0.15551986 D79986 at	HGZ379- HT3997_s_a 0.15548089 t 0.15535207 X02750_at
0.236997 0 0.236944 0.236929 0		0.236507 0.236507 0.236465	0.2364	0.236382	0.236255	0.236173	0.23607	0.235834	0.235540		0.235474	0.235346	0.235173	0.235096	0.234949
0.2812586 C 0.281104 C 0.2809657 C		0.2804482 0.2802991 0.2802726	0.2802726	0.2800324	0.2798555	0.2796672	0.2796137	1.0752034 0.2794659	1.0750905 0.2793669		0.2792509		0.2790005	0.278919	0.2787188
1.0787251 0 1.0787251 1.0784053 0		1.0777758 (1.0770123 (1.0766983 (1.0764946		1.0755459	1.0754781	1.0753374	1.0752034	1.0750905	1.0104043	1.0731243	1.0722156	1.07211	1.0717362	
370 Leukemia 1 371 Leukemia 372 Leukemia	373 Leukemia 374 Leukemia 375 Leukemia		379 Leukemia	380 Leukemia	381 Leukemia	383 Leukemia	384 Leukemia	385 Leukemia	386 Leukemia	387 Leukemia	388 Leukemia	390 Leukemia	391 Leukemia	392 Leukemia	394 Leukemia 395 Leukemia

Clone W2-6 mRNA from chromosome X	at	0.15273067 U66052	0.232722	0.2764401	1.0551009	425 Leukemia	425
Heterochromatin protein HD4He gamma mDNA	U26312_s_a t	0.15283552	0.232751	0.2765085		424 Leukemia	424
Mutated in multiple advanced cancers protein (MMAC1) mRNA		0.15292238 U92436 at	0.23286	0.2765358	1.0571856	423 Leukemia	47.
Ardinine-rich nuclear protein mRNA	क	0.15296148 M74002	0.232909	0.2765918	1.057281	Leukemia	422
Striatum-enriched phosphatase (STED) mDNA mortical and		0.15302981 U27831 at	0.232923	0.2767044	1.0577866	421 Leukemia	421
M33684_s_a (clone lambda-16-1) non-receptor tyrosine phosphatase 1 (PTPN1)		0.1531345	0.232995	0.276747	1.0580108	420 Leukemia	42(
XIII	S74221_at	0.15328898 S74221	0.233013	0.2/67587	1.0581961	renkemia	†
Herpesvirus associated ubiquitin-specific protease (HAUSP)		0.15338008 Z72499 at	0.233075		1.0595453	4 18 Leukemia	7 7
Helix-Loop-Helix Protein Delta Max. Alf. Splice 1		HG2525 0.15345937 HT2621	0.233204		1.0595994	417 Leukemia	41,
Br140 mRNA	M91585_at	0.15353741 M91585	0.233336	0.2/69/49	1.0005/29	renkelilla	+
EST: Futilian tetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)	1 1	0.15362586	0.233364		1.06085	415 Leukemia	41.
RNA-BINDING PROTEIN FUS/TLS	0.15372121 X71428 at	0.15372121	0.233519	0.2770811	1.0012388	414 Leukeiiila	+
HPRT1 Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	0.15381987 M31642_at	0.15381987	0.233641		1.0615326	413 Leukemia	4
	11	0.15389264 X14789	0.233751	0.2772995	1.063674	412 Leukemia	4
Dopamine D1A recentor dene complete evon 1 and evon 2 E and	M85247 at	0.1539706 M85247	0.233791		1.0642318	411 Leukemia	41
Cosmid CRI-JC2015 at D10S289 in 10sp13		0.15408665	0.233895	0.2776266	1.0646759	0 Leukemia	410
PTCH Patched (Drosonhila) homolog	U43148 at	0.15412694 U43148	0.233977		1,0651479	409 Leukemia	8
Branched-chain amino acid aminotransferase (ECA40) mDNA		0.15423803 U62739	0.234001	1	1.0653403	408 Leukemia	49
BA I 1 mRNA for nuclear RNA helicase (DEAD family)	23/166 at	0.1545441/ 23/166 0.15428428 M40283	0.2341	0.2778528	1.0655652	407 Leukemia	8
Rab GDI mRNA		0.1544765 D13988	0.234156		1.0657307	405 Leukernia	₹
KIAA0144 gene	D63478_at	0.15459642 D63478	0.234281		1.0671936	404 Leukemia	4
PRE-MRNA SPLICING FACTOR SRP75		0.1546605 L14076	0.234335	.1. 1	1.0675877	403 Leukemia	8
Signaling inosital polymbosulata 5 phosphatase SID 440 mDNA	्री कि	0.15477511 U57650	0.234388	0.2783461	1.0676644	2 Leukemia	402
at IRE1 Interferon remilatory factor 1	v.	0.15486541 1.05072	0.234422	0.2784211	1.0677823	401 Leukemia	40
ATP5F1 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	X60221_at	0.15492117 X60221	0.234555	0.278449	1.0688711	400 Leukemia	40
Tumor-associated 120 kDa nuclear protein p120, partial cds(carboxyl terminus)	D13413_ma 11_s_at	D 0.15501659	0.23456	0.2784782	1.06919	399 Leukemia	36
Clone 23933 mRNA sequence	U79273_at	0.15510282 U79273	0.234595	0.2784956	1.0693145	398 Leukemia	35
Bone marrow serine protease gene (medullasin) (leukocyte neutrophil elastase gene)	0.155257 Y00477 at	0.155257	0.234722	0.2785358	1.069673	397 Leukemia	36
PTB Ribosomal protein L26	0.15531787 X17206_at		0.234745	1.0706985 0.2786484	1.0706985	396 Leukemia	55
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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. gand, gand, gand, gand gand gand, ga

007		L				4A461140_a	AA461140_a EST: zx64f12.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
470 Le	426 Leukemia	1.0545149	0.276352	0.232625	0.152/0753		clone 796271 5', mRNA sequence, (from Genbank)
427 Let	427 Leukemia	1.0544431	0.2763338	0.232553	0.15260927	HG2325- HT2421 at	Retinoic Acid Receptor, Gamma 2
428 Lei	428 Leukemia	1.0544137	0.2761261	0.232497	0.15254888 Y12856	1	AMP-activated protein kinase alpha-1, partial
429 Leukemia	ukemia	1.0544074	0.2761194	0.232414	0.15247752 J04102	J04102 at	ETS2 V-ets avian erythroblastosis virus E26 oncogene homolog 2
430 Leukemia	ukemia	1.0542761	0.2760035	0.232393	0.15239303 D38076 at	J38076 at	RANBP1 RAN binding protein 1
431 Leukemia	ukemia	1.0539241	0.2758793	0.23235	0.1522458 D21261	D21261 at	SM22-ALPHA HOMOLOG
432 Leukemia	ukemia	1.0537413	0.2758634	0.232301	0.15223864 S82297	S82297 at	BETA-2-MICROGLOBULIN PRECURSOR
433 Leukemia	ukemia	1.0536019	0.2758448	0.232237	.0.15216245 X58521	X58521_at	NUCLEAR PORE GLYCOPROTEIN P62
,						62317	Choline kinase isolog 384D8 3 gene extracted from Chromosome
434 Leukemia	Jkemia	1.0533165	0.275672	0.232159	0.15205857	3_at	22q13 BAC Clone CIT987SK-384D8 complete sequence
					-	HG2705-	
· !						HT2801_s_a	
435 Leukemia	Jkemia	1.0530785			0.15198444		Serine/Threonine Kinase (Gb:Z25427)
436 Leukemia	Jkemia	1.0516443	0.2755635	0.231966	0.15195596 L38932	_38932_at	GT197 partial ORF mRNA, 3' end of cds
							SLC16A1 Solute carrier family 16 (monocarboxylic acid transporters),
437 Leukemia	Jkemia	1.0512185		0.231956	0.15186423 L31801	_31801_at	member 1
438 Leukemia	ıkemia	1.0496935	0.2754662	0.231905	0.151854 L24804	24804 at	(p23) mRNA
439 Leukemia	Jkemia	1.049624	0.275438	0.231852	0.1517252	Y08302 at	MAP kinase phosphatase 4
440 Leukemia	Ikemia	1.0492315	0.2753522	0.231656	0.15156926 U10117	J10117_at	CALMODULIN
441 la Ikamia	ikemis	1 0/87151	0.275995	0.00464	V 17 V 17 V 0	X60003_s_a	
1077	יוייייייייייייייייייייייייייייייייייייי	1017040	0.202012.0	401670	0.151347341	, in the second	CAMP-KESPONSE ELEMENT BINDING PROTEIN
442 Leukemia	Kemla	1.0486447	0.2751431	0.231605	0.1514889 L37368_at	.37368_at	(clone E5.1) RNA-binding protein mRNA
						HG3214-	The state of the s
443 Leukemia	ıkemia	1.048322	0.275055	0.231562	0.15140463 HT3391 at		Metallopanstimulin 1
AAA II aukamis	Komis	1 047834E	0.2750406	70000	7		L43579 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
107	ועבווומ	1.047.0040	0.27.30.190	0.231534	0.15132624 L43579	တ	at 110298, mRNA sequence
445 Leukemia	ıkemia	1.0478203	0.2750187	0.231424	0.15108965	U70064_s_a t	Lysosomal trafficking regulator (LYST) mRNA partial cde
446 Leukemia	ıkemia	1.0443496	0.2750171	0.231419	0.15104818 D86550	at	Serine/threonine protein kinase
						1	L44L gene (L44-like ribosomal protein) extracted from Human
447 Leukemia	Ikemia	1.0442094	0.2750001	0.231389	0.15101625 3 at)2/_rna	Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44.
448 Leukemia	kemia	1.0440782	0.2749421	0.231361	0.15099755 X99687 at	-	Methyl-CpG-binding protein 2 intron 2
-		1	1			ω.	
449 Leukemia	Kemia	1.043317	0.2749179	0,231219	0.1508406 t		Bak protein mRNA
450 Leukemia	kemia	1.0429516	0.274821	0.23114	U.150769651	U90543_s_a	Butvrophilin (BTE1) mRNA
451 Leukemia	kemia	1.0428103	0.2747208	0.231121	0.1507386 L14813	at	CELL Carboxyl ester linase like protein

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, '		4 0425364	0 2746482	0.234054	0.150642661t	D12//3_s_d	AMPD3 Adenosine monophosphate deaminase (isoform E)
∵ i '	452 Leukennia	1.046,0004	1.046.03004 0.2740404	0 234048	0 15060385 L 13434	व	Chromosome 3p21.1 gene sequence
I	453 Leukemia	1.0421928	1.0421929 0.2143910	0.230926	0.1504897 M13792	at	ADA Adenosine deaminase
•	454 Гепкеппа	1,0413241	0.004/7.0	0.400040	×	rna	Put. HMG-17 protein gene extracted from Human HMG-17 gene for
4	4551 eukemia	1.041905	0.2745036	0.230858	0.15043059 1	at	non-histone chromosomal protein HMG-17
1							
_	456 Leukemia	1.0416474	0.2744603	0.230701	0.15036479 HT311	ਲ	Ribosomal Protein L30
	457 Leukemia	1.0408605	1.0408605 0.2743904	0.23067	0.1502489 D42085	at	KIAA0095 gene
1						X66894_s_a	O CHICAN CONTRACTOR CONTRACTOR
	458 Leukemia	1.040831	0.2743227	0.230606	0.15015577 t		FACC Fanconi anemia complementationi giroup c
اتــا	459 Leukemia	1.0405996	1.0405996 0.2743053	0.2305	0.15008208 X9/249		Leucine-rich printary response protein i
1	460 Leukemia	1.040179	1.040179 0.2742777	0.230493	0.15002976 Y13247	13247_at	FD19 mKNA
Η.		000000	0 27 40204	0.930/81	RC_A 0.14999582183_at	RC_AA2625 83_at	EST: zs22c11.s1 NCI_CGAP_GCB1 Homo sapiens curve corre- IMAGE:685940 3', mRNA sequence. (from Genbank)
	461 Leukemia	1.0390300		0.230401	0 14993085 M95627	195627 at	Angio-associated migratory cell protein (AAMP) mRNA
ᆈᆝ-	462 Leukemia	1.038020	0.2/4/302	0.230423	0 14083393 736715		Net transcription factor
_ [463 Leukemia	1.0397133	1.039/ 133 0.2/41/40	0.200230	0.000001		EST. ae32ff3.s1 Gessler Wilms tumor Homo sapiens cDNA clone
	464 l eukemia	1.0395787	0.2739714	0.23025	0.14977348 03 at	13_at	897533 3', mRNA sequence. (from Genbank)
Ц.,						M68895_rna	
	465 Leukemia	1.0393885	0.2739418	0.230143	0.149686551	at	Alcohol dehydrogenase 6 gene
1-	466 Leukemia	1.0383989		0.230089	0.14955644 U49082	J49082 at	Transporter protein (g17) mKNA
41_	2000				The state of the s	RC_AA3484	EST: EST54858 Hippocampus II Homo sapiens cUNA 3 eng, nikina
	467 Leukemia	1.0373524	0	0	0.14946723 12	12_at	sequence. (from Genbank)
1	468 Leukemia	1.036781	0.273836	0.229964	0.14934695 M91467 at	M91467 at	HTR1E 5-hydroxytryptamine (serotoriii) receptor 12
<u> </u>			1		0.44020703	D29675_s_a t	Inducible nifric oxide synthase gene, promoter and exon 1
	469 Leukemia	1.0300333	- 1		l	M21505 of	HI A DNA Major histocompatibility complex, class II, DN alpha
	470 Leukemia	1.0365255	0.2736316	0.229899	- [
	471 Leukemia	1.0360969	0.2736087	0.2298	0.14909622 HT830	н <u>с</u> 830- НТ830_at	Potassium Channel (Gb:L02750)
-			4			HG1112-	. !
	472 Leukemia	1.0360832		0			Ras-Like Protein Tc4
-	473 Leukemia	1.0355002	0.2734777	0.229663		X89985 at	BCL/ B cell lympholina protein / B
1==	474 Leukemia	1.0348488	0	0	- (J02923_at	LCP1 Lymphocyte cytosolic protein 1 (L-piasini)
1.5	475 Leukemia	1.0345237	7 0.273225	0		- 11:	Kab geranyigeranyi transierase, apria-subumi
-	476 Leukemia	1.0342258					ILTA INEREUKIII I, alpria
+-	477 Leukemia	1.0341363	3 0.2730961	0			DEK FROTEIN
100	478 Leukemia	1.0338426				U50553 at	Helicase like protein z Ilikiwa Pagos Pagandel de katuliana tayin substrate 2
15	479 Leukemia	1.0335699	0	0		M64595 at	TACC Res-related Go bottom toxin substrate 2 Thursd reconstructoring TRIPS mRNA 3' end of cds
1-	400 Loughania	4 0220010	0002200	0 00004B	0 148494661 40411 21	140411 21	Involg receptor litteración (Train of minimo), o cara or caca

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1.0326773 0.2729941 0.22911 0.14841114 J03592 at ANT3 Adenine nucleotide translocator 3 (liver)	<u> </u>	0.2729103 0.229048 0.1483176 U03486_at	0.2728589 0.229027 0.14821225 U85430_at	0.2727933 0.228894 0.14812903	302689 0.2727467 0.228818 0.14805987 t CALMODULIN-RELATED PROTEIN NB-1	201200 0 2727061 0 228695 0 14797784 HT3263 at Splicing Factor Sc35. Alt Splice Form 3	HG1595-	1 0298699 0.2725866 0.228628 0.14787337 Heterogeneous Nuclear Ribonucleoprotein I, Alt. Splice 2, Ptb-1	0.228598 0.1478017 X60188 at	294064 0.2724558 0.228523 0.14767988 X98085 at TNR Tenascin R (restrictin, janusin)	292233 0.2724338 0.228461 0.14762366 S49592 s at Transcription factor E2F like protein [human, mRNA, 2492 nt]	AFFX-	HUMGAPDH	275176 0.2723585 0.228377 0.14754903 at AFFX-HUMGAPDH/M33197 5 at (endogenous control)	AFFX.	HUMGAPDH	0000000	0.27.22809 0.228249 0.14741004 at-2	Gamma-aminobutyric acid transporter type 3 [numari, retai brain, 1984 0 2722254 0 228172] 0.14733319 S75989 at mRNA, 1991 ntl	0.2721809 0.228101 0.14730573 M13450_at	261896 0.2721535 0.228052 0.14727719 J02683 s at ANT2 Adenine nucleotide translocator 2 (fibroblast)	0.2721463 0.228036 0.14723867 M21064	0.227913 0.14717765 U15009 at	239787 0.2719609 0.227896 0.14708897 X04391_at CD5 CD5 antigen (p56-62)	'at	0.14696284 M65217_at	at	1,0225275 0.2717126 0.227563 0.14687638 X98260 at M-phase phosphoprotein, mpp11	0.2716422	0 074 170 V 0 074 170 V 0 0 140 T 170 V 0 0 140 T 170 V 0 0 1
73 0.27299	31 0.27299	1		1	į.	1	1	9 0 27258	34 0.27249	34 0.27245											i	1	1		52 0.27179	35 0.27177	88 0.27176			ŧ
1.032677	1.0326481	1.0317615	1.0317472	1.0310644	1.0302689	1 0301290	2000	1 029865	1.029726	1.0294064	1.0292233			1.0275176			, , , , , , , , , , , , , , , , , , ,	1.02/51/6	1 0268674	1.0266908	1.0261896	-	├-	1.0239787	1.0239	-	-		 	+
481 I eukemia	482 Leukemia	483 Leukemia	484 Leukemia	485 Leukemia	486 Leukemia	187 Loukemis	בכמוכווים	488 eukemia	489 Leukemia	490 Leukemia	491 Leukemia			492 eukemia	5000			493 Leukemia	494 l eukemia	495 Leukemia	496 Leukemia	497 Leukemia	498 Leukemia	499 Leukemia	500 Leukemia	501 Leukemia	502 Leukemia	503 Leukemia	504 l eukemia	י בייייייייייייייייייייייייייייייייייי
481	482	483	484	485	486	197	P	488	489	490	491			492	3			493	494	495	496	497	498	499	500	501	502	503	504	5 1

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1909	506 Leukemia	1.0214908	0.2712591	0.227302	0.1466067 Y00414_s	क्र	
202	einkemia	1.0212971	0.271244	0.227212	0.1465708 Z14000	at	RING1 Ring tinger protein 1
800	508 laukemia	-	0.2711166	0.227133	0.14651588 D87073	at,	KIAA0236 gene
	500 Leakonia		0 2710729	0.227066	0.14639397 \710871	ä,	Twist gene
2 5	Leunchille	1.0104591	0.270876	0.227055	0.14633761 X80907	aţ	P85 beta subunit of phosphatidyl-inositol-3-kinase
	это гепкетпа	1.015450	0.21.00				NAD+-dependent succinate-semialdehyde dehydrogenase (SSADH)
7	51111 eukemia	1.0191745	1.0191745 0.2707692	0.226955	0.14623317 L34820	at	mRNA, 3' end
12	510 Leukernia	1.0187136	1 0187136 0.2706109	0.226861	0.14619271 U85245	at	Phosphatidylinositol-4-phosphate 5-kinase type II beta mkivA
7 7	513 Loukemia	1 0184958	0.27059	0.22677	0.14607468 U79718	at	Endonuclease III homolog mRNA
2 2	Leunchina	1 0181412		0.226723	0.14601307 X86681	ä	Nucleolar protein, HNP36
+ K	515 lankamia	1.0180436	10	0.226658	0.14594299 U25165	at	Fragile X mental retardation protein 1 homolog FXR1 mKNA
					Ī	HG2441-	
						HT2537_s_a	
16	516 Leukemia	1.017392	0.2704442	0.226655	0.14586835 t		Retinoblastoma Protein, Mutated
317	517 Leukemia	1.0171125	0.2704426	0.226608	0.14581361 U05040	05040 at	FUSE binding protein mKNA
				·			Phosphatidylinositol (4,5)bisphosphate 5-phosphatase nomog
118	518 Leukemia	1 0170559	0.2703212	0.22658	0.1457779 U45975	45975_at	mRNA, partial cds
2	בפמוס		ı				EST: yp83a08.r1 Homo sapiens cDNA clone 194006 5' similar to
2	540 1 outomia	4 0166558	0 2702766	0 226507	0,14567302 H51825 at		contains L1 repetitive element; (from Genbank)
2	Fernelina	20010			<u>x</u>	9	EST; aa47h07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
520	520 Leukemia	1.016489	0.2700983	0.226478	0.14554566 20	0_at	IMAGE:824125 3', mKNA sequence, (Ironi Genidalin)
					×	X85137_s_a	
321	521 eukemia	1.0157963	0.2700755	0.226348	0.1455456 t		Kinesin-related protein
523	522 Leukemia	1.0152906	1	0.226342	0.14545943 M22490_at	122490_at	BMP4 Bone morphogenetic protein 4
1					2	M20747 s a	a SLC2A4 Solute carrier family 2 (facilitated glucose transporter),
523	523 aukemia	1.015287	0.2698444	0.22629	0.14542662 t		member 4
3	- Course		1 .		X	X98248_rna	
524	5241 eukemia	1.0150449	0.2696536	0.226121	0.14531155 1	at	Sortilin
525	525 Leukemia	1.0141498		0.226105	0.14525439 L20298	20298 at	Transcription factor (CBFB) mKNA, 3 end
526	526 Leukemia	1.0135081	1	0.22607	0.14516947 U05659	J05659_at	HSD17B3 Hydroxysteroid (17-beta) denydiogeniase 3
						X12671_rna	Hnrnp a1 protein gene extracted from Hurrian gene for neterogeneous
527	527 Leukemia	1.0129399	9 0.2694492	0.22601	0.14511096 1	at	nuclear ribonucleoprotein (hnRNP) core protein A1
		1				U36759_s_a	
528	528 Leukemia	1.0113257		0	0.14498425		Pre-T cell receptor appra-type chain precursor, mixing
525	529 Leukemia	1.0109144	4 0.2693585	0.225767	0.14488634 X85372	x85372_at	Sm protein r
		1				X99586_s_a	
530	530 Leukemia	1.0106939	9 0.2691579	0			Ubiquitin-homology domain protein PIC1 mKNA
53	531 Leukemia	1.010581	1	0	0.14475243 U69141 at	U69141 at	GCDH Glutaryl-Coenzyme A denydrogen ase

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

1 0097235 0 2690202 0 225238 0 14462133 Z15114 at PRKCG Protein kinase C, gamma	0.225205	HG3426-	0.14450201 t 13610_s_a 13610_s_a	0.2687259 0.225114 0.14444768 D17427 at		0.2686367 0.225089 0.1444042 U72512_at	0.2685562 0.225052 0.14434643 X82877_at	0.2685473 0.224985 0.14426583 D26068_at	0.2684391 0.224962 0.14419374 L22342 at	0.2684355 0.224962 0.14416265	R33581 0 224901 0.144072491t Histone deacetylase HD1 mRNA	0.268364 0.224838 0.14393923 D14878_at	0.2683569	RC_AA2053 EST: zq79d12.s1 Stratagene hNT neuron (#937233) Homo sapiens con a control of the cont	RC AA2563	0.2682143 0.224679 0.1437358 80_at	0.14366606 U43965 at	1.0037664 0.2680817 0.224473 0.1435526 D86965 at KIAA0210 gene	0.224413 0.14348514 U59736_at	335161 0.2678291 0.224413 0.14342432 U71601 at Zinc finger protein zfp47 (zf47) mRNA, partial cds	0.224385 0.14339615 U49070 at Peptidyl-prolyl isomerase and essential mitotic regulator (PIN1) mRNA	0.2675588 0.224244 0.14334439 Z12830 at	AB006782_a	0.267399 0.224198 0.14328918 t	0.2673563 0.224189 0.14317745 L26247_at	0.267208 0.224188 0.14307486 U48730_at	0.2671715 0.224109 0.14300162	0.267164 0.224084 0.14297684	0 00 74 000
0097235 0 2690	1,0094302 0,2689		1 0094115 0 2688	1 0091236 0.2687		1.008249 0.2686	1	1.0080395 0.2685	4	L	4 0063584 0 2683			1 0052041 0 2683		1.0041918 0.2682	1.003964 0.2681	1.0037664 0.2680	1.0036104 0.2679	1.0035161 0.2678	1.0030602 0.2677	1		1.0027859 0.267	1,0025429 0.2673	1.0021206 0.267	1.001407 0.267	1.000783 0.26	750000000
533 Dukamia 1	+-		F3E Loukemis 1	+-	+-	537 Leukemia	├	\vdash	+	-			-	545 Loukemis 1	+	546 Leukemia 1	-	+-	├	550 Leukemia 1	551 Leukemia 1	+	+-	553 Leukemia 1	554 Leukemia 1	├-	556 Leukernia	557 Leukemia	+

								-			1				_		1	7		_	_	1	T	1		1	1	T		1	1		7
FST: zx11d03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 786149 3' similar to TR:E246888 E246888 CHROMOSOME XVI READING FRAME ORF YPL146C.;, mRNA sequence. (from	Genbank) NE-kanna-B n65delta3 mRNA, spliced franscript lacking exons 6 and	7, partial cds	Guanine nucleotide-binding protein G-s-alpha-3 gene extracted from	M21142_cds Human guanine nucleotide-binding protein alpha-subunit gene (G-s-	alpha)	at SB1.8/DXS423E	Lipid-activated protein kinase PRK1 mRNA	Clone 53BP1 p53-binding protein mRNA, partial cds	Alpha-CP1 mRNA	Protein kinase (JNK2) mKNA	ADRB3 Adrenergic, beta-3-, receptor	CUTL1 Cut (Drosophila)-like 1 (CCAAT displacement protein)	SIAT4A Sialytransferase 4A (beta-galactosidase alpha-2,3-	sialytransferase)	Amiloride-sensitive epithelial sodium criarmer yanıma subumbura ve v	5' end, partial cds	TALLY Kibosomai protein, raige, r. o	Thromboveno A9 receptor	I BAAZK Hillomboxane Az rezeptor	ADENVI OSLICCINATE I YASE	Adding to the solution of the state of the solution of the state of th	BKAF V-fal mulle salcolla vitai o loggono monda e	Clone lambda 5 semaphorin mRNA		Laminin, A Polypeptide	SH3 domain-containing protein SH3P17 IIIRNA	TK1 Thymidine kinase 1, soluble	Endogenous retroviral H protease/linegrase-derived On Himself, at and putative envelope protein mRNA, partial cds	Protein tyrosine kinase PYK2 mRNA	DGCR6 protein	EST: yj91a03.r1 Homo sapiens cDNA clone 1560/6 5. (nom	(Genbank)
	A4488	28.0	5 00000		M21142_cds F		sat	at_	ä		T	M29932_s_a t			at		, si	Ħ,	J27325_s_a	+	ร์ ูซิ	ชี .	at		HG2028-	HT2082_at	U61166_at	M15205_at	<u>_</u>	U43522 at	X96484 at		R73164 at
	1	0.1428782 63 at	0 14276932 †			0.14270826 2 s at	0.14259373 S78271	0.14251819 U33053	0.14248449 U09477	0.14242002 Z29505 at	0.14235973 M32405 at	0.14231849	0.14224017 M74099 at		0.1421362 L13972		0.14204963 U48936	0.14198643 M17885		0.141912161	0.14183213 X02/51	0.14178798 103007	0.14172333 M95/12	0.14165999	The state of the s	0.14163777 HT2082	0.14156242 U61166	0.14151382 M15205	0.14139701 U88898	0.14136915 U43522	0.14127295 X96484		0.14120594 R73164
		0.223965	0.223924	770077		0.223792	0.223738	0.223724	0.223595	0.223556	0.223426	0.223363	0.223345		0.223304		0.223269	0.223243		- 1		0.223133	0.223013	0.222993	1_		0.222837		0 222645	O			0.222402
		0.2670581	500730 U	0.401040		0.2669815	0 2668725	0.2668605	0.2668501		0.2666691	0.0885188	0.2003100	2007	0.2663127		0.2662605	0.266175	1	0.2661211	0.9954985 0.2661073	0.995369 0.2660707	0.2660021	0.2658814		0.2658759	0.2658689		0.2857613	0 993485 0 2657197	0.265673		0.265554
		1.0003803 (4 0000004	1.000000.1		1.0001686	0 9993553			0.9980555	0.9979395	0.007848	(- 1	0.9971064		0.997104	0.9964346		0.996066	0.9954985	0.995369	0.9946226	0.9946206		0.9945748	0.9943095	0.9942491	0 00/1005	0.334155	0.9930201		0.9928292
The second secon	,	559 Leukemia		560 Leukemia		561 Leukemia	560 Loukemia	+-	+-	7			567 Leukerilla	רפחעפווומ	569 Leukemia		570 Leukemia	571 Leukemia		572 Leukemia	573 Leukemia	574 Leukemia	575 Leukemia	576 Leukemia		577 Leukemia	578 Leukemia	579 Leukemia		300 Leunemia	582 Leukenia		583 Leukemia
-		259 L		1095		561	582	5631	564	5651	5661	107	200	000	569	3	570	571		572	573	574	575	576	5	577	578	579	202	200	2 2	700	583

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				and the country
0.9923522	2 0.2654958	0.222351	0.1410583 M19483 at	A1P5B A1P synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
0.9922085	0.265288	0.222326	0.1410289.793784.91	DNA sequence from clone RP3-398C22 on chromosome 22q13 Contains part of the gene for a novel protein (the ortholog of mouse
0.991748	0			KIAA0127 gene
0.9908701	0.265223	0.222072	11 1	DLG2 Homolog 2 of Drosophila large discs
0.9904501	0.2650642	0.221918	0.14086024 L07261 s a	0.14086024 L07261 s at Alpha adducin mRNA partial cds including alternate expres A and B
0.9902272	0.2650642	0.221815	AB006190_a	Adlianorin 6
0.9900854	1		0.14071418 X52882 at	T-COMPI FX PROTFIN 1 AI PHA SHIRLINIT
0.9894392	1 1	0.221781	0.14069244 U25029 at	GRL Glucocorticoid receptor alpha (alternative products)
0.9892231	0.2648208	0.221759	0.14060697 D88613 at	HGCMa
0.9888067	0.2648111	0.2217	0.14056556 M26683 at	SCYA2 Small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-je)
0.988426	0.2647232	0.221685	0.1405043 L43575 s at	at (clone EST02946) mRNA
0.9883249	0.2645627	0.221627	AA091752_a 0.14045231 t	Homo sapiens histone H2A F/Z variant (H2AV) mRNA complete ode
0.9883074	0.2645522	0.221519	0.14043207 55_at	
0.9878091	0.2644228	0.224464	HG3578-	
0.9871443	T .	0.221449	0.14023927 737986 at	Autolmmune Antigen, Thyroid Disease-Related Antigen
0.9866265	1	0.221425	0.14017594 U14973 at	40S RIBOSOMAL PROTEIN S20
0.986596	0.2643457	0.221401	0.14011833 X65873 at	KINESIN HEAVY CHAIN
0 0865050	0.064330E	0.004470	X98534_s_a	
0.986397	1	0.221173	0.140085951	VASP gene, exons 4 to 13
0.300337 0 9860925		0.2211/1	0.14002/34 M88468 at	MVK Mevalonate kinase
0.9859214	1	0.221008	0.1399155 X63692 at	26S PRO LEASOME REGULATORY SUBUNIT P31 DNMT DNA methyltransferasa
0.9854552		0.220998	ti I	Glutathione-S-transferase homolog mRNA
0.9852542		0.220894	0.13979514 Y14140 at	G protein gene encoding beta 3 subunit exon 1 and promoter
0.9849866	0.2640067	0.220879	0.13975918 D79991 at	KIAA0169 gene, partial cds
0.9843043	0.2639483	0.220787	0.13967182 1 s at	Of p65 gene encoding p65 subunit of transcription factor NE-kannaB
0.983847	0.2639208	0.220699	0.13959935 U41387 at	Gu protein mRNA, partial cds

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in their at their interview.	<u></u>	HG3523- HT4899 s a	1	0.22053 0.13938545 D55716_at	0.220465 0.13928382 M21259_at	0.9817628 0.2637195 0.220452 0.13922866 U96131 at HPV16 E1 protein binding protein mKNA	0 2262001 0 2262001 0 22045 0 13048889 S78771 s. at RING3 PROTEIN	0.2030401 0.22043 0.10310000 0.001	0.2635061 0.220441 0.13913223 030313 at	0.9795336 0.2634919 0.220345 0.13896683,303249 at 137 AZ 1369668191 production protein (clone L1-57) [human, HeLa cells,	0.979215 0.2634905 0.220288 0.13890687 S83364 at mRNA Partial, 366 nt]		HSAC07/X0	0.9791006 0.2634052 0.220201 0.13887055 0351_5_at AFFX-HSAC07/X00351_5_at (endogenous control)	AFFX-	HSAC07/X0	0.9791006 0.2633874 0.220063 0.13877283 0351_5_at-2 No info for gene	0.2631836 0.220025 0.13870098 L08187 at	0.2631825 0.22001 0.1386441 D14663_at	0.9781168 0.2631512 0.219925 0.13855246 D86966 at KIAA0211 gene	X62153_s_a	0.2629488 0.219873 0.138449 U15172_at	HG4297-	-	0.9772505 0.262822 0.219774 0.13831814 U58766 at FX protein mRNA	7	0.2627664 0.219734	0.2627564 0.219641 0.13810454 1034182	0.2626424 0.219598 0.13802/16 U34343_at	0.219579 0.13796322 X52889 at	0.219511 0.13790503 L27841 at	0.219493 0	0.2624117 0.2194 0.1378033 L40410 at Inyrold receptor lineactor (11% 3) 11% 3.1%	0.2623586 0.219373 0.13768956 M641/4 at	0.9757196 0.2623353 0.21937 0.13765173/A76556 at Mrr v.17 mpv.11 uch sensy 1.55 miles at 1.55 miles
	9836288 0.263		0.982669 0.263	9820164 0.263	9819489 0.263	.9817628 0.263		3815141 0.20	.9809588 0.26	.9795336 0.26		- L		9791006 0.26				9787955 0.26	0.978353 0.26	0.9781168 0.26				0.977672 0.26	1			 0.9769992 0.26						1	1
	611 Leukemia 0.		612 Penkemia	+	1	_	-	+	-	618 Leukemia 0	610 Leukemia	O TO FEATURE III		620 ankamia 0	-		621 eukemia C	+-	+-	+	+	+	+	627 Leukemia	+	+-	1	 631 Leukemia	632 Leukemia	633 Leukemia	634 Leukemia	635 Leukemia	-	637 Leukemia	638 Leukemia

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						GABPB2 GA-binding protein franscription factor, beta subunit 2
639	639 Leukemia	0.9752443	0.262287	0.219365	0.13759807 U13045_at	
640	640 Leukemia	0.9752169	0.2622797	0.219279	0.13754712 D29954_at	HYPOTHETICAL MYELOID CELL LINE PROTEIN 6
641	641 Leukemia	0.97521	0.2622731	0.219261	0.13752021 X54304_at	Myosin regulatory light chain mRNA
642	642 Leukemia	0.9751254	0.2622283	0.21926	0.13747294 D00860_at	PRPS1 Phosphoribosyl pyrophosphate synthetase subunit I
643	643 Leukemia	0.9747022	0.2621803	0.219174	0.13735367 D86979 at	KIAA0226 gene
					U66828_s_a	
644	644 Leukemia	0.9746139	0.2620894	0.219118	0.13735338 t	Carnitine palmitoyltransferase I (CPTI) mRNA
					U40391_rna	
645	645 Leukemia	0.9743862	0.2620511	0.219061	0.13724798 1 at	Serotonin N-acetyltransferase gene
646	646 Leukemia	0.9731653	Į	0.219031	0.13724132 X07024 at	TRANSCRIPTION INITIATION FACTOR TFIID 250 KD SUBUNIT
						EVI2B PROTEIN PRECURSOR TROPIC VIRAL INTEGRATION SITE
647	647 Leukemia	0.9730851	0.9730851 0.2619634	0.218993	0.13720119 M60830 at	2B PROTEIN)
648	648 Leukemia	0.9730682	0.9730682 0.2619074	0.218949	0.13714243 D00596 at	TYMS Thymidylate synthase
					Y07829 xpt4	Exon A2 from H.sapiens gene encoding RING finger
948	649 Leukemia	0.9729919	0.2617965	0.218936	0.13706204 at	protein./ntype≂DNA /annot=exon
						Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346
920	650 Leukemia	0.9729461	0.2617878	0.2189	0.13694704 S87759 at	lut.
351	651 Leukemia	0.9728951	0.2617784	0.218828	0.1368517 U61234 at	Tubulin-folding cofactor C mRNA
352	652 Leukemia	0.9719777	0.2617541	0.218817	0.13678911 L09604 at	INTESTINAL MEMBRANE A4 PROTEIN
553	653 Leukemia	0.9710791	0.9710791 0.2617541	0.218652	0.13676417 U32849 at	Hou mRNA
354	654 Leukemia	0.9710065	0.2616389	0.2186	0.1366572 U51241_at	CMKBR3 Chemokine (C-C) receptor 3
355	655 Leukemia	0.9708858	0.2615778	0.218598	0.13659933 M81601_at	TRANSCRIPTION ELONGATION FACTOR S-II
				-	U41068_cds	
929	656 Leukemia	0.9701346	0.2615139	0.218563	0.13654675 2_s_at	collagen alpha2(XI) (COL11A2) gene
						Fragile X locus M2C containing an unidentified open reading frame, 3'
927	657 Leukemia	0.9697877	0.2615116	0.218419	0.1364635 M16282_at	end
928	658 Leukemia	0.969676	0,969676 0.2613365	0.218308	0.1363978 U25435_at	Transcriptional repressor (CTCF) mRNA
629	659 Leukemia	0.9696209	0.2612992	0.218243	0.1363728 U52830_at	Cri-du-chat region mRNA, clone CSC8
					M13058_s_a	
099	660 Leukemia	0.9692056	0.2610472	0.218234	0.13633299 t	PRH1 Proline-rich protein HaeIII subfamily 1
661	661 Leukemia	0.9688708	0.2610467	0.218224	0.13622816 U32581_at	Lambda/iota-protein kinase C-interacting protein mRNA
662	662 Leukemia	0.9686209	0.2610361	0.218216	0.13619027 J04948_at	Alkaline phosphatase
663	663 Leukemia	0.9685306		0.218163	0.13613686 U79252 at	Clone 23679 mRNA
664	664 Leukemia	0.9681338	0.2609831	0.218139	0.13607603 D86958_at	KIAA0203 gene
665	665 Leukemia	0.9675313	0.2609794	0.218102	0.1360675 U60666 at	Testis specific leucine rich repeat protein (TSLRP)
999	666 Leukemia	0.9675012	0.2609684	0.218006	0.13601229 M14764 at	NGFR Nerve growth factor receptor
299	667 Leukemia	0.9672784	0.2609606	0.217996	0.13590613 U51477_at	Diacylglycerol kinase zeta mRNA
899	668 Leukemia	0.9669724	0.2608967	0.217986	0.13586837 U19345 at	AR1 protein (AR) mRNA

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	70na nellucida alvonrofein 2 (7D2) m.DNA	Opposen z (zrz) nikwa	ZNF74 Zinc finger protein 74 (Cos52)	RET Ret proto-oncodene (multiple endocation procession Marking)	MEN2B and medullary thyroid carcinoma 1. Hirschsprung disease)	RNA		Protein phosphatase 2A B56-alpha mRNA	ATP synthase B chain, 5'UTR (sequence from the 5'cap to the start	Transcription factor E2F like protein fluman mRNA 2402 pt	111 764.7 (111 111 11 11 11 11 11 11 11 11 11 11	SNRPR Small and our ribound out the state of	and a containment to the control of	CP-1 mRNA	Proliferation call and phosphodiesterase mRNA	Chloride channel (putative) 2139hn	do	Guanine Nucleotide Exchange Factor 1	IEII C-III	SOF 14H IIIKNA	EST: ze39h02.s1 Soares retina N2b4HR Homo sapiens cDNA clone	361395 3, mRNA sequence. (from Genbank)	I A CHAIN	Pta-1 profile		at Mylerid differentiation	Enhancer of zeste homolog 2 (EZH2) mRNA
		SYNAPTORREVIN 1	ZNF74 Zinc finger					Protein phosphatase 2A B56	ATP synthase B ch	Transcription facto	Heme A: famesultr			CC chemokine STCP-1 mRNA	Proliferating 6911 2	Chloride channel (putative) 2139hn		ADOC3 Appliage	Transcription factor SHDT4H C-DNA	ITGB8 Integrin heta 8		361395 3', mRNA s	Small and in the control of the cont	Pta-1 profein		PROBABLE G PRO	Enhancer of zeste h
HG982-		M36200 at		M57464 s a	+	U79528_s_a t	U18271_cds	L42373 at	D28383 at	U47677_at	5.	X17567_s_a t	U83239_s_a	136798 at	105614 at	230643 at	HG960-	11 900 at	J43923 at	A73780 at	RC_AA0175	7 at (59/17 at	Щ	11		170451 at	
HG982- 0 13571836 HT082 -					0.135536761	0.13545358	0.1354333	0.13534908 L42373	0.13531955 D28383 at	0.13526542 U47677	0.13520783 1 at	0.13512626		0.13498931136798 at	0.13493621.105614	0.13491368 Z30643	HG960-	0.13476059 X01388 at	0.13470088 U43923 at	0.13458802 M73780 at	0.134E602 47	0 13451457 X59417	0.13441157 05187	0.13437547 X97302	T01001000000	0.134261821170451	0.13420233 U61145 at
0.217973	0.21	0.21	0.217889		0.217845	0.217693	0.21769	0.217666	0.2176	0.217553	0.217538	0.217453	0.247444	0.217416	0.217369	0.217339	0.24732	0.217247	0.217211	0.217169	0.216952	0.216931	0.216913	0.216764	0.946747	0.21673	0.216691
0.2608065	1	0.2606816	0.2606805		0.2606419	0.2606378	0.260536	0.2604676	0.2604107	0.260329	0.2602753	0.2601953	0.2601803	0.2601281	0.2600382	0.2599831	0.2599669	0.259932	0.2598941	0.2598401	0.2596897	0.259655	0.2596369	0.2595855	0.2595796	0.2595498	0.2595474
0.9659351	0.9656111	0.965321	0.9650875		0.9648359	0.9646308	0.9645846	0.9643921	0.9643776	0.9643621	0.9643193	0.9643027	0.9641039	0.9636247	0.9632511	0.9631376	0.9631153	0.9630888		0.9622974	0.9620204	0.9619097	1	0.9614296	0.9614214		0.9611721
669 Leukemia	670 Leukemia	671 Leukemia	672 Leukemia	-	o/3 Leukemia	674 Leukemia	675 Leukemia	676 Leukemia	677 Leukemia	678 Leukemia	679 Leukemia	680 Leukemia	681 Leukemia	682 Leukemia	683 Leukemia	684 Leukemia	685 Leukemia			688 Leukemia	689 Leukemia	╁		692 Leukemia	693 Leukemia	-	695 Leukemia (
9	9	9	9		ō	67	19	19	29	29	29	89		89	89	89	68	989	89	89	389)69	69	69	693	694	969

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[마마마마 마리 프트프트로 루트루트로 동문[★] ★] 저[저[작[작] 소[의 유[유]유]유]하]하]하	0.9611367 0.2594988 0.2	0.961077 0.2594677 0.216644 0.13406864 J04168 at	0.9610701 0.25945 0.216573 0.13402414 X74330 at	0.9608819 0.2594353 0.21656	1) G600604 0 2502276 0 2407740	0.0500670 0.203036 0.210348 0.13393667 X16983_at	6 100000	0.959936 0.2592751 0.216423 0.13386457 L37360_s_at	0.9598551 0.2592553 0.21639	0.9597926 0.2592183 0.21629	0.9597082 0.2591952 0.216254 0.13371414 HT3339 at	0.9594044 0.2594648 0.24624 0.472227 X93511 s.a	0.133037671	0.9588862 0.2591352 0.216188 0.13356024 t	0.9586842 0.2591317 0.216152 0.13345881 X78992 at	U.3304130 U.Z39114/ 0.216116 0.13340378 Z30426 at	0.9578203 0.2591139 0.216085 0.1333872 t	0.9575109 0.259071 0.216084 0.13329651134844	0.9573796 0.2590636 0.215986 0.1332223 1151004 31	0.9571899 0.2590485 0.215943 0.13316225 D86988	0.95/1832 0.2589642 0.215898 0.13314246 U72517 at	0.9567441 0.2588719 0.215849 0.13311845 HT2375 3	0.9563329 0.2587676 0.215798	0.9561603 0.2587351 0.21569 0.1330000 HG172-	0.9558069 0.2586827 0.215676 0.13294743136927 at	0.9557663 0.2586317 0.215662 0.13287725 X99584	0.9552177 0.2583399 0.215651 0.13283037/Z48054 at	0.9551695 0.2583044 0.215635 0.13277273 X14329 at	0.9545414 0.2581682 0.215605 0.13267013 L38696 at	0.9542512 0.2580179 0.215003 0.13263838/232/65 at	0.10001:0 1:01:
1 의의의의 의의 희 희희 의 의 된 된목(로) 국 국(국(국(국) 국(국) 국(국) 국(국) 국(국) 국(국)				699 Leukemia 0.96	700 Leukemia 0 og	+	+-	702 Leukemia 0.9		704 Leukemia 0.95	705 Leukemia 0.95	706 Leukemia 0.95	+-		709 Leukemia 0.95	-	710 Leukemia 0.95			-	7 14 Leukernia 0.957		716 Leukemia 0.956			-		$\neg +$	723 Leukemia 0.954	+	-

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				HT/	s	*
725 Leukemia	a 0.9540494	0.2579221	0.215509	0.13248448 t	•	Transformation-Related Protein
						TCRBV1S1A1N1 gene extracted from Human germline 1-cell
			-		<u> </u>	TRY3 TCRBV27S1P TCRBV22S1A2N1T TCRBV9S1A1T.
-,						TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P,
						TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT,
	·					TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1,
						TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1,
···	<u></u>					TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T,
						TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T,
				106	N66059_cds	TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1
726 Leukemia	a 0.9538851	0.2578969	0.215386	0.13244924 7_e		of 3)
727 Leukemia	a 0.9535385	0.257876	0.215378	0.13238396 M92287_at	2287_at	GCND3 Cyclin D3
				AA	310450_a	AA310450_a EST: EST181264 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA
728 Leukemia	a 0.9532822	0.2577776	0.215375	0.13236117 t		sequence. (from Genbank)
729 Leukemia	a 0.952901	0.2577533	0.215314	0.13233696 U20979_at		Chromatin assembly factor-I p150 subunit mRNA
				위	HG1728-	
				노	HT1734_s_a	
730 Leukemia	0	0.2577446	0.215302	0.13232188 t		Non-Specific Cross Reacting Antigen (Gb:D90277), Alt. Splice Form 2
731 Leukemia	-	0.2577249	0.215274	0.13226175 Y08976_at	3976_at	FEV protein
732 Leukemia	a 0.9517539	0.2577067	0.215239	0.1321784 M55040 at	5040_at	ACHE Acetylcholinesterase (YT blood group)
				iOX	X05855_s_a	
733 Leukernia	0	- 1	0.215236	0.13211556 t		EEF1G Translation elongation factor 1 gamma
734 Leukemia	a 0.951547	0.2576326	0.215131	0.13202384 X79865_at	3865_at	Mrp17 mRNA
	-	i		XX	X76942_s_a	
735 Leukemia		1	0.215048	0,13195118t		72.1 protein
736 Leukernia			0.214993	0.13191958 J02888_at	2888_at	NMOR2 Quinone oxidoreductase (NQO2)
737 Leukernia	a 0.9511837	0.2575435	0.214969	0.1318432 X80822 f_at	0822_f_at	Ribosomal protein L18a
738 Leukemia	-		0.214803	0.13181144 L25876 at	5876_at	Protein tyrosine phosphatase (CIP2)mRNA
739 Leukemia	a 0.9503995	0.2574296	0.214731	0.13175596 D63485_at	3485_at	KIAA0151 gene
				M3	M38449_s_a	
740 Leukemia		0.2574226	0.214725	0.1316795 t		Transforming growth factor-beta mRNA, clone pTGF-beta-trp114
741 Leukemia	-	0.9500089 0.2573983	0.214666	0.131628 D64154 at	4154 at	Mr 110,000 antigen
742 Leukemia	-		0.214582	0.1315667 X98482	8482 r at	TNNT2 gene exon 11
743 Leukemia	ia 0.9492815	0	0.214458	0.13155843 Y11681_at	1681_at	Mitochondrial ribosomal protein S12
744 Leukemia	la 0.9492169	0.25716	0.214448	0.13153282 M17733	7733_at	Thymosin beta-4 mRNA
7AE Louivomin	70101057	0.0574570	074/1370	0 13117/67 M6/108 at	11108 at	Herlin 1 mBNA 3' and

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Title:	Genetic Markers for Tumors
Invento	ors: Sridhar Ramaswamy, et al.

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0.94 10300 0.2330000 0.212300 0.12471_cds	0 1302186
1	U12471 cds
0.13018301 1_at	0.212986 0.13018301 1_at gene, partial cds
0 9410585 0 2556603 0.212861 0.13015068 D28588_at	0,212861 0,13015068 D28588_at
0.0407704 0.0555643 0.012698 0.13012204 M15182 at	0.212698

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						L1CAM gene (neural cell adhesion molecule L1) extracted from Human Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-
	405040		0.040808	U	112_rna	acetyltransferase related protein (TE2), renin-binding protein (KbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase
771 Leukemia	0.9399531	0.2553393	0.212597	0.13000831 U35459	at 35459 at	(IRAN) geries, and Adzoluz gerie Bomapin mRNA
772 Leukemia	0.9396234	1	0.212595	0.1299605 M55422		Krueppel-related zinc finger protein (H-plk) mRNA
773 Leukemia	0.939461	0.2552339	0.212486	0.1299194 D87453	87453_at	KIAA0264 gene, partial cds
774 Leukemia	0.9388696	0.2552214	0.212377	0.12987974 D.	30758 at-2	0.12987974 D30758 at-2 KIAA0050 gene product
775 Leukemia	0.9388696		0.212352	0.12981263 D30758	30758 at	KIAA0050 gene
776 Leukemia	0.9384459	0.2551932	0.212205	0.12975152 Y10055	11 11	Phosphoinositide 3-kinase
777 Leukemia	0.9384245	0.2551447	0.212176	0.12971516 X64037	64037_at	GTF2F1 General transcription factor IIF, polypeptide 1 (74kD subunit)
778 Leukemia	0.9381435	0.2550916	0.212133	0.12968494 U91327	91327_at	Chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence
779 Leukemia	0.9378268	0.2549949	0,212125	HG4332 0.12960064 HT4602	HG4332- HT4602_at	Zinc Finger Protein Znfpt1
		•	-			PHOSPHORYLASE B KINASE ALPHA REGULATORY CHAIN,
780 Leukemia	0.9368298		0.21209	0.12954417 X80497	80497_at	LIVER ISOFORM
781 Leukemia	0.9364706	0.2547897	0.212073	0.12952755 S72487	72487_at	Platelet-derived endothelial cell growth factor mRNA
782 l e ikemia	0.0364332	0.2546488	0.212023	M910	M91029_cds	AMD deaminese (AMPD2) mBNA
783 Leukemia	0.9363817	- 1	0.21194	0.1294122 L35263 at	35263 at	CSaids binding protein (CSBP1) mRNA
784 Leukemia	0.9349624	0.2546057	0.211892	0.12931158 D79992 at	79992 at	KIAA0170 gene
785 Leukemia	0.9349452		0.211864	0.12928033 U76992	76992_at	Tat-SF1 mRNA
786 Leukemia	0.9347235	0.254467	0.211837	0.12921658 U50535	50535_at	BRCA2 region, mRNA sequence CG005
787 Leukemia	0.9344146	0.2544412	0.211825	0.12920801 U85946	85946_at	Brain secretory protein hSec10p (HSEC10) mRNA
788 Leukemia	0.9343216		0.211786	0.12910709 U72066	72066_at	CtBP interacting protein CtIP (CtIP) mRNA
789 Leukemia	0.9341505	0.2542551	0.211669	0.12908219 D50405	50405_at	RPD3 protein
790 Leukemia	0.933996	0.2542496	0.211644	H 0.12902167 H	HG37- HT37_at	Iron-Responsive Element-Binding Protein
cimodina 1 M7	0.0228408	0.0549497	0.244630	U 479000E79	to 7 7 6 706	PMS8 mRNA (yeast mismatch repair gene PMS1 homologue), partial
/ 3 Leunei IIIa	0.3000400	- 1	07011770	0.12033312 D	12086 cde	ous (C-terrificial region) EGEA agas (francforming profein) avtracted from Human francforming
792 Leukemia	0.9334282	0.2539729	0.211521	0.12895635 1_at	at at	1_at protein (hst) gene
793 Leukemia	0.933028	0.2538656	0.211474	U 0.12888967 t	U24056_s_a t	Inward rectifier K+ channel protein (hirk2) mRNA

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		L) 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Γ	EDAD EK506 hinding protein 12-rapamycin associated protein
794 L	Leukemia		0.2538239	0.211457	0.12884386 L340/5 at		The India and India protein (Nin7-1) mRNA partial cds
795	795 Leukemia	0.9324823	0.2538115	0.21143	0.1288017 U83843 at	1	11V-1 Net Interacting protein (wip)
702	706 I euromia	0 0324226	0.2537694	0.211416	0,12870218 t	z_a	Proteasome subunit p44.5
1 06 /	Gunellia				HG		The life meting Coll Nuclearlas Antigen 120 Kds
797	797 Leukemia		0.2537421	0.211372	0.1286966/HI1110 at		Hatemananis ribonicleonrotein A0 mRNA
7981	798 Leukemia	0.9321988	0.2537384	0.21125	U.12863120 U23603 at	G	ופנפוסחפו מספים במספים
700	700 leukemia	0 9319191	0.2537329	0.211221	0.12862206 t]	Proto-oncogene BCL3 gene
800	800 Leukemia		0.2536258	0.211174	0.12851934 M21186_at	1186_at	CYBA Cytochrome b-245, alpha polypeptide
3	Formation				X04	X04085_rna	Catalase (EC 1.11.1.6) 5 frank and exon 1 mapping to chromosome
801	801 Leukemia	0.9312192	0.2535904	0.211075	0.12850428 1_at	ıt	11, band p13 (and joined CDS)
803	802 Leukemia	0.9310812	0.253555	0.211001	0.12842086 Z15115 at	3115 at	TOP2B Topoisomerase (DNA) II beta (180KU)
803	803 Leukemia	0.9309754	0.2534992	0.210981	0.12839296 U88726_at	3726_at	Symplekin mRNA, partial cds
		1		0.000	0.4000007E D67460	7460 of	EST: yi33b11.r1 Homo sapiens cuivA cione 1410z1 5. (iloni Genhank)
804	804 Leukemia	0.9309714	0.2534063	0.210918	0.12833273 R07400	7315 of	OBLIDATION FACTOR 2
805	805 Leukemia	0.9308714	0.2533648	0.210861	0.1282023 AU	1313 at	מסטברעון ווסמאס סיים ביים
					AF HU	AFFX- HUMGAPDH	
808	ROG I euskernia	0 9307855	0.2533316	0.210856	0.12820283 at-2	/////5519////_at-2	Glyceraldehyde-3-phosphate dehydrogenase
3	Logicalia	2000	1		AF	AFFX-	
					HO	HUMGAPDH	
807	807 Leukemia	0.9307855	0.2533222	0.210815	0.12815712 at		AFFX-HUMGAPDH/M33197_M_at (endogenous control)
					AF	AFFX-	
					H	HSAC07/X0	
808	808 Leukemia	0.9303823	0.2532826	0.210732	0.12813866 03	51 M at-2	0.12813866 0351 M at-2 No info for gene
}			1	_	AF	AFFX- HSAC07/X0	
συσ	800 Lenkemia	0 9303823	0.2532705	0.210646	0.12808098 0351 M_at	51 M at	AFFX-HSAC07/X00351 M at (endogenous control)
200	Louis	20000					Chorionic somatomammotropin CS-1 gene extracted from Human
		0.0008865	0.0530/03	0.210593	0 1280541	J03071_cds 3 f at	growth hormone (GH-1 and GH-2) and chorlonic somatomammotropin (CS-1, CS-2 and CS-5) genes
0	O I O FERNEI III	0.3530003	1			HG2415-	
811	811 Leukemia	0.929739	0.2532407	0.210573	0.12801737 HT2511	T2511_at	Transcription Factor E2t-2
0,40	olomoshio I c	0 9296195	0.253229	0.21052	0.12797187 X01715_at	01715_at	precursor (exons 1 and 2)
212	812 Leukerilla	-	1		1		

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					X9716	EIJ	TFE3 transcription factor gene extracted from H.sapiens TFE3 gene,
800	ejmodijo i 808	0 9227675	0.2520623	0 209269	0.12667598 1 at	: 	exons 1,2,3 (and joined CDS)
0000	eunellila	0.9221.818 0.2520628	0.2520438	0 209255	0.12659852 U73328	at	DLX7 Distal-less homeobox 7
038	039 Leukellila	0.9221312 0.232310	0.2520.00	0.209225	0.12652707 X68486	at	ADENOSINE A2A RECEPTOR
040	040 Leuneillia	0.3220210	0.60606		RC	1315	
841	84411 eukemia	0.9221103	0.2520043	0.20922	0.12648968 02_at		Homo sapiens lok mRNA for protein kinase, complete cds
8421	842 Leukemia	0.921907		0.209099	0.1264545 D11086 at		IL2RG Interleukin 2 receptor gamma chain
0.12	CONCELLIC	20.0				X80763_s_a	
843 L	843 Leukemia	0.921872	0.2518983	0.209092	0.12641974 t		HTR2C 5-hydroxytryptamine (serotonin) receptor 2C
844	844 Leukemia	0.9214814		0.209065	0.12634583 D79993_at		KIAA0171 gene
845	845 Leukemia	0 9213948	0.2517596	0.209003	0.12629886 M99439_at		Transducin-like enhancer protein (1LE4) mKNA, 3 end
846	846 Leukamia	0 9212307	0.251704	0.208911	0.12628059 J03930 at		ALKALINE PHOSPHATASE, INTESTINAL PRECURSOR
040	COUNCILIE	0.02.1200					Putative envelope protein; orf similar to env of Type A and Type B
							retroviruses and to class II HERVs gene extracted from Human
					90	30269 cds	1160269 cds endogenous retrovirus HERV-K(HML6) proviral clone HML6.17
847	847 I pukamia	0 9205834	0.2516705	0.20886	0.12626049 3 at	at	putative polymerase and envelope genes, partial cds, and 3'LTR
1	CONCING	0.000			9X	X68985 s a	
848	848 leukemia	0.9205387	0.2516325	0.208859	0.12620391 t		HLF Hepatic leukemia factor
849	849 Leukemia	0.9201732	1	L	0.12618372 U13395	13395_at	Oxidoreductase (HHCMA56) mRNA
						X98178_s_a	
850	850 Leukemia	0.9199151	0.9199151 0.2515667	0.208515	0.126131711		MACH-beta-4 protein
851	851 Leukemia	0.9197949	0.9197949 0.2514162		0.12609671 X80230	äţ	mRNA (clone C-2k) mknA for serine/intercent close in chicase
852	Leukemia	0.9192909	0.9192909 0.2514091	0.208476	0.1260078 U07802	07802_at	ERF-2 mKNA
					主	HG4312-	
					工	HT4582_s_a	
853	853 Leukemia	0.9192454	0.251401	0.208428	0.12593469 t		Transcription Factor liia
3							ATP50 ATP synthase, H+ transporting, mitochondrial F1 complex, U
854	854 Leukemia	0.9189531	0.251372		0.12589332 X83218	83218 at	subunit (oligomycin sensitivity conferring protein)
855	855 Leukemia	0.9188577	0.2513019		0.12582584 U47742 at	47742 at	Monocytic leukaemia zinc finger protein (MOZ) innwa
856	856 Leukemia	0.9187594	1 0.251271	0.208303	0.1257509 X61970_at	61970_at	PROTEASOME ZETA CHAIN
						U54644_s_a	
857	857 Leukemia	0.9183492					UB Tubby (mouse) nomolog
858	858 Leukemia	0.9181675	5 0.2510666	0.208235			ZNF177 KRAB zinc finger protein (alternative products)
859	859 Leukemia	0.9181058	0.9181059 0.2510518	I		151478 at	Sodium/potassium-transporting A l Pase Deta-5 Subunit IIII NA
860	860 Leukemia	0.917455	5 0.2510499			70219 at	5'UTR for unknown protein (clone ICRr pour Cueso)
961	laıkemia	0.9174279	9 0.2510319	0.208161	0.12551421	(96401_at	
8						AA010933_s	
862	862 Leukemia	0.9173979	9 0.2510196	3 0.208133	0.12549268	at	clone 359800 5', mKNA sequence. (Iloili Gelibalik)
		10010	0.0500508	0.008418	0 12541647	X14085_s_a +	GGTB2 Glycoprotein-4-beta-galactosyltransferase 2
863	863 Leukemia	0.910073					

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864 Leukemia				0.208108	0.1253755 D50930_at	KIAA0140 gene
865 Leukemia	-	0.9162563		0.208106	0.1252812 100091 s	ਰ
866 Leukemia	-+		0.2509249	0.2000.10		\top
867 Leukemia	+	0.9139024	0.2309100	0.201012	0.12511995 M34079 at	T
808 Leukernia	+	0.9130040	0.2508367	0.207837	0.12508899 D50924 at	
869 Leukernia	+	0.9153140 0.2505192		0 207802	0.12504318 U73824 at	P97 mRNA
ovo ren	+	0.9151601			M37984 rna	+
871 Fukemia	kemia	0.9148254	0.250789	0.207763	0.1250134 1_at	
872 Leukemia	kemia	0.9141761	0.2507533	0.207757	0.1249382 D21235_at	
873 Leukemia	kemia	0.9140734	1	0.207751	0.12490247 L12535 at	-
010	NGII II G	200	1		The state of the s	EST: zn84h08.r1 Stratagene lung carcinoma 937218 Homo sapieris
					AA129373_a	
874 Leukemia	kemia	0.9134827	0.2506689	0.207702	0.12485853 t	RADIXIN.;, mKNA sequence. (Iroin Gendann)
					U43753_cds	
875 Leukemia	Ikemia	0.9133811		0.207652		
876 l eukemia	kemia	0.9125423	0.2506206	0.207602	0.12473374 U01877 at	
877 I eukemia	kemia	0.9123278		0.207582	0.12465767 U94585 at	
878 eukemia	kemia	0.9120681		0.207578	0.124619 M73047	at TPP2 Tripeptidyl peptidase II
	2					GCK Glucokinase (hexokinase 4, maturity onset diabetes of the young
879 l eukemia	ıkemia	0.9120664	0.250536	0.207563	0.12460999 M90299	at 2)
880 Loukemia	kemia	0.9119291	10	0.20754	0.12460559 D83779_a	at KIAA0195 gene
884 Purkemia	Kemia	0 9117222	-1	0.207429	0.124566995 D86964_at	
2 200	cieros.	0.011687/	-	0.207429	0.12445831 X78924 8	at HZF1 mRNA for zinc finger protein
862 Leukeilila	JKeilila	0.311001.4	Щ.	211111111111111111111111111111111111111		GNA15 Guanine nucleotide binding protein (G protein), alpha 15 (Gq
883 Laukemia	ikemia	0.9115527	0.2503907	0.207416	0.1244223 M63904_at	
ood Louisonia	oi modi	0.0444603		0 207415	0.12435378 X14675	at Bcr-abl mRNA 5' fragment (clone 3c)
885 P	885 Leukennia	0.9108548		0.207395	0.12433449 U44975 at	
886 8	886 Leukemia	0.9105541		0.207306	0.1242954 U52426_at	
				1	AA194091	1_a [EST; zr37a11.r1 Soares NhHMPu S1 Homo saptens culve close
887 Le	887 Leukemia	0.9103949	9 0.2503051	0.207298	0.1242209351	Retinoblastoma susceptibility protein (RB1) L486W 4 bp deletion
						mutant (resulting in premature stop at amino acid 490) gene, exon 16
888	888 Leukemia	0.9100632	0.250275	0.207249	0	at
889 Le	889 Leukemia	0.909886	3 0.2502447	0.20723	0.12411578 U09414	at ZNF137 Zinc finger protein 137 (clone priz-50)
					M60284_s	σ,
890 Le	890 Leukemia	0.9090841	1			Neurokinin A receptor (NK-ZK) gene, exon 3
891 Le	891 Leukemia	0.9090649	- 1		0.1239694 064444	
892 Le	892 Leukemia	0.908672	2 0.2501059	0.20708	0.12393310 103443	

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Commo Amindonish daid A Lin A Lin A Commo	EST: EST65883 Jurkat T-cells I Homo sapiens cDNA 3' end similar to arrestin heta 2 mRNA sequence (from Carbart).	Clone 23947 mRNA, partial cds	AKT1 V-akt murine thymoma viral oncodene homolog 1	mRNA sequence (15a11-13)	Zinc-finger protein mRNA	Anti-mullerian hormone tyne II recentor precinsor gons	alled negretary beauty and feller	Olfactory Receptor Or17-209	MYO5A Myosin VA (heavy nolymentide 12 myoyin)	Chloride channel (putative) 2163hn			Human noty(A)-hinding production processed as a second processed a	Genbank)	ZNF37A Zinc finger protein 37a (KOX 21)	Dra Dolymorphy Carles C	ARF1 ADP-ribosylation factor 1	(clones lambda-hPKC-beta[15,802]) protein kinase C-beta-1	HCF1 gene related mRNA secritarios		0.1230509 M29960 at RIAAUZU3 gene	CIC-1 muscle chloride channel protein	at Major Histocompatibility Complex, Class I, E (Gb:M21533)		at Small Nuclear Ribonucleoprotein U1, 1snrp	GRIKS Glitamata racentor ignotrosis List F	Lactate dehydrogenase B gene exon 1 and 2 (EC 1.1.1.27) (and	Jonieu CD3) P40phox
HG3255- 0 12394436 HT3432 at		0.12383939 U79275 at	0.12380146 M63167 at	0.123785995 X69636 at	0.123669334 U18543 at	0.123598896 U29700 at	HG4114-	0.12358783 HT4384 at	0.12356066 L19401 at	0.12348593 Z30644 at	HG3725-	H13981_s_a 01 t	U64661 ma	98 1, f at.	0.12330822 X69115_at	HG919- 0.12328922/HT919_at	0.12322194 M84332 at	0.12319439 X07109 at	0.123168916 L20010 at	20707	0.1230509 M29960 at		HG2917- 0.12296216 HT3061 f at	HG4557-	0 12292500 1114902 1 at	a te	94 rna	94 at
	0											0 12342701		0.12340398	0.123308	0.123289	0.123221	0.123194	0.1231689	0 100101	0.12305	0.1230025	0.122962	0 1000306	0.122939	0.12286	0.122841224 1 at	0.1228223
0.20701	0.20			- 1		0.206832				0.206775	-	0.206745		0.206739	0.206667	0.206647	0.206585	0.206558	0.206507	0.206446	0.206425	0.206387	0.206373	0.206358	0.206338	0.206245	0.206211	0.206191
0.2500552			-	- 1		0.2496952				0.2496363		0.2495985	1		0.2493704	0.2492801	0.2491589	0.2491176	0.2491112	0.2490465		0.2490419	0.2490404	0.2490275	0.2490068	0.2488888	0.2488687	0.2487737
0.9085007	0.9083749	0.9083691	0.9078417	0.9070624	0.9066877	0.9066489		0.9065944	0.9064214	0.9062026	,	0.9059651		0.9058428	0.905811	0.9051306	0.9046862	0.9045205	0.9044616	0.9044505	0.9040746	0.904036	0.9039833	0.9039499	1	0.9030672	0.9026195	0.9026141
893 Leukemia	894 Leukemia	895 Leukemia	896 Leukemia	897 Leukemia	898 Leukemia	889 Leukemia	-	900 Leukemia	901 Leukemia	902 Leukemia		903 Leukemia		904 Leukemia	ano renkemia	906 Leukemia	907 Leukemia	908 Leukemia	909 Leukemia	910 Leukemia	911 Leukemia	912 Leukemia	913 Leukemia	914 Leukemia	 	916 Leukemia		918 Leukemia

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919 Leukemia 920 Leukemia 922 Leukemia 922 Leukemia 924 Leukemia 925 Leukemia 925 Leukemia 926 Leukemia 929 Leukemia 930 Leukemia 931 Leukemia 933 Leukemia 935 Leukemia 935 Leukemia 935 Leukemia 936 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia 937 Leukemia	-	0.9024774 0.2487323 0.206089 0.122652991L06505 at	0.9020752 0.248686	0.9011635 0.2486772	0.9011166 0.2486669 0.206008 0.12254101 Y07683 at	X15393_rna	0.9010781 0.2486655 0.205984	ia 0.9008008 0.2486445 0.205957 0.12245452 M81829 at Somatostatin receptor isoform 1 gene	nia 0.9003726 0.2486363 0.20594 0.122392185 K02574 at NP Nucleoside phosphorylase	HG243-	0.9003377 0.2486186 0.205879 0.122306354 HT243_s_at	EST: aa22d08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	AA455706_a IMAGE:813999 5' similar to TR:G473407 G473407 NST-1.;; mRNA	0.9002245 0.2485976 0.205863 0.12226481	0.899919 0.2485244 0.205821 0.1222 U49395 at	nia 0.8998531 0.2485087 0.205794 0.12218475 W27182 at sapiens cDNA, mRNA sequence. (from Genbank)	nia 0.8995121 0.2484315 0.205736 0.12217356 X92098 at Transmembrane protein rnp24	nia 0.8986859 0.2484161 0.205624 0.12210798 U01212 at Olfactory marker protein (OMP) gene	EST: zs26b03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone RC_AA2628 IMAGE:686285 3' similar to contains Alu repetitive element, contains o.8986375 0.2483782 0.205554 0.122053765 81_at element MIR repetitive element;, mRNA sequence. (from Genbank)	HG2915- HG2915- HG2915- HG2915- HG2915- HG2915- HG2915- HG2915- HG29178-270 0 2482400 0 206512 0 422025 1 4 Major Histocompatibility Compley Class 1 E (Gh-M20022)	0.897563 0.2483039 0.205479		RC AA2869 IMAGE:701489 3' similar to contains Alu repetitive element;, mRNA	0.8974713 0.2482811 0.20546 0.121927254 11 at	0.8973967 0.248277 0.20538 0.121908285 X92720 at	0.8972819 0.2482292 0.205257 0.12183682 U11090 at	nia 0.8972813 0.2481745 0.205205 0.121799651t Human transformer-2 alpha (htra-2 alpha) mRNA, complete cds	0.8956457 0.2481677 0.205203 0.12175766	
	2707000	0.902464	0.9020752	0.901163	0.901116	***************************************	0.901078	0.900800	0.9003726		0.900337.			0.900224	0.89991	0.899853	0.899512	0.898685	0.898637	0 807637	0.89756	2000		0.897471	0.897396	0.897281	0.897281	0.895645	To the state of th

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942	942 Leukemia	0.8952051	0.2481435	0.205145	RC_A 0.12165498 78 at	A2814	IEST: zs96f03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711485 3', mRNA sequence. (from Genbank)
9431	943 Leukemia	0.8950702	0.2480213	0.205083	0.12159608 D49738	9738_at	Cytoskeleton associated protein (CG22) mRNA
					_	AB003177_a	
944	944 Leukemia	0.8947564	- 1	0.205081	0.121546224 t		Proteasome subunit p27
945	945 Leukemia	0.8946782	0.2479715	0.205025	0.12150546 M96982	6982_at	SPLICING FACTOR U2AF 35 KD SUBUNIT
946	946 Leukemia	0.8945187	0.2479644	0.205015	0.12145257 U11791	1791_at	CCNH Cyclin H
							Mitochondrial serine hydroxymethyltransferase gene, nuclear encoded
947	947 Leukemia	0.8938792		0.204998	0.12140477 U23143	3143_at	mitochondrion protein
948	948 Leukemia	0.8938088		0.204938	0.12134344 D43949	3949_at	KIAA0082 gene, partial cds
949	949 Leukemia	0.8938009	0.2478486	0.204907	0.12130175 D38145	8145 at	Prostacyclin synthase
950	950 Leukemia	0.893652	0.247844	0.204864	0.12127993 U58032	8032 at	Myotubularin related protein 1 (MTMR1) mRNA, partial cds
951	951 Leukemia	0.8931956	0.2478319	0.204808	0.121241406 U83246	3246 at	Copine I mRNA
952	952 Leukemia	0.893191	0.2478187	0.204665	0.12119114 M63582 at	3582 at	THYROLIBERIN PRECURSOR
	- ~				90	U67932 s a	Communication and the second s
953	953 Leukemia	0.8930505	0.2478007	0.204653	0.12118194 t		CAMP phosphodiesterase mRNA, 3' end
					M3	M31520_rna	Unknown protein gene extracted from Human ribosomal protein S24
954	954 Leukemia	0.8924748	- 1	0.204621	0.121117234 1_8		mRNA
955	955 Leukemia	0.8924127	0.2474866	0.204548	0.12107544 U81802	1802_at	Phosphatidylinositol 4-kinase
926	956 Leukemia	0.8923035	0.2474573	0.204532	0.12104357 M55150 at	5150 at	FAH Fumarylacetoacetate
957	957 Leukemia	0.8922968	0.2474407	0.204504	0.12102167 X53793	3793 at	MULTIFUNCTIONAL PROTEIN ADE2
958	958 Leukemia	0.8920471	0.247371	0.204501	0.12096786 U58334	8334 at	Bcl2, p53 binding protein Bbp/53BP2 (BBP/53BP2) mRNA
1656	959 Leukemia	0.8917607	0.2473075	0.204473	0.12094204 U09607	9607 at	JAK3 Janus kinase 3 (a protein tyrosine kinase. leukocyte)
					AA	97 a	EST: csq3770.seq.F Human fetal heart. Lambda ZAP Express Homo
1096	960 Leukemia	0.891744	0.2472879	0.204473	0.120924175 t		sapiens cDNA 5', mRNA sequence. (from Genbank)
961	961 Leukemia	0.8912273	0.2471743	0.204416	0.12086799 D26599	6599 at	Proteasome subunit HsC7-I
							EST: yq23c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone
1000	11000	*000000	7	0000			274547 5' similar to SP:A44264 A44264 ALL-1=TRITHORAX
706	30Z Leukernia	0.6908304	0.247164	0.204407	0.1207982 R84329	4329 at	HOMOLOG - HUMAN;, mRNA sequence. (from Genbank)
C	1	7	11	1	AB	AB002559_a	
303	903 Leukernia	0.8904554	0.247153	0.204351	0.120/338651		Hunc18b2
964 [964 Leukemia	0.8899966	0.2470384	0.204282	0.12068681 L37033	7033_at	FK-506 binding protein homologue (FKBP38) mRNA
965	065 e Ikemia	0.8800022	0.2470349	0.004067	U82	U82275_s_a	Homo sapiens leucocyte immunoglobulin-like receptor-7 (LIR-7)
200	- Cancilla	0.0000000	0.247.0515	0.204237	0.1200410111		mrivA, complete cas
1996	966 Leukemia	0.8898465	0.2470211	0.204217	0.12061267 X56468	at	14-3-3 PROTEIN TAU
1/96	967 Leukemia	0.8897659	0.2469349	0.204202	0.12057196 U09367	<u>a</u>	ZNF136 Zinc finger protein 136 (clone pHZ-20)
1896	968 Leukemia	0.8896914	0.246884	0.204057	0.12051495 D00762	at	PROTEASOME COMPONENT C8
1 696	969 Leukemia	0.8895212	0.2468418	0.204041	0.1204946 D85376	at	TRHR Thyrotropin-releasing hormone receptor
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D13720_s_a TYROSINE-PROTEIN KINASE ITK/TSK	0.12043469 M94880_f_at HLA-A MHC class I protein HLA-A (HLA-A28,-B40, -Cw3)	0.12039278 U02632_at Calcium-activated potassium channel mRNA, partial cds	0.120345 M34667_at PLCG1 Phospholipase C, gamma 1 (formerly subtype 148)		A4653	sat		0.120152734 HT2811_at Tyrosine Kinase (Gb:Z25437)	0.12012257 M60750 f at Histone H2B.1 (H2B) gene	0.12006155 X69433 at IDH2 Isocitrate dehydrogenase 2 (NADP+), mitochondrial	0.12003669 U73379 at Cyclin-selective ubiquitin carrier protein mRNA	0.11999413 X70040_at MST1R Protein-tyrosine kinase RON	 , AA4787		0.11987577 U59878_at Low-Mr GTP-binding protein (RAB32) mRNA, partial cds	M14328_s_a M14328_s_a ENO1 Enolase 1. (alpha)	RC_AA4364	0.11981014 73_s_at 753062 3', mRNA sequence. (from Genbank)	/15465_s_a		14 X89267_at UROD Uroporphyrinogen decarboxylase	0.11970311 Z35102_at Ndr protein kinase	0.11967517 L35035_at Ribose 5-phosphate isomerase (RPI) mRNA	0.1196234 S54005 s at THYMOSIN BETA-10	0.11962046 U44839 at Putative ubiquitin C-ferminal hydrolase (LIHX1) mRNA	at		äŧ	0.119402386 Y08612_at RABAPTIN-5 protein
0.120472044 t		0.120392	0.1203	0.120318	0.12025077 42 at	0	1	1	0.120122	0.120061	0.120036				0.119875	0.11983562	No. Allegan	0.119810		0.11976837 t	0.119759604 X89267	0.119703	0.119675	0.11962;	0.119620	0.119576	0.1195082	0.119458	0.11940238
0.203998	0.203982	0.20398	0.203948	0.203894	0.203789	0.203749	0.203659	0.203648	0.203593	0.203545	0.203503	0.2035	- !	0.203456	0.203434	0.203419		0.203318		0.203298	0.203272	0.2032	0.203158	. 0,203149	0.203117	0.203058	0.203051	0.202959	0.202943
0.2467485	0.2466843	1 1	- 1	0.2465504	0.2465305	0.2465275	0.2465051	0.2464889	0.2464766	0.2464487	0.2464101	0.2462968	6	0.2461633	0.2460937	0.24607		0.2460543		0.2460309	0.2460168	0.2460154	0.2459939	0.2459908	0.2459807	0.2459711	0.2459466	0.245915	0.2459047
0,8883051	0.887951	0.8871638	0.8865705	0.8857626	0.8853456	0.8847793	0.8847271	0.8843932	0.8842357	0.8840365	0.8836122	0.8835117		0.8833022	0.8822857	0.8821642		0.8820331		0.8820094	0.8817014	0.8817	0.8812661	0.8810147	0.8809319	0.8808945	0.8808035	0.8806957	0.8805698
970 Leukemia	971 Leukemia	972 Leukemia	973 Leukemia	974 Leukemia	975 Leukemia	976 Leukemia	977 Leukemia	978 Leukemia	979 Leukemia	980 Leukemia	981 Leukemia	982 Leukemia		983 Leukemia	984 Leukemia	985 Leukemia	The state of the s	986 Leukemia		987 Leukemia	988 Leukemia	989 Leukemia	990 Leukemia	991 Leukemia	992 Leukemia	993 Leukemia	994 Leukemia	995 Leukemia	996 Leukemia
970	971	972	973	974	975	976	977	978	979	980	981	982	 Ç	202	384	985		986	1	786	288	686	066	991	992	993	994	995	986

gene gene gener ge

notonin 18 recentor		0 8800616 0.2458545 0.202911 0.11930436 M69039 at PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT PRECURSOR	AA247450 a EST: csg2873.seq.F Human tetal neart, Lambda ZAP Express norm	sapiens cDNA 5', mRNA sequence. (from Genbank)		1000 Leukemia 0.879577 0.2457878 0.202777 0.119230516 HT945 s. at Nucleic Acid-Binding Protein (Gb:L12693)
10202020101000K at 15	997] Leukemia 0.8804677 0.2458731 0.202834 0.11838382 0.10833 0.	1930436 M69039_at P	AA247450 a E	9274154 t	HG945-	9230516 HT945 s_at N
A COCOCO	0.202934 0.1	0.202911 0.1		0.879728 0.2457946 0.202783 0.1192741541		0.202777 0.1
10000100	0.2458731	0.2458545		0.2457946		0.2457878
10000	0.88046//	0.8800616		0.879728		0.879577
	Leukemia	l eukemia		ogo l erikemia	Convolution	Leukemia
	997	900	3	000	3	1000

FIG. 5M2

12

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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				Me man Me	38519 mar	17. 14.01 " M68519 May "teen " and and and the first that
11.000	0.9519866	0.716035	0.623983	0.46932647 1 8	at	Pulmonary surfactant-associated protein SP-A (SFTP1) gene
2		1				SP-C1 gene (pulmonary surfactant protein SP-C) extracted from
			-	700	3890_rna1	J03890_ma1 Human pulmonary surfactant protein C (SP-C) and pulmonary
2 1 1100	0.7843286	0.6722338	0.575029	0.43865538 at		surfactant protein C1 (SP-C1) genes
2	201010			-		PULMONARY SURFACTANT-ASSOCIATED PROTEIN B
31 und	0.7770512	0.7770512 0.6453148	0.555386	0.42221874 M24461_at		PRECURSOR
2						PULMONARY SURFACTANT-ASSOCIATED PROTEIN A
411100	0.70441	0.6270386	0.543154	0.41103396 M30838 at		PRECURSOR
P. C.				RC	-	EST: aa74c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
51110	0.5994884	0.6157392	0.534078	0.4015687 95 at		IMAGE:826656 3', mRNA sequence. (from Genbank)
2						EST: HFBEST-56 Human fetal brain QBoqin2 Homo sapiens cDNA,
9	0.5743588	0.5743588 0.6103535	0.526218	0,39522386 W36279 at	36279 at	mRNA sequence. (from Genbank)
S. S.				RC	C AA4602	RC_AA4602 EST: zx67d07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
7 Trund	0.5524321	0.5524321 0.6019864	0.521174	0.38843518 57_at	_at	clone 796525 3', mRNA sequence. (from Genbank)
00118	0.5518032	0.5969788	0.515836	0.38385049 M34516 at		Omega light chain protein 14.1 (lg lambda chain related) gene, exon 3
0						
9 Luna	0.5428825	0.5915497	0.510164	0.37928408 M:	34516 r_at	0.37928408 M34516 r at Omega light chain protein 14.1 (Ig lambda chain related) gene, exon 3
0						EST: ab17g09.s1 Stratagene lung (#937210) Homo sapiens cDNA
				X	C_AA4868	RC_AA4868 clone 841120 3' similar to contains LTR7.b2 L1 R7 repetitive element
10 Lung	0.5341072	0.5888677	0.506043	0.3755257 90_t_at	J r at	", mkna sequence, (nom cenbank)
				S.	71043 ma	S71043 ma Ig alpha 2≕immunoglobulin A heavy chain allotype 2 {constant region,
1111 mg	0.5240091	0.5847114	0.501227	0.37162906 1 s at	s at	germ line} [human, peripheral blood neutrophils, Genomic, 1799 nt]
6.151				Ř	RC_D60670	
12 Lung	0,4905479	0.5814767	0.499201	0.36866218	at	
13 Ling	0.4863556	0.5791841	0.495004	0.36580577 V00563_at	00563_at	Immunoglobulin mu, part of exon 8
		١		A	AA197134_a	
14 Lung	0.4858377	7 0.5730248	0.492127	0.362679031		clone 629373 5', mRNA sequence. (from Genbank)
				2	187789 s.a	M87789_s_a (hybridoma H210) anti-hepatitis A IgG variable region, constant
15 Lung	0.4805647	0.4805647 0.5705465	0.489537	0.3595831 t		region, complementarity-determining regions mRNA
The state of the s						

FIG. 6A

ent, pros, pros, pros, pros, entre pros, entre pros, entre pros, entre pros, entre pros, entre pros, etc., entre pros, etc., entre pros, etc., entre pros, etc., entre pros, etc., entre pros, etc., entre pros, etc., entre pros, etc., entre pros, e

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

A 4 100 7	Non-specific cross reacting antigen	XUZ419_IIIB 1 s at UPA gene	at	s at-2 Glucokinase (hexokinase 4) regulatory protein	Superior Avier S S1 Homo sapiens	RC_AA0102 EST: zi08f07.s1 Soares fetal liver spieer in the Source community at a connect of the spiece connection of the	U43203_s_a	t TIF1 franschpublitetimiquon town y tumor NbHOT Homo sapiens cDNA		AA470056_a [EST: zt94g06.r1 Soares testis INTL Hollio sapicitis common AA470056_a [EST: zt94g06.r1 Soares (from Genhank)	t 730042.5, mKNA sequence, mon conserva-	Homo sapiens mRNA for KIAA0758 protein, partial cds	22 at 668699 3', mRNA sequence. (from Genbank) ICAM1 Intercellular adhesion molecule 1 (CD54), human rhinovirus	at	, 7		a, a	Ū	53 at Inwardly rectifying potassium chariful and sapiens cDNA	RC_AA0558 ES I: zfzucto.s I soules real notation Genbank) 41 at clone 377486 3', mRNA sequence. (from Genbank)	M63438_s_a GLUL Glutamate-ammonia ligase (glutamine synthase)	224 at Homo sapiens Chromosome 16 BAC civille Cli 301 Clivillo	s a	EST: zq39h04.s1 Stratagene film Heulon (#351, zd3) House care	RC_AA1668 element;contains element MSR1 repetitive element ;, mRNA	st sequence, (from Genbank)	
CO. Marin state	0.486864 0.3572573 19_s_at	0.35/6987			100000	0 34818494	0.47.79.0	0.476154 0.34659567 t	0.34489632		0.472729 0.3429253	0.470869 0.34167662 43 at	0.46862 0.34006745 22_at	0.467713 0.33858126 M24283		0.46604 0.336/2//4/11/2002	0.464088 0.33499742 W69970	0.462975 0.333811	0.461234 0.3323383 U52153 at	0.460066 0.33100665 41	0.32952955 t	_				0.455358 0.32613403 38 at	0.453866 0.3251219
	0.5673447 0.48			0.505507	0.5620012		0.5588/28	0.5572204	0 5546945	0.00400.0	0.5527822	0.550931	0.5500904	0.54962		0.5486178	0.5476252	0 5470738	0.5458446	0 5446066	0 543770	0.343772	0.53775			0.5359457	0.5346007
	0.4702581		0.4672205	0.4516379	0.4516379		0.4462894	0.4449928	0.4406042	0.4400042	0.4359149	0.4341773	0.4233249	0 7077940	10.1424	0.4223579	0,4220618	0.4046633	0.4210000			0.4199409					0.4124332
	161 100	Single Control of the	17 Lung	18 Lung	19 Lung		20 Lung	21 Lund		22 Lung	23 Lung	24 Lung	25 Lund		Se Lung	27 Lung	28 Lung		29 Lung	30 Luig	3.1 Lung	32 Lung	33 Lung	34 Lung		35 Lung	36 Lung

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

3.5	0.32375416 U78735 at ABC3 A IT-unange and part of delta (guanine nucleotide Eukaryotic translation elongation factor 1 delta (guanine nucleotide	0.3226801 R29657 at exchange protein) AA249437 a EST: j3966.seq.F Human fetal heart, Lambda ZAP Express Homo	0.3217235 t sapiens cDNA 5, mRNA sequence. (1.27) HG2809-	a a	0.31965977 R53717 at Genbank) RC AA4417 EST: zw62c02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA RC AA4417 EST: zw62c02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	0.3186317791 at clone 774626 3', mixty sequence (1.3186317791 at EST: zv39e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	 0.31748506 t Genbank) EST: 43f5 Human retina cDNA randomly primed sublibrary Homo		M10014_cds M10014_cds	11499106 1 at Fibrinogen gamma chain altu yanının pina Elibrinogen gamma chain altu yanının pina (2007) Homo	AA075427_a EST: zm87a05.r1 Stratagene ovarian cancer (#53.12.13) romans AA075427_a conjane cDNA clone 544880 5', mRNA sequence. (from Garage)	31411502/t M29874 s_a CYP2B6 Cytochrome P450, subfamily IIB (phenobarbital-inducione).	0.31338766 t polypeptide 6	M20778 s.a Homo sapien, alpha-3 (VI) collagen	111313 s a	0.31187356 t AZM Apna-2-111au 09000mm- AA447811_a	0.3109486 t Regulator of G-protein signaling to	0.31013918 t Sex hormone-binding globulin Sex hormone-binding globulin Apple 18 to 1	0.30944195 t AA329542 a EST: EST33182 Embryo, 12 week II Homo sapiens cDNA 5' end,	101	0.3073002 X80062 at SA IIINWA
Transfer of the second	0,452733 0.3	0.451402 0.	0.449812 0.	0.449059 0.3	0.448258 0.3	0.447251 0.	 0.44688 0		0.44540/	0.444204		0.443824 (0.443207		0,441875	0.441396	0.440206	0.439549	0.43922	0.438483	1 1
	13	0.5316177 0.	0.5313253 0.	0.529942 0	0.5297486 0	0.5291454	 0.5283682	0.5267935	0.5267584	0.5253698		0.5251259	0 524534	0.0	0.5232443	0.5219135	0.5215501	3 0.5213429	3 0.5211844	5 0.5204216	3 0.5187517
	0.4114828 0.53234	0,4040549 0.	0,4038739 0.	0.3929638	0.3905684 0	0.3883479 0	0.3872517		0.38344	0,3819989		0.381848	0 0704047	0.3/3/2/1	0.3786208	0.3782215	0.3763703	0.375766	0.3726443	0.3725365	0.3704493
	37 Lung 0.					42 Lung	431 una	44 IING	45 Lung	78 I IIDG	S. D. D.	47 Lung		48 Lung	49 Lung	50 Lung	5411 upd	50 Lung	53 Lund	54 Lung	55 Lung 56 Lung

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

57 Lung	0.3685979	0.5173218	0 436855	D 30647877 t	D10216_s_a	POU domain, class 1, transcription factor 1 (Pit1, growth hormone
58 Lung	0.3647298	1	0	0.30571705 M93221	193221 at	M6PR Mannose recentor
						EST: zk97d12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490775 5' similar to db:L32179 Human arvlacetamide
59 Lung	0.3634779	0.5160826	0.434849	0.30507278 t	AA122302_a	deacetylase mRNA, complete cds. (HUMAN);, mRNA sequence. (from Genbank)
				₩ ₩	A206236 a	Zq54c06.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 645418 5' similar to TR:G1229022 G1229022 AA206236 a Al 1 OGRAFT INEL AMMATORY EACTOR 1 : TROMA CONTROL 1 : TROMA CONTROL 2 : TROMA CONTROL 3 : TROMA CONTRO
60 Lung	0.3618056	0.5157224	0.434509	0.30417424 t		(from Genbank)
61 Lung	0.3602638	0.5155481	0.433437	0.30350277 t	AA419502_a t	
62 Lung	0.3599641	0.5151172	0.432445	0.30296737 D82675 at		EST: similar to none, mRNA sequence, (from Genhank)
63 Lung	0.3595377	0.5140513	0.43226	X 0.30227515t	X81832_s_a t	GIPR Gastric inhibitory polypeptide receptor
64 Lung	0.3595038	0.513129	0.431413	RC_A 0.3017711317_at	A0106	EST: zi09f12.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
65 Lung	0.3559342	0.5122271	0.430571	0.30128786 U01102	at	UGB Ulerodobin
66 Lung	0.3551648	0.5118072	0.429952	0.3006298 L38025_at	at	CNTFR Ciliary neurotrophic factor receptor
67 Lung	0.3545549	0.3545549 0.5115729	0.429614	0.3000475	09858 at-2	0.3000475 Y09858 at-2 H.sapjens mRNA for unknown protein (from Conhant)
68 Lung	0.3545549	0.3545549 0.5113397	0.429585	0.2995665 Y09858 at	09858 at	Unknown profein
69 Lung	0.3529823	0.3529823 0.5100895	0.429083	0.2991551 X	98330 at-2	0.2991551 X98330 at-2 Ryanodine recentor 2 (cardiac)
70 Lung	0.3529823	0.3529823 0.5099303	0.428567	0.29860464 X98330 at	i	RYR2 Ryanodine recentor 2 (cardiac)
71 Lung	0.3496571		0.428254	0.29803205 U21128 at		LUM Lumican
72 Lung	0.3483737	0.5089282	0.427949	0.2975029 X87159_at	1	Beta subunit of epithelial amiloride-sensitive sodium channel
73 Lung	0.3478406	0.5087081	0.427465	RC_A 0.29693455 12_at	A4781	EST: zt89e03.s1 Soares testis NHT Homo sapiens cDNA clone 729532 3', mRNA sequence. (from Genhank)
74 Lung	0.347209	0.5081029	0.426163	0.29632545 t	AB002328_a t	Human mRNA for KIAA0330 gene, partial cds. (from Genhank)
75 Lung	0.3460515	0.5066884	0.425931	Hi H: 0.29575261	HG3242- HT4231_s_a	Calcium Channel Voltage Catad Alaka 45 Cata at 10 Cata
76 Lung	0.3454287	0.506658	0.425813	0.29526493 D17793	at	DDH1 Dihydrodiol dehydronenase
77 Lung	0.3416797		0.425146	0.294682 U17077 at	ä	BENE mRNA, partial cds
78 Lung	0.3394485	0.5054468	0.425012	0.29430637 W16804 at	1	NCK adaptor protein 1
79 Lung	0.3377888	0.3377888 0.5051784	0.423829	A/ 0.29379308 t	AA046840_a t	CCAAT/enhancer binding protein (C/EBP). delta

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80 Lung

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5C5 mRNA, putative complete cds	0.2927943 U25041 at-2 Ribosomal profein mitochondrial 112	ADH7 Alcohol dehydrogenase 7 signa suhimit (class IV)	EST: zv11b06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	EST: aa19f07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	013/33 3, MKIVA sequence. (from Genbank)	CAMERI Chemokine (C.C.) recentor 1		Osteoblast specific factor 2 (OSF-2os)	AB000221_a Small inducible cytokine subfamily A (Cys-Cys), member 18,	Monorary and activation-regulated	Ribosomal protein S29	EST: zd37c12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 342838 5', mRNA sequence. (from Genbank)	EST: zx46a12.s1 Soares testis NHT Homo sapiens cDNA clone	EST: zx63h02.r1 Soques total fetus Nb2HF8 9w Homo sapiens cDNA	Mitochondrial 1 25-dihydroxyydramin D3 24 hydroxydae mbNA	אייים של איים	EST: zi04g05.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429848 3. mRNA sequence (from Genhank)	1000	RC_AA0555 EST: zf21f02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 377595 3', mRNA sequence. (from Genbank)	Paraoxonase 3 (PON3) mRNA, 3' end of cds	Proline-rich Gla (G-carboxdutamic acid) nolynentide 2	EST: zs95h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:/052793, mRNA sequence. (from Genbank)	EST: zr57e11.r1 Soares NhHMPu S1 Homo sapiens cDNA cione	EST: Human HL60 3'directed Mbol cDNA, HUMGS01869, clone	Inpudou, IIIININA Sequence. (IIOIII Genbank)
0.29332182 U25041_at	U25041 at-2	X76342 at	AA411756_a		109708 at	0.29039747 D10925 at	D13666_s_a	0.28965738 U43944 at	AB000221_a	0.2030430 t	W73544 at	and a second	W67675 at	RC_AA4539 97_at	AA461426 r	L13286 at		A0098	AA479826_a t	RC_AA0555	60 <u>r</u> at	L48516_at	RC_AA4305 52_at	_AA2806	at	WZZ/621_a	RC_D20888	5
0.29332182	0.2927943	0.29232162 X76342	0.291763751	0 20132702 04	0.29098588109708	0.29039747	Crosses of	0.28965738	A 200000 0	0.2030436	0.28807667 W73544		0.28//18/4 W6/6/5	0.2874054 97	78704917	0.2865247 L13286	The state of the s	0.28622055 09_at	0.28579881		0.28523868 60 r at	0.28482866 L48516	0.28458977	OCKORROOO	0.2841813387	0.2838734	0.28347975	
0.423658	0.423195	0.42275	0.422723	0.42207	0.421176	0.420608	07 7007 0	0.419688	0.440674	0.419325	0.419012	0.77	0.418708	0.418117	0.417838	0.417477		0.416854	0.416236		0.416063	0.41583	0.415777	744	0.41480	0.414412	0.414252	
0.337722 0.5046392	0.5041449	0,5037944	0.5035952	0.5032396		0.3308455 0.5016013	0.5000428	0.5008838	0.5007274		0.5006619	100100	0.489504	0.4990037	0.4987492	0.4984739		0.4976095	0.4973751		0.4964509	0.4959161	0.4948879	0.4025004	0.48330001	0.4923228	0.4920196	
0.337722	0.337722	0.3370443	0.3366936	0.3350614	0.3310624	0.3308455	0 329923	0.3295958	0.3281576	0.3276698	0.3271097	0 2045004	0.3243924	0.323945	0.3238139			0.3228559	0.3203585			0.3191325	0.3189789	0.3487366		0.3185722	0.3164977	

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors pour pours pour grant mont est mont pour grant pour grant pour grant pour grant grant pour grant pour grant

			-	H. that that H. Bath that	Olono
				RC AA2561	EST: zr79a09.s1 Soares NhHMPu S1 Homo sapiens curva cione
	0.3163303	0 4917606	0.413722	0.28317362 53 i at	681880 3', mRNA sequence. (from Genbank)
104 Lung	0.3100300	0.4915778		at	RXRA Retinoid X receptor, alpha
105 Lung	0.3102/17	0.4913110	0.413415	at-2	Retinoid X receptor, alpha
106 Lung	0.3162///	0.3162/// 0.49123/3	0.1001.0	0.0000088 M50499 at	TISSUE FACTOR PATHWAY INHIBITOR PRECURSUR
107 Lung	0.3148296	0.4909871	0.413030	U.ZOZOZOGO WOOTO	RC. AA4914 EST: ab04a05.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
	0.0405484	0 4005869	0 412112	0.28164613 65 at	clone 839792 3', mRNA sequence. (from Genbank)
108 Lung	0.3133401	1	7117117	A4257	EST: zw47g09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cUINA
1001	0.3131494	0.4901651	0.411985		clone 773248 3', mRNA sequence. (from Genbank)
Ja Lui g	2	- 1		HG2614-	
11011	0.31157	0.4901148	0.411572	0.28100762 HT2710 at	Collagen, Type Viii, Alpha 1
n rain			The second secon	RC_AA1484	
111 Lung	0.3114629	0.4900665	0.411247	0.28065553 80_s_at	Flavin containing monooxygeriase 3
				RC_AA0400	EST: ZK46c06.ST Soares pregram access many close 485870 31 mRNA sequence, (from Genbank)
112 Lung	0.3111804	0.4891412	0.410739	0.28039536 62 s at	EST: 4128 Himan retina cDNA randomly primed sublibrary Homo
			0	20000000000000000000000000000000000000	capiens chNA mRNA sequence. (from Genbank)
113 Lung	0.3110718	9	0.409556	0.260U0497 W20035 av	At DH3 Aldehyde dehydrogenase 3
114 Lung	0.3106906	0.488937	0.408829	0.279466 13 M/ 4542 : at	
			0.400527	NO 27822872 96 r at	Ferritin, light polypeptide
115 Lung	0.3100885	0.4800/20		RC A46208	
	0.3409994	0 4885174	0.408111	0.27884746 89 at	1055586 3', mRNA sequence. (from Genbank)
n lo Luig	0.0102201			0.27860078 W25781 at	Homo sapiens clone 23698 mRNA sequence
11/ Lung	0.310103		_	RC AA0355	
	0.000	1 0 4977547	0.407374	0.2782199 14 at	
118 Lung	0.3093511			RC AA3473	
-	0.2000408	0.487529	0.407007	0.27806336 93 at	sequence. (from Genbank)
119 Lung	0.3030100	10	_	0.27772397 Y09267 at	Flavin-containing monooxygenase 2
1201 ung	0.000013	- 1		11	Canicular multispecific organic anion transporter
121 Lung	0.308141	0.4003400			EST: zw82c11.r1 Soares testis NHT Homo sapiens cDNA clone
				AA448101	AA448101 a 782708 5' similar to SW:A412_PLAFA P15847 41-2 PROTEIN
2011	0.3077937	7 0 486472	0.40635	0,27707386	ANTIGEN PRECURSOR: ,, mRNA sequence. (from Genbank)
122 Lung	0.3077347	0		0.27671063	LLGL mRNA
123 Lung	0.30/34/4			000110170	AA043894 a EST; zk57b05.r1 Soares pregnant uterus NbHPU Homo sapiens
	0.2072834	0 4856305	5 0 405303	0.27626926	cDNA clone 486897 5', mRNA sequence. (from Genbank)
124 Lung	0.307203		1		EST: 2s26b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
				RC AA2628	RC_AA2628 IMAGE:686303 3' similar to contains Alu repetitive element;, mKNA
1951 und	0.3069983	33 0.4848718	8 0.404571	0.27588493	sequence. (from Genbank)
Sin Car		70707	0.404178		Human RNA polymerase III subunit (RPC32) mRNA, complete cds
126/Luna	0.306675	0.3066799 0.4848718		1	1

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127 Lung	0.3065006	0.4846845	0.403754	0.27539155 H46074	146074_at	EST: yo13f07.r1 Homo sapiens cDNA clone 177829 5'. (from Genbank)
128 Lung	0.3056957	0.4841858	0.403345	0.27508694 L44574 at	.44574 at	EST: Homo sapiens thymus mRNA (randomly primed, normalized), single-bass segments
129 Lung	0.3042333	0.4836007	0.403323	A 0.27474338 t	VA490685_a	AA490685_a EST: aa45b03.r1 Soares NhHMPu S1 Homo sapiens cDNA clone to 823853.5'. mRNA sequence (from Genhank)
				✓	AA206983 a	
130 Lung 131 Lung	0.3041266	0.4833055	0.402314	0.27447408 t 0.27427304 H62435 at	3.	sequence. (from Genbank) Cholingrais recorder is a sequence.
132 Lung	0.3023016	0.4830277	0.401581	0.2738723 03 i at	RC_AA2358 03 i at	EST: zs42g06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687898.31 mRNA sequence (from Corbon).
133 Lung	0.3022544	0.4825101	0.401088	0.27348357 N48204	148204 at	EST: yv22a08.r1 Homo sapiens cDNA clone 243446 5'. (from Genhank)
134 Lung	0.3016735	0.4821407	0.400811	0.2732604 U91618		Proneurotensin/proneuromedin N mRNA
135 Lung	0.3014633	0	0.400427	0.27292356 T.	57140 s at	0.27292356 T57140 s at Paraoxonase 3
136 Lung	0.2994365	0.481468	0.400271	0.27270302 Li	02326 f at	0.27270302 L02326 f at (clone Hu lambda-17) lambda-like gene
137 Lung	0.2989464	0.4812913	0.400164	RC_A 0.27240446 96 at	RC_AA2930 96_at	EST: zt55b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726225 31 mRNA secuence (from Generally)
138 Lung	0.2985752	0.4812542	0.399905	RC_A 0.27210814 59 at	C_AA4774 9 at	RC_AA4774 EST: zu44c08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 59 at clone 740846 3', mRNA sequence (from Ganbank)
139 Lung	0.2965464	0.4810946	0.39948	0.27188435 61	44537	Homo caniane mBNA for KIAAA770 motolic action
140 Lung	0.2961333	0.4806972	0.399182	0.27159443 M16973	at	C8B Complement component 8, beta polymentide
141 Lung	0,2960797	0.4802434	0.39881	0.271245 1_at	'60_rna	Laminin S B3 chain (LAMB3) gene
142 Lung	0.2951559	0.479978	0.398544	RC_A 0.270909185_at	A4166	Homo sapiens Munc13 mRNA, complete cds
143 Lung	0.2951044 0.4799131	0.4799131	0.398312	A/ 0.2707115 t	4011479_a	AA011479_a EST: zi01b10.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
144 Lung	0.2948266	0.4796198	0.398208	0.27045232 M62505	ज	C5R1 Complement component 5 recentor 1 (CF2 Hand)
145 Lung	0.2944621	0.4792813	0.397764	RC_A 0.2700249941_at	A4775	EST: zu41a09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740536 3' similar to TR:G1144330 G1144330 CREB-RP. ;, mRNA sequence. (from Genbank)
146 Lung	0.2939202 0.4790747	0.4790747	0.397602	D7 0.26977727 t	D79206_s_a	SDC4 Syndecan 4 (amphiglycan, ryudocan)

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147 Lung	0.2914589	0.2914589 0.4786702	0.397298	D10537_s_a 0.26932248 t	MPZ Myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)
148 Lung	0.2914589	0.4783935	0.39646	D10537_s_a 0.2690792 t-2	Myelin protein zero (Charcot-Marie-Tooth neuropathy 1B)
149 Lung	0.2898674	0.4781693	0.396126	RC_AA4546 0.26867762 67 at	EST: zx99h03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 811925 3', mRNA sequence. (from Genbank)
150 Lung	0.2898594	0.4780451	0.395776	0.26845086 U08021_at	Nicotinamide N-methyltransferase (NNMT) mRNA
					EST: yp88f07.r1 Homo sapiens cDNA clone 194533 5' similar to contains Alu repetitive element; contains L1 repetitive element;. (from
151 Lung	0.2892954	0.477616	0.395687	0.2681705 R86178_at	Genbank)
152 Lung	0.2885685	0.4775392	0.395578	M55998_s_a 0.26800632 t	Alpha-1 collagen type I gene, 3' end
153 Lung	0.288322	0.288322 0.4771822	0.394955	RC_AA2339 0.26776683 57_at	RC_AA2339 EST: zr27e04.s1 Stratagene NT2 neuronal precursor 937230 Homo 57_at sapiens cDNA clone 664638 3', mRNA sequence. (from Genbank)
154 Lung	0.2881756	0.477153	0.394793	AA082023_e	AA082023_a EST: zn35d10.r1 Stratagene endothelial cell 937223 Homo sapiens t cDNA clone 549427 5', mRNA sequence. (from Genbank)
155 Lung	0.2880437	0.4766433	0,394412	N72380_s_a 0.26727933 t	EST: yv38f12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 245039 5', mRNA sequence. (from Genbank)
156 Lung	0.2880289	0.476529	0.394247	RC_AA6085 0.26688108 79_s_at	Paired-like homeodomain transcription factor 2
157 Luna	0.2879598	0.4765055	0.394054	RC_AA0478 0.266726176 at	EST: zf50b08.s1 Soares retina N2b4HR Homo sapiens cDNA clone 380343 3' similar to contains Alu repetitive element;contains element L1 repetitive element;. mRNA sequence, (from Genbank)
158 Lung	0.2872478		0.393871	0.26648134 99_at	RC_AA4588 EST: zx88d07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 99 at clone 810829 3', mRNA sequence. (from Genbank)
159 Lung	0.2870744	0.475351	0.392849	U58496_s_a	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1
160 Lung	0.2869344	0.4750723	0.392529	M17183_s_a 0.2658185 t	Parathyroid hormone-related protein mRNA
161 Lung	0.2849524	0.4749866	0.392386	RC_AA6209 0.26562515 65_at	EST: af88f01.s1 Soares testis NHT Homo sapiens cDNA clone 1049113 3' similar to SW:PUA1_MOUSE P28650 ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME; contains Alu repetitive element;, mRNA sequence. (from Genbank)
162 Lung	0.2849164	1	0.392209	RC_D20171 0.2653295_at	EST: Human HL60 3'directed Mbol cDNA, HUMGS01145, clone pm2260, mRNA sequence. (from Genbank)

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cDNA	s cDNA	4 clone	s cDNA	clone	cDNA	lone			lar to	one	DNA	one	90

164 Lung 165 Lung 166 Lung	0.2846965 0.2844742 0.2829887			Ď(RC AA4534	(monitor in contract in the co
	0.2844742	0.4735598	0.391638	0.2649537 31_at	ੂੜਾਂ	EST: zx32g10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788226 3', mRNA sequence, (from Genbank)
).2829887	0.4733726	0.391583	RC_A 0.2646426 95 at	RC_AA0170 95 at	EST: ze37h12.s1 Soares retina N2b4HR Homo sapiens cDNA clone 361223 3', mRNA sequence (from Genhank)
		0.4731536	0.39143	0.26436642 35	RC_AA4960 35 at	
	0.2827876	0.4730274	0.390832	RC_A 0.26403245 11 at	RC_AA4958	
168 Lung	0.282494	0.472829	0.390482	0.26365912 t	AA485585_a t	
	0.2821531	0.4727932	0.390371	RC_AAZ 0.2633431 03 f at	2358	
	0.2819685	0.4727181	0.389973	0.26310006 MZ0902	20902 at	APOCI Andinomotein Cl
	.2817782	0.2817782 0.4723372	0.389887	0.26284868 M21305	ज	Alpha satellite and satellite 3 innetion DNA sequence
172 Lung (0.2811393	0.4723207	0.389765	0.2626506 J04056	at "	CBR Carbonyl reductase
173 Lung C	0.2810333	0.4720445	0.389511	X1595z 0.26250052 1_s_at	X15954_ma 1_s_at	MBP1 gene, exon 1 (and joined CDS)
174 Lung	0.279982	0.4719756	0.389102	0.26218 at	383703_i	EST97119 Testis I Homo sapiens cDNA 5' end similar to similar to
175 Lung	0.279511	0.471948	0.388998	RC 0.26192585 12	_AA2341 _at	EST: zr74a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669104 3', mRNA sequence. (from Genhank)
176 Lung 0	0.2792959	0.471922	0.388748	RC_A 0.2616987 76 at	A4875	EST: ab23g01.s1 Stratagene lung (#937210) Homo sapiens cDNA clone 841680 3', mRNA sequence (from Genhank)
177 Lung 0	0.2788754	0.4717746	0.388623	RC_A 0.261507 06 at	A2279	EST: zr57d06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667499 3', mRNA sequence (from Genhank)
178 Lung 0	0.2788578	0.471641	0.388283	0.26125085 t	416829_a	AA416829_a EST: zu08e03.r1 Soares testis NHT Homo sapiens cDNA clone t 731260 5', mRNA sequence. (from Genhank)
179 Lung	0.278733	0.4715191	0.388099	0.26096424 t	.027760_a	AA027760_a EST: HPLA_CCLEE_40f6ar HPLA CCLee Homo sapiens cDNA,
180 Lung 0	0.2786865	0.471338	0.387806	0.26075655 1 s at	_ ma	Hebatocyte growth factor-like profein gene
181 Lung 0	0.2786642	0.4710641	0.387796	RC_A 0.2605786 47_at	4195	EST: zv04a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 752624 3', mRNA sequence. (from Genbank)
182 Lung	0.278047	0.4709638	0.387473	0.26028854 U30999 at		U30999 Homo sapiens MV3 melanoma Homo sapiens cDNA clone memd, mRNA sequence
183 Lung ().276639	0.276639 0.4708279	0.386837	AFFX- 0.2600507 3_at-2	J	AFFX-PheX-3_at (miscellaneous control - 11k chips)

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184 Lung	D	0.276639	0.4699768	0.386803	AFF. 0.25985834 3_at	X-PheX-	AFFX-PheX-3_at (endogenous control)
		00000000	A 40000A O	0.000	A A DEOE2246+	AA047045_a	EST: zf50d12.r1 Soares retina N2b4HR Homo sapiens cDNA clone 380375 5' similar to contains Alu repetitive element;, mRNA
gun car	Ō	0.270720		0.300732	0.23333340	-	Sequence: (11011) Certibatin)
186 Lung	ğ	0.2761711	0.4692693	0.386704	0.2593366	C20545	EST: HUMGS0002073, Human Gene Signature, 3 -directed CDNA sequence, mRNA sequence. (from Genbank)
187 Lina	ō	0.2756152	0.4688733	0.386704	RC_A 0.25915623 18 at	A4062	EST: zu65e08.s1 Soares testis NHT Homo sapiens cDNA clone 742886 3', mRNA seguence, (from Genbank)
188 Luna	2 0	0.2753333	1	0.386171	0.2589496 [27671 s at	0.2589496 L27671 s at Intercellular adhesion molecule 4. Landsteiner-Wiener blood group
189 Lung	D D	0.2745251	1	0.386088	A 0.2587298 t	AA367473_a	Crystallin, beta B2
190 Lung	Ď	0.2743412	0.4680363	0.385394	0.25824875 t	A437153_a	AA437153_a EST: zv61b01.r1 Soares testis NHT Homo sapiens cDNA clone t
191 Lung	g	0.2739779	0.4680098	0.385391	0.2581156 U35340 at		CRYBB1 Crystallin beta-B1
192 Lung	Bi	0.2733802	0.4676982	0,385331	U203 0.25782692 6_at	U20391_rna 6_at	Folate receptor (FOLR1) gene
193 Lung	Ď	0.2732106	0.4673478	0.385189	0.25753233	03934_s_at	0.25753233 J03934 s. at NMOR1 NAD(P)H:menadione oxidoreductase
							EST: 20c4 Human retina cDNA randomly primed sublibrary Homo
194 Lung	ĝ	0.2726639	0.4672887	0.384898	0.25737914 W27099_at		sapiens cDNA, mRNA sequence. (from Genbank)
		777777		200	7.00	_AA6207	EST: af90f08.s1 Soares testis NHT Homo sapiens cDNA clone
Bunn cal	<u>g</u>	0.2124411	- (0.384/25	0.25/12/34 82		1049319 3', mKNA sequence. (from Genbank)
196 Lung	Ď	0.2721126	0.4670309	0.384471	0.25696772 304970	04970_at	CPM Carboxypeptidase M
							EST: zx89g02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810962 3' similar to SW:MV10_MOUSE P23249 PUTATIVE
197 Luna		0.2709255	0.4665315	0.384406	RC_AA4 0.25674567 02 s at	594	GTP-BINDING PROTEIN MOV10.;, mRNA sequence. (from Genbank)
			1			HG491-	
198 Lung	βį	0.2701913	0.4665315	0.384145	0.25656185 HT491_at	1T491_at	Fc Receptor lib3 For lgg, Low Affinity
199 Lung		0.2690204	0.4664357	0.384121	0.25643316 18	R at 8 at	RC_AA3720 EST: EST83940 Parathyroid gland tumor I Homo sapiens cDNA 3' at end, mRNA sequence. (from Genbank)
200 Lung		0.2685316	0.4654056	0.383995	0.2560336 M87499 at	7499 at	UNG Uracil-DNA glycosylase
201 Lung		0.2683346	0.4653634	0.383518	0.2558822 t	AB002366_a t	KIAA0368 gene, partial cds
202 Lind	Di	0.2682895	0.4647388	0.383131	0 25561267 t	AC002086_a	PAC clone D.1525N14 from Xo23. complete secuence
203 Lund	g 0	0.2682696		0.382982	0.25542003 X74039	(74039 at	Variant urokinase plasminogen activator receptor (uPAR2) mRNA, partial cds
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Inventors: Sridhar Ramaswamy, et al.

204 Lung	0.2681348	0.4644563	0.382882	0.2552324 X54925 at		MMP1 Matrix metalloprofeinase 1 (interstitial collacenase)
205 Lung	0.2668635	0.464408	0.382328	0.2550093 D26129_at		RNS1 Ribonuclease A (pancreatic)
206 Lung	0.2667076	0.4642426	0.382286	RC 0.25474834 17	RC_AA4192 17 at	EST: zv34h10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755587 3. mRNA sequence (from Genhank)
207 Lung	0.2660186	0.4642034	0.382111	0.2544974 X52228	228_at	MUC1 Mucin 1, transmembrane
208 Lung	0.2652287	0.4641261	0.381949	0.2543377 D79565	565 at	Human aorta cDNA 5'-end GEN-281C02, mRNA sequence. (from Genbank)
209 Lung	0.2652253	0.4638998	0.381842	0.25415117 M18728	728 at	NCA Non-specific cross reacting antigen
210 Lung	0.2649988	0.4635157	0.381611	0.2538488 U95301	301_at	Phospholipase A2, group X
241 1 100	0.26/782	0.4634952	000000000000000000000000000000000000000	RC	45211	EST: aa70h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826343 3' similar to WP:C09F5.2 CE01774;, mRNA
212 Ling	0.204102	ł	0.301338	0.2537095511		sequence. (from Genbank)
213 Luna	0.2030349		0.381114	0.25355068 X07820	at at	MMP10 Matrix metalloproteinase 10 (stromelysin 2)
S. S. S. S. S. S. S. S. S. S. S. S. S. S	00001:0	- 1	0.301042	0.2326223 737 808	ä	IGL@ Immunoglobulin lambda light chain
214 Lung	0.2634412	0.4626113	0.38087	RC_ 0.25311196/41_e	RC_AA4042 41 at	EST: zv63c01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 758304 3' similar to TR:G412267 G412267 UNCOUPLING PROTEIN + mRNA sequence from Coupling
215 Luna	0.263259	0.4623666	0 380820	RC A	A4769	EST: zu38c05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
216 Lung	0.2632494		0.380665	0.5263985 104080 at		clone /40264 3, mKNA sequence. (from Genbank)
			0.00000	0.20202020		C13 Complement component 1, s subcomponent
217 Lung	0.2631691	0.4618928	0.380591	0.25234178 t	AA480025_a t	EST: zv18f06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 754019 5', mRNA sequence. (from Genbank)
218 Lung	0.2630112	0.4618654	0.380522	0.25200328 U908	910 at-2	0.25200328 U90910 at-2 Human clone 23564 mRNA securence
219 Lung	0.2630112	0.4618502	0.380008	0,2518673 U90910 at	910 at	Clone 23564 mRNA serillence
220 Lung	0.2627808	0.4612269	0.379785	0.25163764 80 r at	1549	Homo sapiens zinc-finger helicase (hZFH) mRNA complete cds
221 Lung	0.2627209	0.4611526	0.379452	AA40 0.25145218 t	AA400044_a t	Human clone 23803 mRNA, partial cds
222 Lung	0.2625929	0.4610807	0.379284	0.2512403 W68464 at		Homo sapiens mRNA for ADP ribosylation factor-like LAK, complete cds
223 Lung	0.2623043	0.460708	0.379116	0.2510612_at	17510_s	AA147510_s EST: zl50c12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA_at clone 505366 5', mRNA sequence. (from Genhank)
224 Lung	0.2619781	0.4603861	0.378938	0.25085554 W26091 at		EST: 20h8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence (from Genhank)
225 Lung	0.2616983	0.4602705	0.378533	0.25066435 t	AA477715_a l	EST: zu44e10.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740874 5' mRNA sequence (from Conhant)
226 Lung	0.2611458	0.4598296	0.378524	0.25050667 t	AA096343_a I	EST: 19342.seq.F Fetal heart, Lambda ZAP Express Homo sapiens CDNA 5", mRNA sequence (from Canbank)
227 Lung	0.2611255	0.4596179	0.378396	0.2502798 U57721	at	L-kynurenine hydrolase mRNA

		L			The second secon
228 Lung	0.260941		0.378269	0.2501868 M19481 at	Follistatin gene
229 Lung	0.2606874	0.4589527	0.377927	0.24997187 U89717_at	RDH1 Retinol dehydrogenase 1 (11-cis)
000	0 0004000	1	110110	RC_AA5987	G cintum citoroxodum and C
230 Lung	0.2604209	0.4583380	0.377071	0.24980038 02_at	ວ ເມລາວ ກ່າວປ່ອກອາປະຕິ ກ່າວປ່ອກອາປະຕິ ກ່າວປ່ອກອຸກຸລາວປ່ອກອຸກຸລາວປ່ອກອຸກຸລາວປ່ອກອຸກຸລາວປ່ອກອຸກຸລາວປ່ອກອຸກຸລາວປ່
2311 und	0.2603552	0.4582492	0.377406	RC_AA1820 0 24960165101 i at	RC_AA1820 EST: zp62f10.s1 Stratagene endothelial cell 937223 Homo sapiens 01 i at cDNA clone 624811.3' mRNA sequence. (from Genbank)
		1		AA431603 a	
232 Lung	0.2600594	0.4581787	0.3772	0.24940409 t	
233 Luna	0.2599597	0.4577981	0.377166	RC_AA4878 0.24916701 79 at	EST: ab12a04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone 840558 3. mRNA sequence. (from Genbank)
234 Lung	0.2595257		0.377067	0.24900065 W94795 at	Zinc finger protein 143 (clone pHZ-1)
				. RC_AA6098	EST; af08c07.s1 Soares testis NHT Homo sapiens cDNA clone
235 Lung	0.2589462	0.4576144	0.376934	0.24892284 73_at	1031052 3', mRNA sequence. (from Genbank)
236 Lung	0.2588362	0.4575812	0.376602	M13686_s_a 0.24865182 t	M13686_s_a PULMONARY SURFACTANT-ASSOCIATED PROTEIN A PRECURSOR
				RC_AA0745	RC_AA0745 EST: zm17f04.s1 Stratagene pancreas (#937208) Homo sapiens
237 Lung	0.2588171	0.4571579	0.376432	0.24852368 14_at	cDNA clone 525919 3', mRNA sequence. (from Genbank)
				₹	
238 Lung	0.2587827	0.4570878	0.376238	0.24832734 at	Claudin 4
239 Luna	0.2586628	0.4570521	0.376141	YEL019c/M 0.24815279 MS21 at	No info for gene
)				U75272 s a	
240 Lung	0.2571341	0.4570198	0.375894	0.24797288 t	PGC Gastricsin (pepsinogen C)
241 Lung	0.257126	0.4567713	0.37581	0.24773003 L15388_at	G PROTEIN-COUPLED RECEPTOR KINASE GRK5
242 l ma	0.257074	0 4567229	0.375642	0 24751059 N41669 at	EST: yw90d03.r1 Homo sapiens cDNA clone 259493 5'. (from Genhank)
2				RC AA0354	America
243 Lung	0.2569361	0.2569361 0.4564265	0.37563	0.24729508 82 at	Homo sapiens clone 24655 mRNA sequence
				RC_AA0019	
244 Lung	0.2565171		0.375295	- 1	cDNA clone 427905 3', mRNA sequence. (from Genbank)
245 Lung	0.2564692	0.4560823	0.375261	0.24699226 M11147_at	
246 Lung	0.2564633	0.4554453	0.375238	AA477891_a 0.24680512 t	EST: zu34e12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739918 5', mRNA sequence. (from Genbank)
247 Lung	0.2562718	0.4553228	0.374868	M83667_rna 0.24652603 1_s_at	NF-IL6-beta protein mRNA
248 Luna	0,2558699	0.4548869	0.374733	0.24635512 65 at	RC_AA0106 EST: ze19f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA 65 at clone 359459 3', mRNA sequence. (from Genbank)
					The state of the s

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040	0.0553034	0.0553034 0.4548366	0.374488	0.24627477 at	D25718	EST: Human colon 3'directed Mbol culvA, holyscortost, sione cm1380, mRNA sequence. (from Genbank)
249 Luliy	0.253333	0.4546747	0.37416		_AA6217 at	EST: af54e12.s1 Soares total fetts N02rtro 3W from Suprans clone 1035502 3', mRNA sequence. (from Genbank)
250 Lung	0.2341 340		1,000	0.245926001.25880	5880 c at	Enoxide hydrolase 1. microsomal (xenobiotic)
251 Lung	0.2542415	0.4546261	0.374077	0.24303039	2	EST: ye04h07.r1 Homo sapiens cDNA done 116797 5' similar to
-	0 2542160	0.4543322	0.373829	0.24569415 T89571	f at	contains Alu repetitive element; (from Genbank)
252 Lung	0.2342103		0.00			SLC9A1 Solute carrier family 9 (sodium/hydrogen exchanger), isolottii
253 1100	0.2539989	0.4542571	0.373699	0.24545069 X76180 at		1 (antiporter, Na+/H+, amiloride sensitive)
254 Lind	0,2537951		0.373522	0.2453531 X87843	at	Cyclin H assembly factor
	2010040	0.4520768	0.373385	HG3400- 0 24507011 HT3579	at	Nestin
255 Lung	0.2030490	0.7330483 0.4333100	0.00			EST: vi94e03.r1 Homo sapiens cDNA clone 146908 5. (from
250	0.2536239	0 4537005	0.373333	0.24477062 R81003_at		Genbank)
ก็มกา ๑๓ฺ	0.200250	1		K.	3	EST: aa68f12.s1 NCI_CGAP_GCB1 Homo sapiens curve cione
257 Lina	0.2532515	5 0.453271	0.373097	0.24461727 33 at		IMAGE:826127 3', mRNA sequence. (Ifotti Gettidality)
		l	000000	RC_A	A0253	EST; ze/4h04.s1 sodiles letal iteal (1957) (
258 Lung	0.2532487	7 0.4531776	0.372902	0.2444123	44483	EST: 2,02606 s1 Soares NHHMPu S1 Homo sapiens cDNA clone
050	0.2526551	1 0.4531004	0.372707	0.24432798 94_at	A4100	767266 3', mRNA sequence. (from Genbank)
260 Lung	0.2525689		0.372399	0.2441121 M60047	. 11	Heparin binding protein (HBp1/) mKNA
264 Lung	0.2520721		0.372217	0.24392939 L42601	at	f at KERATIN, TYPE II CY I OSKELE I AL OD
2621 und	0.2515372	2 0.4522601	0.372131	0.24384682 X03350	at	ADH2 Alcohol denydlogeriase z (dass 1), bota polyperias CDNA
202	1 0		0.372052	RC_A 0.2434447179 at	A2923	EST: zt51h09.s1 soares ovary unitor incline suprained su
263 Lung	0.7314039		0.012.002			
	_				AA0341	EST: zi06g11.s1 Soares fetal liver spleen 1NFLS S1 Homo saplens
264 Lung	0.2512445	5 0.45218	0.371709	0.24330080	AA3937	EST: zv64f06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
285 1100	0.2510947	17 0.4520143	0.371691	0.24313627 66_at		clone 758435 3', mRNA sequence. (from Genbank)
607 Lui 19	0.2510839		L	0.24289817 D21239	D21239_at	C3G protein
fun 7007	20107:0	1	1	0.24273656	HG3517- HT3711 at	Aloha-1-Antitrypsin, 5' End
267 Lung	0.251063	33 0.4518838	\bot	0.6421 3300	AA095022 a	AA095022 a EST: cp2494.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
268 l una	0.2508122	22 0.4518792	0.371246	0.24254175		cDNA 5', mRNA sequence. (from Genbank)
	0 2505688	88 D 4518583	0.371176	0.24230699	RC_AA2567 00 at	Interferon (alpha, beta and omega) receptor 2
Zey Lung	0.53000	00 0:40	ļ		RC_AA1259	
270 Lung	0.25010	0.2501076 0.4517699	0.370847	0.24218002 69_at	69 at	CIONE 31 1390 3, IIININ 36406160, IIININ 30406160

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. agen, group, group, group group, grou

Docke	t No.: 2825.2020-002
Title:	Genetic Markers for Tumors
Invente	ors: Sridhar Ramaswamy, et al.

						AA490758 a	
271 Lung		0.2493669	0.4517632	0.37067	0.241965 t	-	No info for gene
272 Luna		0.2492503	0.4517419	0.37066	0 24183054 41 at	RC_AA4030	Call that rationic acid hinding protoin 4
				2	1000011	חביים איזינים	ספוימים ופיוויסוס מסומ-חווימיוול לווחווים לווחווים מסומים ו
273 Lung		0.2488994	0.4512726	0.37039	0.24164191167 s at	67 s at	Paranyonaca 3
						RC AA4366	EST: 2W55004 st Soares total fetus Nh2HE8 Gw. Homo canions aDNA
274 Lung		0.2485074	0.4512726	0.370234	0.24142757 19_at	19 at	clone 773959 3', mRNA sequence. (from Genbank)
275 Ling		0.2470669	0.4500642	0 970044	000000000000000000000000000000000000000	RC_AA1470	EST: zo32a02.s1 Stratagene colon (#937204) Homo sapiens cDNA
610 Luig		1	0.4500012	0.3/0041	U.2412/822 6/_at	6/_at	clone 588554 3', mRNA sequence. (from Genbank)
276 Lung	0.2470958	0958	0.4508456	0.369826	0.24110112	0.24110112 R39467 f at	
						X02761_s_a	
277 Lung		- 1	0.4508456	0.369599	0.24089013t	-	FN1 Fibronectin 1
278 Lung		0.2468594	0.450728	0.369407	0.24080303 U18991	U18991 at	RPE65 Retinal pigment epithelium-snecific protein (65kh)
279 Lung		4644	0.2464644 0.4505417	0.369224	0.24056235 M83772	M83772 at	FMO2 Flavin-containing monooxygenase 2
280 Lung		3113	0.2463113 0.4504213	0.369217	0.24039806 L07765	L07765 at	CES2 Carboxylestease 2 fliver)
281 Lung		2243	0.2452243 0.4496022	0.368663	0.24017109 Y12556 at	Y12556 at	AMP-activated protein kinase heta-1
282 Lung			0.4494774	0.368508	0.2400353	0.2400353 M32578 at	HLA-DRB1 Major histocompatibility complex class II DR heta 1
283 Lung	0.2449677		0.4493105	0.368338	0.23982677 H18713 at	H18713 at	H.sapiens mRNA for aminonentidase P-like
20						100	
284 Lung	0.2449493	- 1	0.4492599	0.368215	0.23971696 57 at		clone 789030 3', mRNA sequence. (from Genbank)
285 Lung	0.2447449	7449	0.449254	0.3677	0.23965551	AA114949_a	AA114949_a UDP-N-acteylglucosamine pyrophosphorylase 1; Sperm associated
					200	AA248469 2	
286 Lung	0.24	0.244619	0.4490928	0.367492	0.23940934	t t	sapiens cDNA 5', mRNA sequence, (from Genhank)
					_	HG3431-	
	W. A 4					HT3616 s a	
287 Lung	0.2439476		0.4490151	0.367249	0.23927197 t	1	Decorin, Alt. Splice 1
28811103	0.0495030	0000	0000			The state of the s	EST: yh44b01.r1 Homo sapiens cDNA clone 132553 5'. (from
200 Luiig	0,2438	0000	0.448853	0.356966	0.23907928	0.23907928 R25944 f at Genbank)	Genbank)
289 Lung	0.2421348		0,4489121	0.366873	0.23886372\D79603 at	D79603 at	EST: Human aorta cDNA 5'-end GEN-286H04, mRNA sequence.
						0	EST: ze62e11.s1 Soares retina N2b4HR Homo saniens cDNA clone
290 Lung	0.242	2101	0.242101 0.4486721	0.366676	0.23872155 05 at		363596 3', mRNA sequence. (from Genbank)

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

	7111				
291 Lung	0.2418224	0.4483815	0.366662	0.23854859 R67702 at	Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyltransferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae)bacterial, worm and yeast hypothetical genes, and the GNB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG islands, ESTs, STSs, and GSSs.
292 Lung	0.241485	5 0.4482195	0.366486	RC_AA2364 0.23836564 60 at	
293 Lung	0.24 0591	1 0.4480375	0.366363	RC_AA4493 0.23823951 06_at	
294 Lung	0.2407021	0.4478584	0.366068	RC_AA4240 0.2380642 13 at	ļ
295 Lung	0.2406482	2 0.4476039	0.365884	0	EST: yx19f02.r1 Homo sapiens cDNA clone 262203 5' (from Genbank)
296 Lung	0.2405345	5 0.4472519	0.365732	0.23780748 66 at	-
297 Lung	0.2402408	3 0.4472004	0.365634	0.23751338 U90905 at	Clone 23574 mRNA sequence
298 Lung	0.240171	0.4470855	0.365302	RC_AA1279 0.23746502 64 at	-
299 Lung	0.2398486	3 0.4470855	0.36514	0.23732695 K01396 at	Pl Protease inhibitor 1 (anti-elastase), alpha-1-antitrosin
300 Lung	0.2393439	0.4470831	0.365066	0.23717211 U93869_at	Human RNA polymerase III subunit (RPC39) mRNA_complete cds
301 Lung	0.2393215	0.2393215 0.4469072	0.365001	AA418143_8 0.23687358 t	
302 Lung	0.2392817	0.4468811	0.364987	D26561_cds 0.23681135 2_at	
303 Lung	0.2389897	0.4466466	0.364967	0.23660107 Z47553 at	FMO5 Flavin containing monooxygenase 5
304 Lung	0.2389653	0.4465462	0.364956	M82967_s_a	
305 Lung	0.2389139	0.4464949	0.364728	0.2361749 H81340_at	EST: yu74d04.r1 Homo sapiens cDNA clone 239527 5'. (from Genbank)
306 Lung	0.2387406	0.2387406 0.4463466	0.364603	AA397616_a	AA397616_a 728558 5' similar to TR:G57649 G57649 VOLTAGE-GATED 0.23596013 t POTASSIUM CHANNEL.; mRNA sequence. (from Genbank)
				The state of the s	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)

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307 Lung	0.2386606	0.4461591	0.364413	0.23576084 J04430_s	J04430_s_at	at ACP5 Acid phosphatase 5, tartrate resistant
308 Lung	0.2384605	0.2384605 0.4459762	0.363926	0.23568334		AA421370_a 731074 5' similar to contains MER17.t2 MER17 repetitive element;, mRNA sequence. (from Genbank)
309 Lung	0.2381974	0.2381974 0.4458249	0.363899	0.23559451 X66358 at	1	mRNA KKIALRE for serine/threonine protein kinase
310 Lung	0.2377942	0.2377942 0.4455868	0.363651	RC_A 0.23553509 22_at	A0075	EST: zh98f09.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429353 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)
311 Lung	0.2377663	0.2377663 0.4454852	0.363403	RC_A 0.23538382 33_at	A1646	EST: zo93d04.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 594439 3', mRNA sequence (from Genhank)
312 Lung	0.2376308	0.4451729	0.363267	0.23522367 56_at	A2625	EST: zs2zb09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685913 3', mRNA sequence, (from Genhank)
313 Lung	0.2373599	0.4451073	0.363244	0.23511253	AA287815_a t	AA287815_a EST: zs50g04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
314 Lung	0.2373353	0.4449089	0.363137	0.23500282	RC_D25984 _at	EST: Human colon 3'directed Mbol cDNA, HUMGS06759, clone cm3106, mRNA sequence. (from Genbank)
315 Lung	0.2369185	0.2369185 0.4447673	0.362995	RC_A 0.23480712 39_at	A0531	EST: 2/73e05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510272 3' similar to TR:E243948 E243948 CHROMOSOME VII READING FRAME ORF YGL054C.;; mRNA sequence. (from Genbank)
316 Lung	0.2366281	0.4447151	0.36291	RC_Av 0.23457296 79 at	44889	Homo sapiens cell cycle-regulated factor n78 mBNA complete ode
317 Lung	0.2361669	0.2361669 0.4447031	0.362812	RC_A 0.23443899 50_at	40322	EST: zk19f06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471011 3', mRNA sequence. (from Genbank)
318 Lung	0.2361647	0.2361647 0.4445837	0.362637	0.23431237	AA478131_a	AA478131_a clone 740658 5' similar to TR:G433963 G433963 P18H-REV 107. ;,
319 Lung	0.2359319	0.4444797	0.362621	0.234217931	(57348_s_a	SFN Stratifin
320 Lung	0.235862	0.4444004	0.362557	0.23400162 N34697 at		EST: yx81c11.r1 Homo sapiens cDNA clone 268148 5'. (from Genbank)
321 Lung	0.2356288	0.4443508	0.362268	RC_A 0.2338126 92 at	A6095	EST: af15d11.s1 Soares testis NHT Homo sapiens cDNA clone
322 Lung	0.2352507	0.4443409	0.362126	0.23375657 X76534	ਜ਼	NMB Neuromedin B
323 Lung	0.2352127 0.4442597	0.4442597	0.361905	RC_AA1 0.23355637 97_s_at	RC_AA1560 97_s_at	RC_AA1560 EST: zo45d03.s1 Stratagene endothelial cell 937223 Homo sapiens 97 s_at cDNA clone 589829 3', mRNA sequence. (from Genbank)

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324 Lung	0.2351494	0.4441127	0.361713	0.23342706 t	\\\476517_a	Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 AA476517_a (Hematological and Neurological expressed sequence 1) downstream t
325 Lung	0.2344142	0.4440047	0.361645	0.23331495 t	AF004709_a	Protein kinase mitogen- activated 13
326 Lung	0.234278	f I	Ll	0.23319076 X93921 at		Protein-tyrosine-phosphatase (tissue type: testis)
Lung	0.234278	0.4439402	0.361569	0.2330621 X93921	at-2	at-2 Dual specificity phosphatase 7
328 Lung	0.233664	0.4434984	0.361149	0.23292959 HT537	1 1 10	Collagen, Type Viii, Alpha 2
329 Lung	0.2334355	0.4433608	0.361149	0.23277782 L10125	s at	Human serine/threonine kinase receptor-2-2 (SKR2-2) mRNA, at complete cds. (from Genbank)
330 Luna	0.2333466	0.4432385	0.36080	1 1 1 1 1 1 1	HG3242- HT3419_s_a	
331 Luna	0.2333421		0		AA128724_a	Damo consists and the state of Alpha 1e Subunit, Alt. Splice 2
332 Lung	0.2329953	1	0.360797	0.23223354 [121931 at		FRP1 Frictore highborhood 1
333 Lung	0.2328587	0.442692	0.360785	RC_A 0.23213045161_at	4	EST: zw70f11.s1 Soares testis NHT Homo sapiens cDNA clone
334 Lung	0.2320017	0	0.360615	0.23200329 283745	at	DNA sequence from PAC 45343 contains EST and STS
335 Lung	0.2317447	0.4423266	0.360527	0.23182687 L48513	, at	Paraoxonase (PON2) mRNA
			-	_ <	AA399299 a	EST: zt52e09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA a clone 725992 5' similar to contains element PTR5 renetitive element :
336 Lung	0.2314258	0.4422433	0.360438	0.23169434 t		mRNA sequence. (from Genbank)
337 Lung	0.2313241	0.2313241 0.4421065	0.360438	0.23157692 M90656		GLCLC Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase) catalytic (72 8kD)
338 Lung	0.2312668	0.2312668 0.4420143	0.360013	0.23138015 D11151 at	1	EDNRA Endothelin receptor type A
339 Lung	0.2312089	0.2312089 0.4416896	0.359856	0.2312995 X07696		KRT15 Keratin 15
7	74007660		0	>	 §	The state of the s
340 Lung	0.2312077		0.359846	0.23117815 BP1_at		No info for gene
34 1 Lung	0.2310319	1	0.359609	0.23102877 X92475_at	(92475_at	ITBA1 protein
34 c Lung	0.2310319	0.4409662	0.35918	0.23085321 X92475 at-2 ITBA1 gene	(92475_at-2	ITBA1 gene
343 Lung	0.2309153	0.4409024	0.358989	0.23061915 H66367	at at	EST: yu14avb.71 Homo sapiens cDNA clone 233746 5' similar to contains Alu repetitive element;. (from Genbank)
344 Lung	0.2308357	0.4406858	0.358954	0.23049174 t	A081995_a	AA081995_a Zn26d06.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo t
345 Lung	0.2303604	0.4405938	0.358489	0.23034495 t	A248964_a	AA248964_a EST: kk6741.seq.F Human fetal heart, Lambda ZAP Express Homo to sapiens cDNA 5' mRNA sequence (from Ganbank)
)	,			-1		שמשוטוט סבווים אויים של של של אירו של אירוש אירוש של אירוש של אירוש של אירוש של אירוש של אירוש של אירוש של איר

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346 Lung	0.230249	0.4402882	0.358379	RC_AA4904 0.23023087 61 at	RC_AA4904 EST: aa45a12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 61 at 823870 3', mRNA sequence. (from Genbank)
347 Ling	0.000000	7.07.707.0	0.00000	RC_AA4314	EST: zw70g01.s1 Soares testis NHT Homo sapiens cDNA clone
348 Lung	0.2300901	- 1	0.358028	0.23003279 62 at 0.2399746 M16714 at	/81584 3, mKNA sequence. (from Genbank)
349 Lung	0.2300901		0.357847	0.22978345 M16774 at 2	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102
			10000	או וטוואו טרטט וטבבט טיב	ALTHA CHAIN PRECURSOR
350 Lung	0.2299386	0.2299386 0.4398891	0.357632	RC_AA6098	EST: ae62e05.s1 Stratagene lung carcinoma 937218 Homo sapiens
351 Lung	0.2297726	0.2297726 0.4398526	0.357595	0.2293974 T28246 at	Hensin (fransmemhrane professe sering 1)
352 Lung	0.2293905	0.4395745	0.357466		
353 Lung	0.2282414		0.357359	0.2292258 M20786 at	Perioric linegrated into Indinative Calculonia DNA PLI Alnha-2-niasmin inhibitor (alpha-2 DI)
354 Lung	0.2279826	0.4392837	0.357342	0.22907254 D17716 at	N-acetylglucosaminyltransferase V
355 Lung	0.2279826	0.4390499	0.35719	Mannosyl (alpha-1,6-)-gi 0.22897726 D17716 at-2 alucosaminyltransferase	Mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-
356 Lung	0.2276511	0.4389308	0.357114	RC_AA4656	EST: aa31b01.s1 NCI CGAP GCB1 Homo sapiens cDNA clone
				11	ABO blood group (transferase A alpha 1.3-N.
1					acetylgalactosaminyltransferase; transferase B, alpha 1-3-
35/ Lung	0.227571	0.4387819	0.35707	0.22858873 U15197 at-2	
					ABO ABO blood group (transferase A, alpha 1-3-N-
358 Lung	0.227571	0.4383889	0.356992	0.22850904 U15197 at	acetylgalactosaminyltransferase; transferase B, alpha 1-3- galactosyltransferase)
359 Lung	0.2274778		0.356905	0.22833458 t	INTERLEUKIN ENHANCER-BINDING FACTOR
360 Lung	0.2274309	0.4382207	0.356582	0.22816384 H16876_at	
26.1	0000		1		
SOI LUIG	0.22/429	0.4382066	0.356479	0.22797966 61 at	1030965 3', mRNA sequence. (from Genbank)
362 Lung	0.2274029	0.4381657	0.356466	HG417- 0.22778736 HT417 s at	
363 Lung	0.2267194	0.4379906	0.356311		
· · · · · ·					EST: aa43a01.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
2001	7 7000			AA489716_a	
304 Lung	0.2261014	0.43/9368	0.356146	0.22767206 t	mRNA sequence. (from Genbank)
365 1 1100	0.2259946	0.4370368	0 256026		EST: CHR220376 Homo sapiens genomic clone C22_491 5. (from
366 Lung	0.2253340		0.330030	0.22/320// H5343/ at	Genbank)
6,122,000	0.000022	•	0.330011	0.22730403 M15856 at	LPL Lipoprotein lipase

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3671	367 Lung	0.2257753	0.4379004	0.35571	0.22715753 R33961 at	EST: yh74b06.r1 Homo sapiens cDNA clone 135443 5'. (from Genbank)
368	368 Lung	0.2249175	0.4378383	0.355655		Alpha1-fetoprotein transcription factor (hFTF) mRNA
369 Lung	Lung	0.2249175	0.4378307	0.355551	0.22693585 U93553 at-	0.22693585 U93553 at-2 Fetoprotein-alpha 1 (AFP) transcription factor
370 Lung	nng	0.2248085	0.4377857	0.355499	0.22686562 44 at	EST: zw85c11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 783764 3' mRNA sequence (from Genhank)
371 Lung	nng	0.2240313	0.4377154	0.355092	0.22671953 X67698_at	Tissue specific mRNA
372 Lung	nng-	0.2232322	0.43761	0.355025	AA167824_a 0.2266024 t	
373 Lung	-nng	0.2231333	0.4375583	0.355006	0.22648223 J04513 at	Basic fibroblast growth factor (bFGF) 22.5 kd, 21 kd and 18 kd protein mRNA
374 Lung	5un-	0.2231237	0.4375517	0.354993	0.22640823 D30954 at	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)
375 Lung	-ung	0.2230321	0.4374047	0.354758	0.22624739 M68840 at	MAOA Monoamine oxidase A
376 Lung	ōun -	0.2226568	0.4373781	0.354701	W28902_r_a 0.22611126 t	
377 Lung	nng	0.2224297	0.4372591	0.354173	0.22595744 W37398 at	EST: zc11a10.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321978 5', mRNA sequence. (from Genbank)
378 Lung	nng	0.222415	0.4371029	0.354148	AA442274_a	EST: zv54a06.r1 Soares testis NHT Homo sapiens cDNA clone 757426 5', mRNA sequence. (from Genbank)
370 1 1100	מוו	0 2233001	9770767 0	0.054406	RC_AA4875	
380 Lung	gun.	0.2221375	0.4370183	0.354106	0.2256546 U72513 at	Clone 841656 3', mRNA sequence. (from Genbank)
381 Lung	nng	0.2221208	0.2221208 0.4369998	0.353864		
382 Lung	nng	0.2219176	0.4369082	0.353735	AFFX-DapX- 0.22524932 5 at-2	
383 Lung	nng.	0.2219176	0.4365304	0.353641	AFFX-DapX 0.2251752 5 at	1
384 Lung	ung	0.2218542	0.4363941	0.353457	0.22497497 X52022 at	RNA for type VI colladen alpha3 chain
385 Lung	nng	0.2216734	0.4362356	0.353429		
386 Lung	nng.	0.2216565	0.4361902	0.353312	0.22469103 X68314 at	
387 Lung	gun:		0.436033	0.353193	0.22459164 L07592 at-2	
388 Lung	nng		0.4360034	0.353074	0.22441469 L07592 at	
389	nng	0.221295	0.4359591	0.352986	0.22426459 U25801_at	Tax1 binding protein mRNA, partial cds

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Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

390 Lung	0.2212361	361 0.4356104	0.352714	RC_A 0.22414272 17_at	3C_AA1286 7_at	RC_AA1286 EST: zl15d10.s1 Soares pregnant uterus NbHPU Homo sapiens 17_at cDNA clone 502003 3', mRNA sequence. (from Genbank)
391 Lung	0.2211314	314 0.4355704	0.352636	0.2241315 T55087_	တ	EST: yb45c08.r1 Homo sapiens cDNA clone 74126 5'. (from at Genbank)
392 Lung	0.2201063	0.4355692	0.352476	Α 0.22397614 t	\A364267_a	AA364267_a EST: EST74873 Pineal gland II Homo sapiens cDNA 5' end, mRNA t sequence. (from Genbank)
393 Lung	0.2199532	532 0.4354602	0.352393	0.22389945 t	D83017_s_a t	Nel-related protein
394 Lung	0.2196524	524 0 4352692	0.352348	RC_A	RC_AA4221	EST: zv28g12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
395 Lung	0.2196019			0.22361091 W28763 at	V28763 at	Homo saniens KIAA0431 mRNA partial cds
396 Lung	0.2193915	15 0.4348034	0.352102	RC_A 0.22356348 54_at	RC_AA0172 54 at	EST: ze52b08.s1 Soares retina N2b4HR Homo sapiens cDNA clone
397 Lung	0.21907	0.2190742 0.4344841	0.352101	0.22330593 Y00443	700443 at	Profamine 1
398 Lung	0.21904	0.2190497 0.4342092	0.351846	0.22316453 U46689	146689 at	Microsomal aldehyde dehydrogenase (ALD10) mRNA
399 Lund	0.2181691	191 0 43/1/150	0.354690) 1	U26446_s_a	
P. I.	11.0	- 1	6001000	1 COSS 777.0	00000	Protoporphyrinogen oxidase
400 Lung	0.2181218	118 0.4339353	0.351536	0.22288755 79	79 at	Selenium binding protein 1
401 Lung	0.2178215	15 0.4337802	0.351477	X85116 0.22280458 1 s at	X85116_ma 1 s at	Epb72 dene exon 1
402 l und	0.2477523	73 0 433364B	0.384400	X	X56411_ma	
8.51	0.4.1.4.0		0.331422	0.22203434 1 at	at	ADH4 gene for class II alcohol dehydrogenase (pi subunit), exon 1
403 Lung	0.2172694	94 0.4333493	0.351059	A 0.2224586 t	A504384_a	AA504384_a IMAGE:825218 5' similar to contains element MIR repetitive element ;, mRNA sequence, (from Genbank)
404 Lung	0.2167519	19 0.4331934	0.351059	RC_A 0.22227941 60 at	A6090	EST: af10g04.s1 Soares testis NHT Homo sapiens cDNA clone 1031286 3', mRNA sequence. (from Genhank)
405 Lung	0.21650	0.2165043 0.4331761	0.350608	0.22222474 W25933	V25933 at	EST: 15b2 Human retina cDNA randomly primed sublibrary Homo
406 Lung	0.21637	0.2163794 0.4327171	0.3506	0.2220807 U40434	at c	Pre-pro-medakaryocyte notentiating factor
407 Lung	0.2160962	62 0.4327111	0.350465	0.22189234 57 at	40211	EST: ze65d11.s1 Soares retina N2b4HR Homo sapiens cDNA clone 363861.31 mRNA sequence (from Genbank)
408 Lung	0.2158367	67 0.4323317	0.350414	0.22180302 99	14065	EST: zv15a07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753684 3', mRNA sequence (from Genhank)
409 Lung	0.2158337	37 0.4322483	0.349979	A 0.22170478t	AA028976_a	EST: zk11a03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470188 5" mRNA seri ience (from Ganbank)
410 Lung	0.2156631	31 0.4319767	0.349961	0.22155166 Z33905_at		43kD acetylcholine receptor-associated protein (Rapsyn)
411 Lung	0.2156629	29 0.4319547	0.349961	0.22126713	25878_s_at	0.22126713 L25878_s_at EPHX1 Epoxide hydrolase 1, microsomal (xenobiotic)

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				AA310301_a	
412 Lung	0.2154811		Ì	0.22112909 t	KIAA0331 gene product
413 Lung	0.2153825	5 0.4317125	0.349745	0.22102222 U80811_at	Lysophosphatidic acid receptor homolog mRNA
				AA442383_a	
414 Lung	0.2149317	7 0.4316894	0.349359	0.22088535 t	758227 5', mRNA sequence. (from Genbank)
415 Lung	0.2144865	5 0.431473	0.349329	RC_D60272 0.22075154 i at	EST: Human fetal brain cDNA 3'-end GEN-095A07, mRNA sequence. (from Genbank)
					AA452428 a EST: zx15g01.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
416 Lung	0.2142058	3 0.431373	0.349289	0.22066022 t	clone 786576 5', mRNA sequence. (from Genbank)
147	0.9440677		0,70,70	D38163_s_a	
417 Lung	0.2 1403/1	0.4313075	0.349188	0.22053619 t-2	Collagen, type XIX, alpha 1
418 Lung	0.2140577	0.4312895	0.349178	D38163_s_a 0.22047408 t	COL19A1 Collagen, type XIX, alpha 1
					AA365742_s EST: EST76593 Pineal gland II Homo sapiens cDNA 5' end, mRNA
419 Lung	0.213926	0.4310879	0.349085	0.22033271 _at	sequence. (from Genbank)
420 Lung	0.2138369	0.4310526	0.348985	RC_AA1478 0,22024357 84_at	EST: zl50b04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505327 3', mRNA sequence. (from Genbank)
	1			RC_AA2365	
4Z1 Lung	0.213/4/	0.4309248	0.348899	0.22010231 33_s_at	Ecotropic viral integration site 1
422 Lung	0.2131875	0.4308415	0.348601	X57809_s_a 0.21998385 t	IGL@ Immunoalobulin lambda licht chain
423 Lung	0.2128338	3 0.4306715	0.348535	0.2198807 L42583_f_at	0.2198807 L42583 f at KERATIN, TYPE II CYTOSKELETAL 6D
				RC_AA6096	RC_AA6096 EST: af16b03.s1 Soares testis NHT Homo sapiens cDNA clone
424 Lung	0.2124133	0.430651	0.34851	0.21979778 50 s at	1031789 3', mRNA sequence. (from Genbank)
				M91368_s_a	
425 Lung	0.2120543	0.4305704	0.348472	0.219668 t	
				RC_AA1868	EST: zp73h02.s1 Stratagene HeLa cell s3 937216 Homo sapiens
426 Lung	0.2119022	0.430404	0.348394	0.21951333 04 at	cDNA clone 625875 3', mRNA sequence. (from Genbank)
1					EST: yw36a03.r1 Homo sapiens cDNA clone 254284 5'. (from
427 Lung	0.2117596	0.4303828	0.348296	0.21937673 N75274 at	Genbank)
428 Lind	0.2400002	0 4202400	0.00000	RC_AA5214	EST: aa69e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
120 callg	0.2 109902	- 1	1	0.2 1920320 34 at	IMAGE:826206 3, mKNA sequence. (from Genbank)
429 Lung	0.2103204	0.4303102	0.34806		EST: ZUTSCTTST Soares tests NHT Homo saptens cunA cione 731732 3", mRNA sequence, (from Genbank)
				RC_AA4602	EST: zx67a02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
430 Lung	0.2102232		0.347818	0.21889462 21 at	clone 796490 3', mRNA sequence. (from Genbank)
431 Lung	0.2101254	0.4299512	0.347725	0.21885294 U46499 at	GLUTATHIONE S-TRANSFERASE, MICROSOMAL
432 Lung	0.2099159	0.4297647	0.347623	HG4058- 0.2187152 HT4328 at	Oncogene Amt1-Evi-1, Fusion Activated
			-	Actual Commence of the Commenc	

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433 Lung	0.2097635	5 0.4295103	0.347362	0.218626511t	M31516_s_a t	M31516_s_a DAF Decay accelerating factor for complement (CD55, Cromer blood t
434 Lung	0.2097511	0.429289	0	0.21849224 U78294 at	U78294 at	Arachidonate 15-linoxvoenase second type
i C	1				RC_AA1578	
435 Lung	0.209544	0.4290964	0	0.2183921 14_at	14_at	clone 588917 3', mRNA sequence, (from Genbank)
436 Lung	0.2095305	0.2095305 0.4289351	0.347231	0.21836402 M95740_at	M95740_at	
437 1122	0.000.400.0				M10321_s_a	
437 LUIIG	0.2094368	0.428/938	0.347176	0.21822181 t		
438 Lung	0.2090187	0.4287123	0.346952	RC 0.21810547 71	RC_AA2917	EST: zt45g06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
					11/2	EST: 2x82a03.s1 Soares overy filmor NHHOT Homo serviews Chris
439 Lung	0.2082064	0.428611	0.346904	0.2179941 89_at	89_at	clone 810220 3', mRNA sequence. (from Genbank)
440 Lung	0.2078301	0.4284413	0.34687	RC 0.21785095 46	RC_AA4180 46 at	EST: zv97f10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 767755 3' mRNA segitance (from Ganhank)
441 Lung	0.2068907	0.4283747	0.346675	RC_A	RC_AA2279	EST: zr56a07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
>		- 1		0.5111.5000	20 al	50/380 3, mKNA sequence. (from Genbank)
442 Lung	0.2068767	0.4283747	0.346674	0.217593331	4A085138_a	AA085138 a clone 546132 5' similar to gb:M34539 FK506-BINDING PROTEIN (HI IMAN): mRNA certinage (from Contral)
443 Lung	0.2061588	0.4282722	0.346576	HG3962- 0.21742108 HT4232	HG3962- HT4232 at	Sialvitransferase Stx
444 Lung	0.2059874	0.428027	0.346462	HG4749	7	
			70101010	0.0101212	977	Calminine Calcium-Binding Protein, Mitochondrial
445 Lung	0.2056971	0.4277479	0.346384	0.21727546 45_at	+00+0	Homo sapiens KIAA0439 mRNA, partial cds
						RAGE gene (receptor for advanced glycosylation end products) extracted from Human HLA class III region containing NOTCH4 gene.
					U89336 cds	partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced rikingeviation and products (DACE) and
446 Lung	0.2056753	0	0.346345	0.21713229 3 at		ര്ഷ്ണാര്ഷ് ളൂറ്റോഴുമ്പാല ലാല് പ്രവര്ധം (സ്പ്രാട്ട്) ഇല്ലം, and b unidentified cds. complete sequence
447 Lung	0.2055376	0.427707	0.345998	0.21705247 D87937	37_at	Alpha(1,2)fucosyltransferase, 5'UTR partial seguence
448 Lung	0.2055319	0.4276571	0.345845	RC 0.21698031 61	_AA0545 at	EST: zk83h03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 4894613' mRNA seguence (from Caphaga)
						EST: Homo sapiens thymus mRNA (randomly primed normalized)
449 LUNG	0.2052905	0.4274889	0.345738	0.21689378 L44367	्यं	single-pass sequence, mRNA sequence. (from Genbank)
450 Lung	0.2050517	0.4274542	0.345642	H 0.21673831 t		EST: yr75e04.r1 Homo sapiens cDNA clone 211134 5'. (from Genbank)
451 Lung	0.2050112	0.4274464	0.345535	0.21656497 1 at-2	7_ma	Homeo box dene expressed in FS cells: Rathke nouch homeo hox
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452|Lung

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453 Lung 454 Lung

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0.2048765 | 0.4271686

455|Lung

0,34491

0.2047669 0.4269871

457|Lung

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459 Lung

458 Lung

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0.344231

0.2032563 0.4263962

0.2034993 0.4264408

461 Lung 462 Lung

460 Lung

0.345007

0.2048381 0.4270829

456|Lung

U654 0.21644798 1_at	U65437_ma 1_at	Homeodomain-containing protein (HANF) gene, partial cds
RC 0.2162795 ₅₃	RC_AA4960 53_at	EST: zv72f05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759201 3' similar to SW:RSP5_YEAST P39940 RSP5 PROTEIN: mRNA sequence. (from Genbank)
0.21620359 U89995	U89995_at	DNA binding protein FKHL15 (FKHL15) mRNA
0.21611412	U89995 at-2	0.21611412 U89995 at-2 Forkhead (Drosonhila)-like 15
0.21604095	AA112799_a t	AA112799_a EST: zn62h02.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 562803 5', mRNA sequence. (from Genbank)
RC_A 0.21596743 16 at	RC_AA4494 16_at	RC_AA4494 EST: zx05a09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 16 at clone 785560 3', mRNA sequence. (from Genbank)
RC_A 0.21581881 06 at	RC_AA4248 06_at	Biphenyl hydrolase-like (serine hydrolase)
0.21564978 Y08134	Y08134_at	ASM-like phosphodiesterase 3b
0.21552551	Y08134_at-2	0.21552551 Y08134_at-2 H.sapiens mRNA for ASM-like phosphodiesterase 3b
0.21540318 D55696	D55696_at	Cysteine protease
0.2152159 L42354	L42354_at	(clone 48ES4) mRNA fragment
	RC_AA2349	EST: zr50b04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
0.21512045 76_at	76_at	666799 3', mRNA sequence. (from Genbank)
HG1078-		Section 1 Section 100 MOVED
0.2 1304333	٦	EST:40440 of St-de-center (1100-2000) 11
0.21492204 51_f_at	2243	EST: ZT1ZT1Z.ST Stratagene NNT neuron (#937233) Homo sapiens CDNA clone 648623 3', mRNA sequence. (from Genbank)
		EST: EST17092 Aorta endothelial cells, TNF alpha-treated Homo
RC_AA: 0.21481012 44 f at	RC_AA3043 44 f at	RC_AA3043 sapiens cDNA 3' end similar to EST containing Alu repeat, mRNA 44 f at sequence (from Genhank)
		Insulin-like growth factor binding protein-2 Ihuman, placenta.
0.2146979 S37730_s	S37730_s_at	at Genomic, 1342 nt, segment 4 of 41
	RC_AA4787	RC_AA4787 EST: zv14d09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
0.21461599 26 at	26 at	753617 3', mRNA sequence. (from Genbank)
0 21446498		U27328_s_a Fucosyltransferase 3 (galactoside 3(4)-L-fucosyltransferase, Lewis
0.21434529 U50330 at	U50330 at	BMP1 Bone morphogenetic protein 1
0.21422687 L11353	L11353_at	NF2 Neurofibromin 2 (bilateral acoustic neuroma)
0.21413274 IL4_at		No info for gene
0.2141196 U29091 at		Selenium-binding protein (hSBP) mRNA

0.343966

0.2025169 0.4262234

465 Lung

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464|Lung

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463|Lung

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466|Lung

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0.426129

0.2021588

467|Lung

	PHKG2 Phosphorylase kinase, gamma 2 (testis)	
-	606 at	
	0.34312 0.21393813 M31	
	0.34312	
	0.2014027 0.4250385	
-	0.2014027	

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Docket	No.: 2825.2020-002
Title:	Genetic Markers for Tumors
Invento	ors: Sridhar Ramaswamy, et al.

0.21381254 T61997 at 0.21372266 67 at RC_AA4056 0.213602 98 at 0.2135397 W29115 at 0.2135397 W29115 at 0.21345186 t 0.21345186 t 0.21345186 t 0.2128378 W88988 at 0.2128732 at 0.2128378 W86849 at 0.2128378 W86849 at 0.2128378 W86849 at 0.2128351 t at 0.2128378 W86849 at 0.2128351 t at 0.2128378 W86849 at 0.2128351 t at 0.2128378 W86849 at 0.2128351 t at 0.21283581 L22647 s at 0.21233281 L22647 s at 0.21233281 L22647 s at 0.2128958 X99977 at 0.2128958 X99977 at 0.2128958 X99977 at 0.212853								
0.2013092 0.424717 0.342651 0.21372266 67_at	475	nng.	0.2013618			0.21381254	T61997_at	EST: yb97a01.r1 Homo sapiens cDNA clone 79080 5'. (from Genbank)
0.2001409 0.4244892 0.342415 0.213602 RC_AA4056 0.2008185 0.424482 0.342406 0.2135397 W29115_at 0.2000599 0.4243616 0.342179 0.21345186 t AA279513_a 0.1998813 0.4241411 0.342084 0.21336243 W28988_at 0.1998655 0.424125 0.342075 0.21336243 W28988_at 0.1998655 0.424125 0.342075 0.21336243 W28988_at 0.1998655 0.424125 0.342075 0.21239781 M86849_at 0.1998655 0.4239705 0.341905 0.21239781 M86849_at 0.1998727 0.4239705 0.341905 0.21283978 M86849_at 10.1998727 0.4239786 0.341905 0.21245435 33_at 10.1987727 0.4234348 0.341777 0.21223628 X99977_at 0.1961918 0.4234348 0.341777 0.21223628 X99977_at 0.1972662 0.42342468 0.341715 0.21220771 57_at 0.1977862 0.42342468 0.341331 0.21128989 40_at 0.1977862 0.4227898 0.341321 0.212307762 J02876_at 0.1972662 0.4227898 0.341321 0.2118858 X02612_at 0.1964423 0.4227419 0.341281 0.2118858 X02612_at 0.1964423 0.4227419 0.341161 0.21168528 t U10099_s_at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21168528 t at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.341156 0.21165162 Y08417 s at 0.1958027 0.4227415 0.21165162 Y08417 s at 0.1958027 0.4227415 0.21165162 Y08417 s at 0.1958027 0.4224488 0.4227415 0.421165162 Y08417 s at 0.1958027 0.4224488 0.42417 s at 0.1958027 0.4224488 0.42417 s at 0.1958027 0.42244	476	nng.	0.2013092	ł	0.342651	0.21372266	RC_AA4436 67_at	EST: zw86b07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 783829 3', mRNA sequence, (from Genbank)
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0.1998813 0.4241411 0.342084 0.21318842 20 at M14123_xpt 0.1996655 0.424125 0.342075 0.21297514_at 0.1996655 0.4239705 0.341954 0.21297514_at 0.1993467 0.4239705 0.341954 0.21283978 M36849_at 0.1990886 0.4238464 0.341905 0.212646411_s_at 0.1987727 0.4236789 0.341905 0.21245435 33_at 0.198716 0.42348 0.341777 0.21233281_L22647_s_at 0.1972662 0.423468 0.34177 0.21229628 X99977_at 0.1972662 0.423857 0.341715 0.2122071_57_at 0.1972662 0.422857 0.341715 0.212207762_J02876_at 0.1972662 0.422867 0.341331 0.21199898_40_at 0.1969504 0.4227419 0.341381 0.2118858 X02612_at 0.1964423 0.4227419 0.341161 0.21168528 t 0.10099_s_a 0.1958027 0.4227415 0.3411561 0.21168528 t	480	nng	0.1999584		0.342091	0.21336243	W28988 at	EST: 54f5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
0.1996655	481	nng	0.1998813	1	0.342084	0.21318842	RC_AA4238 20_at	EST: zv33f03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755453 3', mRNA sequence, (from Genbank)
0.1993467 0.4239705 0.341954 0.21283978 M86849 at RC_D19672 at RC_D19672 at RC_D19672 at RC_D19672 at RC_D19672 at RC_D19672 at RC_D19672 at RC_D19672 at RC_D19672 at RC_D196727 0.4236789 0.341905 0.21264641 1 s at RC_D44771 0.1987727 0.4236789 0.341905 0.21245435 33 at 0.1987727 0.4233534 0.341777 0.21233281 L22647 s at 0.1981918 0.4233534 0.341777 0.21233281 L22647 s at 0.1977862 0.4233534 0.341777 0.21233281 L22647 s at 0.1977862 0.423368 0.341715 0.21229628 X99977 at RC_DA4188 0.1977862 0.423857 0.341331 0.21199898 40 at 0.1969504 0.4227888 0.341322 0.2119403 X16832 at 0.1968705 0.4227419 0.341361 0.2118858 X02612 at 0.1968423 0.4227419 0.341161 0.21168528 t 0.1958027 0.341156 0.21165162 Y08417 s at	482	nng.	0.1996655			0.2129751	M14123_xpt 4_at	Neutral protease large subunit from Human endogenous retrovirus HERV-K10./ntvoe=DNA /annot=CDS
0.1991327 0.4239197 0.341923 0.2127732 at K02882_cds 0.1990886 0.4238464 0.341905 0.212646411 s at RC_AA4771 0.1987727 0.4236789 0.341905 0.21245435 33_at RC_AA4771 0.1981918 0.4233534 0.341777 0.21233281_L22647_s_at 0.1987862 0.4232468 0.341777 0.21233281_L22647_s_at 0.1977862 0.4232468 0.341777 0.21229628 X99977_at 0.1972662 0.4232468 0.341715 0.2120971_57_at 0.1972662 0.422857 0.341331 0.21199898 40_at 0.1968705 0.4227419 0.341381 0.21198898 40_at 0.1968705 0.4227419 0.341281 0.2118858 X02612_at 0.1964423 0.4227419 0.341161 0.21168528 t	483	ung.	0.1993467	0.4239705	0.341954	0.21283978	M86849 at	Connexin 26 (GJB2) mRNA
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0.1987727 0.4236789 0.341905 0.21245435 33_at 0.1982116 0.4234348 0.341777 0.21233281 L22647 s_at 0.1981918 0.4234348 0.341777 0.21233281 L22647 s_at 0.1977862 0.4232468 0.341715 0.2122071 57_at 0.1976121 0.423027 0.341614 0.21207762 J02876_at 0.1972662 0.422857 0.341614 0.21207762 J02876_at 0.1969504 0.4227888 0.341331 0.21199898 40_at 0.1964423 0.4227419 0.341281 0.2118858 X02612_at 0.1964423 0.4227419 0.341161 0.21168528 t	485	nng.	0.1990886	1		0.21264641	K02882_cds 1 s at	IGHD gene (immunoglobulin delta-chain) extracted from Human germline IaD chain gene. C-region. C-delta-1 domain
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0.1981918 0.4233534 0.34173 0.21229628 X99977_at 0.1977862 0.4232468 0.341715 0.2122071 57_at 0.1972662 0.422857 0.341331 0.21199898 40_at 0.1968705 0.4227419 0.341381 0.2118858 X02612_at 0.1968423 0.4227419 0.341161 0.21168528 t 0.1958027 0.4226115 0.341156 0.21165162 Y08417 s_at	487	nng.	0.1982116			0.21233281	S	at Prostaglandin E receptor 1 (subtype EP1), 42kD
0.1977862 0.4232468 0.341715 0.2122071 F7_at 0.1976121 0.423027 0.341614 0.212207762 J02876_at 0.1972662 0.422857 0.341331 0.21199898 40_at 0.1968504 0.4227888 0.341322 0.21199898 40_at 0.1968705 0.4227419 0.341281 0.2118858 X02612_at 0.1964423 0.4227419 0.341161 0.21168528 t 0.1958027 0.4226115 0.341156 0.21165162 Y08417 s at	488	gun.	0.1981918		0.34173	0.21229628	ਲ	H.sapiens ARS gene, component B
0.1972662 0.422857 0.341614 0.21207762 J02876 at RC_AA4282	489	nng.	0.1977862			0.2122071	RC_AA4188 57 at	0.212207157 at 767858 3' mRNA sequence (from Genhank)
0.1972662 0.422857 0.341331 0.21199898 RC_AA4282 0.1969504 0.4227888 0.341322 0.2119403 X16832 at 0.1968705 0.4227419 0.341281 0.2118858 X02612 at 0.1964423 0.4227419 0.341161 0.21168528 t 0.1958027 0.4226115 0.341156 0.21165162 Y08417 s at	4901	nng.	0.1976121			0.21207762	J02876_at	FOLATE RECEPTOR BETA PRECURSOR
0.1968705 0.4227419 0.341281 0.2118858 X02612 at	491	nng.	0.1972662			0.21199898	RC_AA4282 40 at	EST: zw51d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773575 31, mRNA sequence, (from Genbank)
0.1968705 0.4227419 0.341281 0.2118858 X02612 at 0.1964423 0.4227419 0.341161 0.21168528 t 0.1958027 0.4226115 0.341156 0.21165162 Y08417 s at	492	nng.	0.1969504		0.341322	0.2119403	1 1	CTSH Cathepsin H
0.1964423 0.4227419 0.341161 0.21168528 t 0.1958027 0.4226115 0.341156 0.21165162 Y08417 s at	493	gun	0.1968705		0.341281	0.2118858	X02612_at	CYP1A1 Cytochrome P450, subfamily I (aromatic compound- inducible), polypeptide 1
0.1958027 0.4226115 0.341156 0.21165162 708417	494	gun.	0.1964423		0.341161	0.21168528	U10099_s_a t	ZÓNA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR
	495	nng	0.1958027	0.4226115	0.341156	0.21165162		s_at CHRNB3 Cholinergic receptor, nicotinic, beta polypeptide 3

496 Lung	0.1954674			0.21149278	A2165	EST: zq94e07.s1 Stratagene NT2 neuronal precursor 937230 Homo
497 Lung	0.1951269	9 0.4224565	0.3			SPRR1B Small proline-rich protein 1B (cornifin)
498 Lung	0.1950906	6 0.422343	0.340617	RC_A 0.21125698 45 at	A2518	EST: zs09e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
499 Lung	0.1949839	0		0.21116346	A0858	Home savient close 24658 mDMA common
500 1 000	0 40 47	1				ייסיוס מקומום בייססס וווראיא אפקומפונפ
Fully	0.1347.046	0.4217040	0.340486	0.21103089 H8/6/1	at	Yw15d02.r1 Homo sapiens cDNA clone 252291 5'. (from Genbank)
501 Lung	0.1946286	0.4215694	0.340345	0.21094948	78129_a	AA478129_a clone 740656 5' similar to SW:BI3_MOUSE P28662 BRAIN PROTEIN t 13;, mRNA sequence. (from Genbank)
						Homo sapiens DNA sequence from PAC 262D12 on chromosome
						1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin,
				711		Neuronectin, Myotendinous antigen)-LIKE gene and a
				(mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene
502 Lung	0.1945925	0.4215353	0.340341	0.21076483 62_at	A0052	preceeded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs
503 [110.0	0 1045424	0.4045004	. 0	AAO	AA099995_a	Zm65e06.r1 Stratagene fibroblast (#937212) Homo sapiens cDNA
66	0.1343421		0.340195	U.Z1067597 t		clone 530530 5', mRNA sequence. (from Genbank)
504 1100	0 1040130	0.4243465	0 0 0 0 0 0	RC /	A2566	EST: zr86h05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
505 1 1100	0.1010100	0.404040		0.0104/02/10		6826173, mKNA sequence. (from Genbank)
film-	0.1930102	0.1930102 0.4213312	0.340048	0.21035962 U64871 at		G protein-coupled receptor GPR-NGA gene
506 Lung	0.1930866	0.4210407	0.340033	RC_A 0.21014266 36_at	A0451	EST: zk66e05.s1 Soares pregnant uterus NbHPU Homo sapiens
		1	2000	00 00711013:0	7001	CUNA CIVITÉ 467 808 3, MKINA Sequence. (from Genbank)
507 Lung	0.1927703	0.4209378	0.339926	RC_A 0.21005228 73_at	A4065	EST: zv11b09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753305 3', mRNA sequence. (from Genbank)
508 Lung	0.1927402	0.420889	0.339847	U510 0.20998116 t	U51010_s_a t	Nicotinamide N-methyltransferase gene exon 1 and 5 flanking region
509 Luna	0.192631	0.420854	0 330807	0 20082015 t	AA402121_a	EST: zt67e02.r1 Soares testis NHT Homo sapiens cDNA clone
0	0.1020	1	0.333021		1	72/418 5, mKNA sequence. (from Genbank)
510 Lung	0.1925233	0.4208244	0.339741	0.2096795 70_at		EST: zt05e04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 376062 3', mRNA sequence. (from Genbank)
511 Lung	0.1922924	0.4208244	0.339713	0.20962334 59 at	A6211	EST: af61g01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 1046544 31, mRNA sequence. (from Genbank)
512 Lung	0.1921844	0.4208062	0.339543	0.2095446.08 at	A2623	EST: zr70g10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
						EST: yi82b05.r1 Homo sapiens cDNA clone 145713 5', (from
513 Lung	0.1919594	0.1919594 0.4204926	0,339518	0.20937859 R78309	at	Genbank)
						A CONTRACTOR OF THE PROPERTY O

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	7 2 4 C	0.4202072	0.990467	RC_AA3938	EST: zv64c05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
514 Lung	0.1915505	0.4203677	0.333431	0.20323030 os at	KERATIN TYPE II CYTOSKELETAL 6D
515 Lung	0.1912515	0.1912515 0.4205647	0.333410	0.20324449 L00203 gt	
516 Lung	0.1910615	0.4202727	0.33931	0.20910385 15_at	
517 l ma	0 19082	0.4200797	0.339181	0.20906146 3 s at	PTHLH gene (parathyroid hormone-like protein A) extracted from Human parathyroid hormone-like protein (PLP) gene
5	000000000000000000000000000000000000000	1	990000	0.2000320041/04448 f at	O ODGODOGALVOLES & AF VEDATIN TYDE II CYTOSKEI ETAL BD
518 Lung	0.1908086	0.4189097	0.333030	0.20033004 VOLUTIO 1 dt	RC. AA4597 Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA,
519 Lung	0.1906331	0.4197833	0.338948	0.20886692 78 s at	complete cds
200	0.4004682	0.4405034	0 33871	RC_AA2846	EST: zt24a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 714026 3' mRNA sequence. (from Genbank)
filin azc	0.1301002		70000		
521 Lung	0.1897348	0.4194072	0.338614	0.2086687 at	
522 Lung	0.1896246	0.4193492	0.338557	0.20855269 M92449_at	LTR mRNA, 3' end of coding region and 3' flank
		1			Human hindlimb expressed homeobox protein backfoot (Bft) mRNA,
523 Lung	0.1895064	- 1	0.338511	0.20846142 U70370_at-2 complete cds	complete cds
524 Lung	0.1895064	0.4192346	0.338359	0.20838776 U70370 at	Hindlimb expressed homeobox protein backloot (Bit) mkNA
					EST: zn99g10.r1 Stratagene colon (#93/204) Homo sapiens cDNA
525 Lina	0 1894303	0 4190782	0.338218	0.208264981	sequence, (from Genbank)
6				D31628 s a	+
526 Luna	0.1891232	0.4189568	0.338168	0.20808844 t	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE
				RC_AA4822	
527 Lung	0.1889508	3 0.418781	0.33799	0.20796324 24_f_at	clone 840868 3', mRNA sequence. (from Genbank)
528 Lina	0.1886343	0.4187364	0.33796	RC_AA2932 0 20783304 66 at	EST: zt28b08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 714423 3', mRNA sequence, (from Genbank)
220		1		X60382_ma	
529 Lund	0.188535	5 0.418455	0.337843	0.20773321 1 at	COL10A1 gene for collagen (alpha-1 type X)
					EST: zv34e11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755564 3' similar to SW:PTN2_RAT P35233 PROTEIN-
C	70070	700000000000000000000000000000000000000	77774	RC_AA4190	
Bun nsc	0.1004340	0 4464404	0.337677		DD4 homolog mDNA 34 ITR radion
531 Lung	0.18/921	1 0.4181424	0.33/63/	0.20/33200 03043/ at	אירו ווטווטוטן ווויאין ט ט ואירוווט טוטוווטון אירו
	0 4075046	0 4470054	783280	AA059489_a	EST: zl96b08.r1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone 512439 5', mRNA sequence, (from Genbank)
332 LUIIY	0.101.321	1			
533 Lung	0.187520	0.1875204 0.4178397	0.337493	0.20733769 06 at	728054 3', mRNA sequence. (from Genbank)

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534 Lung	0.1874888	0.1874888 0.4178062	0.337434	0.20723632 U92971_at	Protease-activated receptor 3 (PAR3) mRNA
535 Lung	0.1874888	0.4177079	0.337288	0.2071424 U92971_at-2	Coagulation factor II (thrombin) receptor-like 2
				AA115605_a	
536 Lung	0.1870525	0.417677	0.337274	0.20709419 t	HEAT SHOCK 70 KD PROTEIN 1
537 Lung	0.1865084	0.4173896	0.337251	0.20700532 D49742 at	HGF activator like protein
538 Lung	0.1864699		0.337199	0.20678568 U79258 at	Clone 23732 mRNA, partial cds
539 Lung	0.1863133	0.4168765	0.337039	0.20670204 N78005_at	Homo sapiens SRp46 splicing factor retropseudogene mRNA
				AA250804_a	
540 Lung	0.1862135	0.4167521	0.336992	0.20656496 t	IMAGE:684360 5', mRNA sequence, (from Genbank)
541 Lung	0.186195	0.4166836	0.336973	RC_AA2363 0.2064239 56 at	Zr54a11.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:667196 31 mRNA segrence
542 Lung	0.1859639	0.4165951	0.336705	0.20635933 D31417 at	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)
		1		X85781_s_a	
543 Lung	0.1857352	0.4163893	0.336634	0.20627302 t	NOS2 gene, exon 27
544 Lung	0.1855199	0.4163481	0.336564	0.20614211 R46311_at	EST: yj53f04.r1 Homo sapiens cDNA clone 152479 5'. (from Genbank)
····				RC AA4303	EST: zw23c04.s1 Soares ovary furnor NbHOT Homo sapiens cDNA clone 770118 3' similar to TR:E243387 E243387 ORF YGR038W
545 Lung	0.185402	0.416087	0.336356	0.20605162 88_at	mRNA sequence. (from Genbank)
546 1 1100	0.4852733	0.4480094	0 238120	RC_AA4460	
547 Lung	0.1032733		0.330138	0.2059/322 2/ S at	Early growth response 2 (Krox-20 (Drosophila) homolog)
o41 Luiig	0.1048999		0.330001	0.20589226 U03056 at	Hyaluronoglucosaminidase 1 (HYAL1) mRNA
548 Lung	0.1849384	0.4157496	0.335964	RC_AA0630 0.20574966 68_at	EST: zf67e04.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 382014 31 mRNA secuence (from Ganhank)
549 Lung	0.184717	0.4155971	0.335957	0.20566192 41 at	EST: zr49a12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666718 3', mRNA sequence. (from Genbank)
		1		RC_AA1612	
550 Lung	0.1845714	0.4154634	0.335825	0.20564336 92_s_at	Interferon, alpha-inducible protein 27
551 Lina	0 1843069	0.4154162	0 335604	0.205E074+	
552 Lung	0.1839211	1	0.335685	0.205439781t	STS-billouing domain gloralnic actor-for protein EST: zw51h07.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773629 5', mRNA sequence, (from Genbank)
553 Lung	0.1837888	0.4150792	0.33558	AB000381_s 0.20533098 at	DNA for GPI-anchored molecule-like protein
757 June	0.1837856	0.4450003	0 325/00	RC_AA2349	RC_AA2349 669570 3' similar to contains Alu repetitive element;, mRNA
304 Luiig	0.1037030		0.333402	0.20313313 Z3 at	sequence, (from Genbank)

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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The same of	0.1792251	0.4130711	0.333878	0.20336556 t		IPL (IPL) mRNA
0.1	0.1789774	0.4130512	0.333833	RC_A 0.20329963 28_at	RC_AA2321 28_at	Sarcoglycan, epsilon
0.1	0.1788631	0.4129976	0.333741	0.20321542 20	RC_AA1957 20_at	33 kDa transcriptional co-activator
0.1	0.1786308	0.4128208	0.333676	0.20308189+	U41163_s_a	Creatine franconter (CL CGA40) working ode
0.1	0.1784864			0.20299609 J03258 at		VDR Vitamin D (1.25- dihydroxyvitamin D3) recentor
		1			3C_AA0228	RC_AA0228 EST: ze71c10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
0.7	0.1784352	0.4125812	0.333453	0.20295717 84_at	34_at	clone 364434 3', mRNA sequence. (from Genbank)
0.1	0.1779975	0.4124382	0.333382	RC_A 0.20284432 40_at	RC_AA1499 40_at	GLUT1 C-terminal binding protein
- 3	270470		0,000	1)545_f	EST: zx89d12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
5 0	0.17.77500	0.4124382	0.333313	0.2027/34		clone 810935 5', mRNA sequence. (from Genbank)
2 2	000111		0.333262	0.202/19/ X51/5/ at	(51/5/ at	HSPA6 Heat shock 70kD protein 6 (HSP70B')
0.7	0.1777500	0.4123559	0.333143	0.20251761 X51757_at-2	(51757_at-2	Heat shock 70kD protein 6 (HSP70B')
0.1	775776	0.1775776 0.4123455	0.333082	RC_A 0.20244415 68_at	२८_AA6091 १8_at	RC_AA6091 EST: af12a10.s1 Soares testis NHT Homo sapiens cDNA clone 68 at 1031418 3', mRNA sequence. (from Genbank)
0.1	0,1773938	0.4123455	0.332971	RC_A 0.2023239 32_at	3C_AA1565 32_at	RC_AA1565 Homo sapiens interferon regulatory factor 6 (IRF6) mRNA, complete 32 at cds
0.1	773851	0.1773851 0.4122714	0.332968	0.20230734 29_at	A0558	EST: zf21d10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 377587 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)
0.1	0.1770672	0.4121855	0.332893	0.2021531	102871_s_at	0.2021531 J02871_s_at CYP4B1 Cytochrome P450 IVB1
0.1	0.1769539	0.4120433	0.332842	RC_A/ 0.20204392 62_at	3C_AA2435 i2_at	RC_AA2435 EST: zs15h06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 62_at IMAGE:685307 3', mRNA sequence. (from Genbank)
0	0 1767123	0.411992	0 332838	RC 0 20108 E4E 31	v6091	EST: af11f03.s1 Soares testis NHT Homo sapiens cDNA clone
5	27 10 1	0.411932	0.0260.0	0.20130343	אטבטע	1031337 3; mKNA sequence, (from Genbank)
0.1	0.1766792	0.4119014	0.332786	0.20189731 30	AAZ581 at	EST: zs35f03.s1 NCT_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:687197 3', mRNA sequence. (from Genbank)
0.1	0.1765536	0.4116339	0.332738	0.20184301 N	/62896 i at	0.20184301 M62896 i at region. (from Genbank)
ć	700327	1,000	1,0000	4	A094752_a	AA094752_a Protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform
-	0.170591	0.4115647	0.332615	0.201/5259		(calcineurin A beta)
0.1	0.1758538	0.4114534	0.332574	0.20171952 U32114 at		Caveolin-2 mRNA
0.1	0.1756858	0.4112209	0.332498	AFF; 0.20159934 3_at	X-LysX-	AFFX-LysX-3_at (endogenous control)

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				Lysx-	
595 Lung	0.1756858		0.332317		AFFX-LysX-3_at (miscellaneous control - 11k chips)
596 Lung	0.1756189	0.4108433	0.332238	0.20147029 D53639_at	Ribosomal protein S26
				AA074407_a	AA074407_a EST: zm15c08.r1 Stratagene pancreas (#937208) Homo sapiens
597 Lung	0.1754493		0.332225	0.2012877 t	cDNA clone 525710 5', mRNA sequence. (from Genbank)
598 Lung	0.1751292	0.4106699	0.332118	0.20117259 X05409_at	ALDH2 Aldehyde dehydrogenase 2, mitochondrial
				DC AA2241	ECT: 7rd EdOE of Chrotonona NITO national produces 027230 Home
599 Lung	0.1751191	0.4106699	0.332109		sapiens cDNA clone 663465 3', mRNA sequence, (from Genbank)
				D20490	EST: Human HL60 3'directed Mbol cDNA, HUMGS01464, clone
600 Lung	0.1749851	0.4106589	0.331931		pm1439, mRNA sequence. (from Genbank)
601 Lung	0.1749773	0.4106361	0.331699	0.20100032 U34877_at	Biliverdin-IXalpha reductase mRNA
602 Lung	0.1746583	0.4105441	0.331498	M12963_s_a	ADH1 Alcohol dehydrogenase 1 (class I), albha polynebtide
)				RC_AA4178	EST: zv05f04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
603 Lung	0.1742481	0.4104374	0.331449	0.20081457 76_at	752767 3', mRNA sequence. (from Genbank)
804 Lina	0 174043	0.4403945	7001000	AA256220_a	AA256220 a EST: zr79b07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
605 Lung	0.17474		0.331397	T	od 1877 5, mknya sequence. (Irom Genbank)
000 Luig	0.17414171	0.4103045	0.951343		PMPZZ Peripheral myelin protein ZZ
ono rnuĝ	0.1741265	0.1741265 0.4102918	0.3312	077 at	Glucocorticoid receptor repression factor 1 (GRF-1) mRNA
607 Lung	0.1740455	0.4101519	0.331197	RC_AA4787 0.2004808 94 at	EST: zv20e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754200 3' mRNA sequence. (from Genhank)
				the state of the s	EST: yi75d09.r1 Homo sapiens cDNA clone 145073 5'. (from
608 Lung	0.174037	0.4101184	0.3311	0.20032713 R77382 at	Genbank)
-					Amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer
609 Lung	0.1740171	0.4100366	0.331065	0.2002879 W27334 at	disease)
610 Lung	0.1738587	0.4100316	0.330924	AA465601_a	AA465601_a EST: aa24h10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
611 Lung	0.1738566		0.330884	X56677 at	MYOD1 Myogenic factor 3
		1		RC_AA2343	EST: zr72a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
612 Lung	0.1736328	0.4098567	0.330859		668918 3', mRNA sequence. (from Genbank)
643	0 1795944		000000	_AA4614	EST: zx68b01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
610 Lung	0.175034		0.330803		Glone /95585 3, mRNA sequence. (from Genbank)
o 14 Lung	0.1730271	0.4097906	0.330/05		Inhibitor of growth 1-like
615 Luna	0.1729905	0.4097636	0.330516	0.19974774/40 at	High-mobility group (nonhistone chromosomal) protein 4
				U47011_cds	
616 Lung	0.172933	1	0.330497		Fibroblast growth tactor 8 (androgen-induced)
617 Lung	0.1727754	0.4096222	0.330496	2_at	Homo sapiens zinc finger protein mRNA, complete cds

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				R	C_AA1820	RC_AA1820 EST: zp62f10.s1 Stratagene endothelial cell 937223 Homo sapiens
618 Lung	0.1726794	0.4096209	0.330155	0.19945705 01	r at	cDNA clone 624811 3', mRNA sequence. (from Genbank)
61911 und	0.1726431	0.4095511	0.330045	A/ 0.19940549 t	AA024428_a F t	EST: ze/3e12.r1 Soares retal heart NbHH19W Homo sapiens cUNA clone 364654 5', mRNA sequence. (from Genbank)
620 Lind	0.172183	L	0.329832	0.19930793 t	X17644_s_a	GSPT1 G1 to S phase transition 1
621 Lund	0.1712534	1	0.329715	RC_AA4 0.19923551 18 s at	498	Human modulator recognition factor I (MRF-1) mRNA, 3' end
622 Lung	0.1710514		0.329715	0.19910565 76 at	A6095	KIAA0331 gene product
623 Lung	0.1710219	0.4093424	0.329587	0.19904129 R33301_at)1 at	EST: yh81g01.r1 Homo sapiens cDNA clone 136176 5' similar to contains MSR1 repetitive element ;. (from Genbank)
624 Lung	0.1709628	0.409292	0.329483	RC_A 0.19899122 35_at	A0567	KIAA0755 gene product
625 Lung	0.1709038	0.4091597	0.329393	X(0.19889487	68264_ma at	X68264_rna MUC18 gene (melanoma associated glycoprotein) extracted from 1_at H.sapiens MGF gene exons 1&2
626 Luna	0.1709003	0.4091567	0.329025	Al 0.1987667.t	AF003521_a	Jagged 2
627 Lung	0.1706247		0.328994	0.19872703 U95090	at	Chromosome 19 cosmid F19541
628 Lung	0.1706247	0.4090124	0.328987	0.19867331	95090_at-2	0.19867331 U95090_at-2 Homo sapiens chromosome 19 cosmid F19541
629 Luna	0.1705484	0.4088767	0.328945	RC_A 0_19856872_49_at	C_AA4497	RC_A44497 EST: zx07e10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 49 at Iclone 785802 3'. mRNA sequence. (from Genbank)
630 Lung	0.1705396	1	0.328934	RC_A 0.19843347 08 at	A4286	EST: zw69c09.s1 Soares testis NHT Homo sapiens cDNA clone 781456 3', mRNA sequence. (from Genbank)
631 Lina	0.1699309		0.328932	0.19835263	A5999	EST: ag28h10.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1090915.3' mRNA sequence. (from Genbank)
632 Lung	0.1697518		0.328778	ļ	13 at	Organic anion transporting polypeptide (OATP) mRNA
						EST: ze74h03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
633 Lung	0.1696738	0.4086568	0.328629	0.19810322 51 at	AU233	cione 304707 3 similar to contains OFK.t1 OFK repetitive element., mRNA sequence, (from Genbank)
				<u>x</u>	A1322	EST: zo06h05.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 566937 3' similar to SW:YBF5_YEAST P34220 HYPOTHETICAL 47.4 KD PROTEIN IN SHP1-SEC17 INTERGENIC
634 Lung	0.1695444	0	0.32833	0.19789805 39_at	g at	REGION.;, mRNA sequence. (from Genbank)
635 Lung	0.1693365	0.408468	0.32826	0.19780265 Z11793	11793 at	Selenoprotein P
636 Lung	0.1693141	0.408138	0.328115	RC 0.19769555 54_	RC_AA4314 54_at	EST: zw/0i01.s1 Soares tests NHT Homo saptens cDNA clone 781561 3', mRNA sequence. (from Genbank)

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al*.

FIG. 6E

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

637 Lung 638 Lung 639 Lung 640 Lung 641 Lung 642 Lung 643 Lung		0.1692346 (0.1691924 (0.1691511 0.168735 0.1679861 0.1678808 0.1678641		0.328104 0.328041 0.32799 0.327775 0.327494 0.327396	0.19753662 at 0.19753116 W58612 at 0.19753116 W58612 at 0.19733652 C01782 at 0.19730447 38 at RC_AA292 0.19723177 05 s at 0.19723177 5 s at 0.19723177 5 s at	319 f le constant de la constant de	13.9 f EST: ab15c03.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840868 5', mRNA sequence. (from Genbank) clone 840868 5', mRNA sequence. (from Genbank) clone 341054 5', mRNA sequence. (from Genbank) clone 341154 5', mRNA sequence. (from Genbank) clone 341154 5', mRNA sequence. (from Genbank) clone 341154 5', mRNA sequence. (from Genbank) clone 341154 5', mRNA sequence. (from Genbank) clone
645 646 647 648	645 Lung 646 Lung 647 Lung 648 Lung	0.1678427 0.1677564 0.1676219 0.1674928	0.4076892 1 0.4076728 0.4076345 3 0.4076067	0.327369 0.327288 0.327237	0.19683264 0.19676338 0.19671354	M88461_s_a t t HG429- HT429_at HG371- HT26388_s_a at	M88461 s a MPY1R Neuropeptide Y receptor Y1 HG429- HT429 at B-Cell Growth Factor 1 HT26388 s Mucin 1, Epithelial, Alt. Splice 9 at B-Cell Soares fetal heart NbHH19W Homo sapiens cDNA
649	649 Lung 650 Lung	0.1670751	0.4075646	0.326983	0.19662581	KC_AA4120 97_at RC_AA4120 82_at AFFX-	clone 366501 3', mRNA sequence. (from Genbank) EST: zt66912.s1 Soares testis NHT Homo sapiens cDNA clone 727366 3', mRNA sequence. (from Genbank)
651	651 Lung	0.1668522	2 0.4069711	0.326899	0.19653678	HUMGAPDH //M33197_3_ st-2 AFFX-	Glyceraldehyde-3-phosphate dehydrogenase
652	652 Lung 653 Lung	0.1668522	0.1668522 0.4069277 0.1667838 0.4068303	7 0.326872	HU /M. 2 0.19647944 st RC RC 2 0.19635656 87	HUMGAPDH /M33197_3_ t st RC_AA4656 87_at	AFFX-HUMGAPDH/M33197_3_st (endogenous control) RNA binding motif, single stranded interacting protein 1

FIG. 6F2

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654 Lung	0.1667251	0.4068004	0.32665	RC_AA6217 0.19628635 51_at	A6217 EST 103	EST: af06c06.s1 Soares testis NHT Homo sapiens cDNA clone 1030858 3', mRNA sequence. (from Genbank)
655 Lung	0.1666787	0.4067025	0.32664	M58286 0.1961289 t	s, a	TNFR1 Tumor necrosis factor receptor 1 (55kD)
656 Lung	0.1663081	0.4065947	0.326593	0.19605476 M69225 at	1	Bullous pemphigoid antigen (BPAG1) mRNA
657 Lung	0.1662385	0.4065902	0.326535	AA328993_s 0.19599803 at	993_s EST mRI	EST: EST32546 Embryo, 12 week I Homo sapiens cDNA 5' end, mRNA sequence, (from Genbank)
658 Lung	0.1658361	0.4064042	0.326349	0.19586013 t		Transcription termination factor. RNA polymerase I
659 Luna	0.1654775	0.4063645	0 326348	X82850_s_a	ļ	1. T. T. T. T. T. T. T. T. T. T. T. T. T.
660 Lung	0.1654435	1		0.19572937 06 at	.0163 EST	EST: ze38e03.s1 Soares retina N2b4HR Homo sapiens cDNA clone 361276.3* mRNA seminance (from Garbark)
661 Lung	0.1653326	0.4063256	0.326291	U11862_s	w.	ABP1 Amiloride binding protein 1 (amine oxidase (conner-containing))
662 Lung	0.1652815	0.4062697	0.325892	RC_AA0209 0.19548824 25 at	ļ	EST: ze64b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone 363741 3'. mRNA sequence (from Genbank)
663 Lung	0.1650641	0.4061297	0.325863	0.19539194 at	T	EST: zf65e11.r1 Soares retina N2b4HR Homo sapiens cDNA clone 381836 5' mRNA segience (from Genhank)
664 Lung	0.1647899	0.4061297	0.325836	RC_AA3983 0.19532411 68 at		EST: zt60g04.s1 Soares testis NHT Homo sapiens cDNA clone 726774.3', mRNA sequence (from Genhank)
665 Lung	0.164668	0.406011	0.325815	0.1952033 M21389 at		KRT5 Keratin 5 (epidermolysis bullosa simplex, Dowling- Meara/Kobner/Weber-Cockavne tynes)
666 Lung	0.1643513	0.405869	0.325575	0.19513659 N28707 at		EST: yx66d11.r1 Homo sapiens cDNA clone 266709 5'. (from Genbank)
667 Lung	0.1641693	0.4057203	0.325569	AF000959_a 0.19505616 t	(U)	Transmembrane protein mRNA
668 Lung	0.1641491	0.1641491 0.4056871	0.325556	0.19498733 17 at	AA4785 EST	EST: zw95d09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784721 3. mRNA sequence (from Genhank)
669 Lung	0.1641174	0.4056812	0.325556	0.19492373 58 at		EST: zx45b04.s1 Soares testis NHT Homo sapiens cDNA clone 795151 3'. mRNA sequence. (from Genbank)
670 Lung	0.1638896	0.4056676	0.325412	0.19482031 W26652	at	EST: 34c6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
671 Lung	0.1637483	0.4055148	0.32536	RC_AA0859 0.19481373 34 at		EST: zn54c11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 562004 3' similar to WP:B0035.3 CE05161 VIRAL NON-STRUCTURAL PROTEIN LIKE: mRNA sequence (from Genbank)
672 Lung	0.1636582	0.4054967	0.32529	0.19469741 02 at	·	EST: zu81d06.s1 Soares testis NHT Homo sapiens cDNA clone 744395 3', mRNA sequence. (from Genbank)
673 Lung	0.1635511	0.4054483	0.325278	0.19450822 X95715	at	Anthracycline resistance associated protein

And the party part

674 Lung	0.1635163	0.4053991	0.325183	C00125_s	C00125_s_a EST: HUMGS0005758, Human Gene Signature, 3'-directed cDNA to sequence, mRNA sequence. (from Genbank)
675 Lung	0.1634756	0.4053788	0.325151	RC_AA3656 0.19430615 91_at	56 EST: EST76520 Pineal gland II Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)
676 Lung	0.1633382	0.4052712	0.325131	0.1941281 R81773 at	
677 Lung	0.1629665	0.4052194	0.325131	0.19411421 37 at	_
678 Lung	0.1629425	0.4051319	0.325034	73205	at H.sapiens mRNA for ITBA2 protein
679 Lung	0.162857	0.405015	0.324802	0.19390991 S67325 a	1
680 Lung	0.1628385	0.4049314	0.32464	0.19384205 U00951	at Clone A9A2BR11 (CAC)n/(GTG)n repeat-containing mRNA
681 Lung	0.1628385	0.4046706	0.324633	0.19378188 U00951	0.19378188 U00951_at-2 Human clone A9A2BR11 (CAC)n/(GTG)n repeat-containing mRNA
682 Lung	0.1626987	0.404662	0.324588	RC_AA4638 0.1935928 61_at	EST: zx97c05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 38 811688 3' similar to SW:RB25_RABIT P46629 RAS-RELATED PROTEIN RAB-25.: mRNA sequence. (from Genbank)
683 Lung	0.1625888	0.4046579	0.324578	2976	at CYB5 Cytochrome b-5
684 Lung	0.1625832	0.4046481	0.324551	0.19351377 N57397 at	
685 Lung	0.1625642	0.4045725	0.324433	RC_AA2817 0.19344255 43 r at	
		ł		AA393903_a	
686 Lung	0.1625272	0.4044692	0.324433	0.19336131 t	729150 5', mRNA sequence. (from Genbank)
687 Lung	0.1624313	0.1624313 0.4044175	0.324413	RC_AA4859 0.1933195945 at	EST: ab40g02.s1 Stratagene HeLa cell s3 937216 Homo sapiens 59 cDNA clone 843314 3' similar to SW:SOH1_YEAST P38633 SOH1 PROTEIN (11 - mRNA sequence (from Ganback)
688 Lung	0.162345	0.162345 0.4044085	0.324361	0820	at FKBP3 FK506-binding protein 3 (25kD)
					Collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic,
689 Lung	0.1622701	0.1622701 0.4043581	0.324304	0.19302377 L02870 s	at
690 Lung	0.1622288	0.1622288 0.4043215	0.323979	0.19302014 Y10260_at	it EYA1A gene
691 Lung	0.162208	0.4043183	0.323945	U83668_rna 0.19296211 at	
692 Lung	0.1620144	0.4042932	0.323915	47	at Placenta copper monamine oxidase mRNA
693 Luna	0.1619355	0.4042848	0.323732	0.19261003 09_at	
694 Lung	0.1618381	0.4042658	0.323732	0.19257444 J04076 at	
695 Lung	0.1618337	0.4041261	0.323615	0.19251408 J04093 s	ä

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Docke	t No.:	2825.2020-002
Title:	Genet	ic Markers for Tumors
Invent	ors: Sri	idhar Ramaswamy, et al.

898 1 1100	0.1617138	0.1617138 0.4039294	0.323484	AA488793 0.19232956 t	AA488793_a Aa54d11.r1 NCI_CGAP_GCB1 n0110 sapiens conviced at AA488793_a AA548757 5', mRNA sequence. (from Genbank)
600			and the state of t	RC_AA4497	
697 Lund	0.161703	0.161703 0.4039294	0.323406		
698 Luna	0.1616854	0.1616854 0.4038564	0.32339	- 1	at-2 Integrin, alpha 8
699 Lund	0.1616854	0.4038201	0.323158	0.19208887 L36531 at	
20				RC_AA1906	
700 Luna	0.1616846	0.403772	0.323007	- 1	
701 Luna	0.1614686	0.1614686 0.4037253	0.323001	ļļ,	at UBIQUITIN CARBOXYL-IEKMINAL HYDROLASE ISOZ IME LI
702 Lung	0.1614486	0.1614486 0.4035651	0.322985	0.19181742 N56451	
6 GOL	0 1814016	0.4034808	0.322871	RC_AA4191 0.19169772 39 at	EST: zv34h05.s1 Soares ovary tumor NbHO1 Homo clone 755577 3', mRNA sequence. (from Genbank)
ה ה	200000000000000000000000000000000000000	000000000000000000000000000000000000000	0.392788	RC_AA2619	
704 Lung	0.1012041	0.4034000	0.322100	BC AA9343	
705 Luna	0.1611828	0.1611828 0.4034121	0.322782	0.19158146 84 s at	
706 Luna	0.1611738	0.1611738 0.4032412	0.322646	0.19145317 M26665	at HISTATIN 3 PRECURSOR
Dull 1702	0.160806	0.160806 0.4030387	0.322293	0.19143632 HT3686_at	
708 Lung	0.1607893	0.4029555	0.322293	0.19137366 X91247_at	
1004	0.4807438	0.4028861	0.322226	RC_AA0338 0 19128461 74 at	338 EST: zk20h04.s1 Soares pregnant uterus Nortr O rioriro saprens cDNA clone 471127 3', mRNA sequence. (from Genbank)
710 Lung	0.1605828		0.322216	0.19121543 X55330	at AGA Aspart//glucosaminidase
7111 und	0.16058		0.322182	0.19113089 U10868	at ALDH7 Aldehyde dehydrogenase 7
712 Lung	0.160527	0	0.322157	0.19104183 M60315	at BONE MORPHOGENETIC PROTEIN 6 PRECURSOR
713 Luna	0.1604544	0,4025697	0.322078	0.19097774 X04011_	at-2 Cytochrome b-245, beta polypeptide (chronic granulomatous disease)
714 Lund	0.1604544	0.4025488	0.322062	0.1909366 X04011	at CYBB Chronic granulomatous disease
715 Lung	0.160289	9 0.4025015	0.321903	0.19076052 M63138	at CTSD Cathepsin D (lysosomal asparty) protease)
				RC_AA2232	
716 Lung	0.159566		- 1		
717 Lung	0.1595563	3 0.4023925	0.321515	0.19051693 Z49	-+
7181 1100	0.1595394	4 0.4023082	0.321482	0.19048667 78	AA4323 EST: zw/6c08.s1 Soares testis INFL Horito Sapieris Curva dolle at 782126 3', mRNA sequence. (from Genbank)
		1			Germline Ig alpha mutant chain gene C-alpha-3 region of the secreted
719 Lung	0.1594579	9 0.4021936	0.321442	0.19042634 MB32220 at	0
720 Lund	0.1594037	7 0.4021498	0.321401	0.19039536	

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Mvosin, heavy nolynentirle-like (110kD)		mRNA, clone RES4-24A, exon 1, 2, 3, 4	Homo sapiens mRNA, exon 1, 2, 3, 4, clone:RES4-24A	RC_AA1590 EST: zo57h03.s1 Stratagene pancreas (#937208) Homo sapiens	cDNA clone 591029 3', mRNA sequence. (from Genbank)	PSEN1 Presenilin 1 (Alzheimer disease 3)	C1R Complement component C1r	EST: 2735h11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 665445 5' mRNA sequence (from Genhank)	EST: 12164T7 Homo sapiens cDNA. (from Genbank)	EST: zt22d02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 713859 3', mRNA sequence. (from Genbank)	EST: zt21e10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713802 31, mRNA sequence, (from Genhank)	EST: ze50a08.s1 Soares retina N2b4HR Homo sapiens cDNA clone	362390 3', mRNA sequence. (from Genbank)	EST: aa86a02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA	clone 838154 3', mRNA sequence. (from Genbank)	KIAA0750 gene product		AA203649_a EST: zx58e12.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	cDNA clone 446734 5', mRNA sequence. (from Genbank)	HOK-2 mRNA for zinc finger protein	Pit (Procedula) to a late	Sin (Drosoprina) Hornolog Z	EST: 1952 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)	EST: zq05e05.s1 Stratagene muscle 937209 Homo sapiens cDNA	clone 628832 3', mRNA sequence, (from Genbank)	CD110 protein	0.18866336 J05582 s at MUC1 Mucin 1. transmembrane	TCN2 Transcobalamin II	Gamma-dlutamyl hydrolase (hGH) mRNA	EST: zs59b05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:701745 3', mRNA sequence. (from Genbank)
RC_D25786 at	\B000464_a		AB000464_a t-2	RC_AA1590	25 at			AA195179_s at	0.189721 H55741 at	A2848		A2926	A0184		A4573		AA157623_s at	1	AA203649_a			898			A1943		at	J05582 s at	L02648 at	a t	AA2925	33_at
0.19019453		0.1900/705t	AB 0.19000174 t-2		0.18994969 25	0.18990836 U40380 at	0.18983312 M14058_at	0.18977161	0.189721		0.18970075 44_at	RC_A 0.18959823 94 at		0.18954493 41_at	0770	0.189418 64 at	0.18934537		000	0.189203161	0.18914019 X82125_at	RC_AA4	0.1001.1020	0.18895441 W26989 at		0.18892865 84_at	0.18886289 Y10506	0.18866336	0.188614951.02648	0.1885562 U55206 at		0.18846686 33
0.32135		0.321342	0.320959	0	0.320935	0.320838	0.320718	0.320644	0.320586		0.320539	0.3204	1	0.320353	0000000	0.320330	0.320289		1000	0.320137	0.320012	0.319602	2000	0,31955		0.31955	0.319524	0.319524	0.319467	0.319298		0.319279
0.4021483	1	0.4021243	0.4021043		0.1583903 0.4019//3	0.4019668	0.1582281 0.4018503	0.4018459	0.4017893		0.4016997	0.4016899	000000000000000000000000000000000000000	0.4010082	0.4042542	0.4013313	0.40129				0.4011586	0.4010572	100101	0.4010132		0.4009562	0.400949	0.400864	0.4008102	0.400767	1	0.4006851
0.1591712	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.1590312	0.1590312	7.00000	0.1583903	0.1583357	0.1582281	0.1580057	0.1576287		0.1576098	0.1574292	0.46770040	0.1373870	0.4573744	0.107.07.41	0.1573352		0.4570465	0.1372403	0.1572429	0 1572165	2	0.1571014		0.1568871	0.1567547	0.1566631	0.1566456	0.1560733		0.1560259
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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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0.1556983 0.4003758 0.319139 0.188247 57_at 0.15526242 0.4002338 0.319108 0.18817091 0.52600_s_a 0.1552629 0.4000708 0.318924 0.18817091 0.56260_s_at 0.1552629 0.4000708 0.318924 0.18817091 0.56260_s_at 0.1552609 0.3999682 0.31887 0.18787578 45_at 0.1540695 0.3997752 0.31873 0.18787578 45_at 0.1537301 0.3996654 0.318283 0.187645 0.18760176 N36588_at 0.1537301 0.3996654 0.318269 0.18773164 at 0.1537301 0.3996654 0.318269 0.18773164 at 0.1537301 0.399654 0.318269 0.18773164 at 0.1537301 0.3996554 0.318269 0.18773164 at 0.1537301 0.3996554 0.318269 0.18773164 at 0.1537301 0.3996554 0.318269 0.18773164 at 0.1538369 0.3994141 0.318128 0.18741755 27_at 0.1538027 0.3994181 0.318128 0.1872227 at 0.1532162 0.3993481 0.318068 0.18714279 HT544 at 0.1528723 0.399235 0.318043 0.18714279 HT544 at 0.1528723 0.3990953 0.317774 0.18703292 57_fat 0.1528723 0.3990953 0.317774 0.18703292 57_fat 0.1528723 0.3990953 0.317774 0.18703292 57_fat 0.18703292 57_fat 0.1870309953 0.317774 0.18703292 57_fat 0.18703292 57_fat 0.1870309953 0.317774 0.18703292 57_fat 0.187030959 0.317774 0.18703292 57_fat 0.18703292 57_fat 0.187030959 0.317774 0.18703292 57_fat 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.1870309959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.18703292 57_fat 0.187030959 0.3177774 0.187030959 57_fat 0.187030959 0.3177774 0.187030959 0.3177774 0.1870309959 0.3177774 0.1870309959 0.3177774 0.187030959 0.3177774 0.18703	745	Lung	0.1558058		0.319159	0.18829513 Y07868_s	at Pirin
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765 Lung	0.1527564	0.3989051	0.317638	RC_AA4486 0.18681543 88_at	RC_AA4486 EST: zx11g04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 88_at clone 786198 3', mRNA sequence. (from Genbank)
				RC_AA4275	RC_AA4275 Homo sapiens regulator of G protein signaling RGS14 mRNA,
766 Lung	0.1527243	0.3988705	0.317583	0.18668638 79_at	complete cds
767 Luna	0.1526961	0.3987791	0.317416	C16161_s_a	EST: Human aorta cDNA 5'-end GEN-234B03, mRNA sequence. (from Genhank)
6				N75215 S A	FST: vw33h05 r1 Homo saniens cDNA clone 254073 5t1 (from
768 Lung	0.1524764	0.3987571	0.317406	0.18656528 t	Genbank)
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769 Lung	0.1524361	0.398697	0.317302	0.18650225 t	HFL1 H factor (complement)-like 1
770 Lung	0.1520901	0.398609	0.317201	0.18638606 M23254_at	CAPN2 Calpain, large polypeptide L2
				U67368_s_a	
771 Lung	0.1519963	0.3985269	0.317098	0.18629472 t	EXT2 Exostoses (multiple) 2
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774 Lino	0.15-5783	0 3984929	0.346024	RC_AA2353	EST: zs40a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
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778 Lung	0.1513683	0.3983211	0.316739	AA495865_a 0.18580435 t	EST: zw05c07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 768396 5', mRNA sequence. (from Genbank)
				RC_AA4279	RC_AA4279 EST: zw53d11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
779 Lung	0.151318	0.3982729	0.316642	0.18563059 44_at	clone 773781 3', mRNA sequence. (from Genbank)
1					EST: yj83f12.r1 Homo sapiens cDNA clone 155375 5'. (from
/80 Lung	0.1510057		0.316614	0.18558958 R69417_at	Genbank)
/81 Lung	0.1509293	0.3981314	0.316604	0.18548734 U09850_at	ZNF143 Zinc finger protein 143 (clone pHZ-1)
782 Lung	0.1509293	0.3980586	0.316573	0.18541473 U09850_at-2	0.18541473 U09850_at-2 Zinc finger protein 143 (clone pHZ-1)
783 Luna	0.1507461	0.397989	0.316551	RC_AA6101 0 18534403 16 i at	EST: af19g10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 1032162 3' mRNA sequence (from Ganhank)
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785 Lung	0.1506853	0.3979476	0.316352	0.18519415 53_at	Inositol 1,4,5-triphosphate receptor, type 3

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805 Lung	0.1481089	99 0.3968687	7 0.314831	0.18348065	sequence. (from Genbank) a EST; zs81h05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
806 Lung	0.1479293	93 0.3968554	4 0.314773	0.1833788	

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00711200	0 4474733	223 0 3968059		0.314682	0,1832981 U27655 at		RGP3 mRNA
SOV LUNG	77.0	000				4	EST: zr85f01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682489 3' similar to contains MER32.b2 MER32 repetitive element ;,
808 1 1100	0.1472	0.1472143 0.3966435		0.314641	0.18323557 25_at		mRNA sequence. (from Genbank)
Sin 200			\	27.70		AA491376_a E	EST: aa65e11.r1 NCI_CGAP_GCB1 Homo sapletts convenients in NCI_CGAP_GCB1 (from Genbank)
809 Lung	0.1467867	867 0.3965822		0.314590	0.16313203	X55448 cds (GRPD nene (glucose-6-phosphate dehydrogenase) extracted from
040	0.146693	693 0 3965822		0.314504	0.18311477	s at	H.sapiens G6PD gene for glucose-6-phosphate dehydrogenase
010 Luig	5	- L					EST: zx36h04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDINA
					RC 0.40200045104	_AA4528	clone 788599 3' similar to SW: KSTo_TAETIN F44302 SVS.
811 Lung	0.1466552	552 0.3962835		0.314498	0.16300613	41 5533 c 3	
812 Lung	0.1465183	- 1	0.3961302	0.314475	0.1829082	t	KIAA0221 gene
813 Lund	0.1460573		0.3960912	0.314452	0.18277606	S72493_s_at	0.18277606 S72493 s at KERATIN, TYPE I CYTOSKELETAL 17
814 Lund		0.1459976 0.3960102	30102	0.31436	0.182711771	N71503_s_a t	N71503_s_a EST; yw32b10.r1 Homo sapiens cDNA clone 253915 5. (iruii t Genbank)
		9000		0.314055	RC_A 0.18268190 at	A1884	EST: zq44d08.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632559 3', mRNA sequence. (from Genbank)
815 Lung	0.1458150			0.014200	0.10201		EST: 2x08f10 s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
-							clone 785899 3' similar to contains Alu repetitive element; contains
						A4494	element MER22 repetitive element ., mRNA sequence. (from
816 Lung	0.1458645		0.3959216	0.314163	0.18262355 75 at	75 at	Genbank)
817 Lung	0.1457587		0.3957494	0.314094	0.18250148 U57094	U57094_at	Small GTP-binding protein mrava
818 Luna	0.1456036		0.3956778	0.314067	0.18238007	0.18238007 X87767_at	
			0 3058528	0 343974	0 18231533	R50247_s_a	EST: yj58b01.r1 Genbank)
0 13 Lui 19			2000			V00535 rna	Interferon beta 1 gene extracted from Gene for human fibroblast
820 Lina	0.1454591		0.3956354	0.313935	0.18223673 2_	32_s_at	interferon beta 1
821 Lung		1.	0.3956173	0.31384	0.18218815 U63973	5 U63973 at	Rhodopsin kinase
822 Lunc		0.1452974 0.3	0.395606	0.313818	0.1821528	3 D87468_at-2	0.1821528 D87468_at-2 Human mRNA for KIAA0278 gene, partial cds
823 Luna		0.1452974 0.39	0.3956012	0.313758	0.18206927 D87468	7 D87468 at	KIAA0278 gene, partial cds
824 Lund		0.1452601 0.39	0.3955233	0.313689		RC_AA4319 957_at	EST; zw77a01.s1 Soares testis NH1 Homo sapiens conva cione 782184 3', mRNA sequence. (from Genbank)
825 Lung		1	0.3954939	0.313687	0.18196057 R15917	7 R15917 at	Homo sapiens gione 24629 IIIINNA sequence
826 Lung		0.1447495 0.39	0.3954457	0.313662	0.18187064	RC_D60033	
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827 Luna	0.1445389	0.3951472	0.313558	AFFX- HSAC07/XI 0.1817814 0351 3 st		AFFX-HSAC07/X00351_3_st (endogenous control)
		1	0030700	AFFX- HSAC07/X0	AFFX- HSAC07/X0	No info for gene
828 Lung	0.1445389	0.3950662	0.313404	0.1816883 95_at	RC_AA2812 95_at	EST: zt08g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712560 3', mRNA sequence. (from Genbank)
D	0.144937		0.313378	0.18145241 t	A074933_a	Zm85b07.r1 Stratagene ovarian cancer (#937219) Homo sapiens AA074933_a cDNA clone 544693 5' similar to gb:J04794 ALCOHOL t DEHYDROGENASE (HUMAN);, mRNA sequence. (from Genbank)
831 Luna	0.1440862	,	0,313332	0.18137266 W25821	at	EST: 14e10 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
832 Lung	0.1439097	0.3949648	0.313265	0.18132702 W26105	at	EST: 22f7 Human retina cDNA randomly primed subjudicy monto sapiens cDNA, mRNA sequence. (from Genbank)
833 Luna	0.1435464		0.3132	RC 0.18126038 57	2_AA2332 at	Transforming growth factor beta 1 induced transcript 1
834 Luna	0.1433436	1	0.313104	0.18126038	5_5	TAP binding protein (tapasin)
835 Lung	0.1433351	0		0.18113275 U84971		Homo sapiens fetal unknown mkNA, complete cus vr72h07 r1 Homo saniens cDNA clone 210805 5' (from Genbank)
836 Lung	0.1432472		- 1	0.161003/3 T002/3 at	7	TVK TVK timesine kinase
837 Lung	0.1431472	2 0.394642	0.312932	0.18092379 LZ1071	EC AA4546	FST: x76a07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
838 Lung	0.1431143	3 0.3946405	0.312908	0.18084158 75_at	5 at	clone 809652 31, mRNA sequence. (from Genbank)
839 Luna	0.1429422	2 0.3944924	0.312861	0.18073787 N	//28585_f_at	0.18073787 M28585_f_at IFNA16 Interferon, alpha 16
840 Lung	0.1428676	6 0.3944664	0.312838	0.1806418 X75308 at		MMP13 Matrix metalloproteinase 13 (collageriase 5)
				0.4006230	\A070326_a	AA070326_a EST: zm68e02.r1 Stratagene neuroepithelium (#937231) Homo
841 Lung	0.1425217	0.3944664	0.312733	0.1000230	RC AA2794	EST: zs85g09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
842 Lung	0.1420535	5 0.3943546	0.312741	0.18053092 67	37_at	IMAGE:704320 3', mRNA sequence. (from Genbank)
843 Lung	0.1420401		0.31271	RC 0.18047878 12	RC_AA4890 12_at	Human pre-B cell enhancing factor (PBEF) mRNA, complete cds
844 Lung	0.1418682	2 0.3942029	0.312684	0.18039018 Z74616 s		at COL1A2 Collagen, type I, alpha-2
845 Lung	0.1417904	4 0.3941631		0	M63835_at	FORM" PRECURSOR
846 Lung	0,1417589	9 0.3940368	0.312477	0.1802316 U90913_at	U90913 at	Clone 23665 mknA sequerice
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847 Lung 848 Lung				RC.	AA1324	RC_AA1324 EST: zo20b01.s1 Stratagene colon (#937204) Homo sapiens cDNA
848 Lung	0.1415097	0.3939755	0.312368	0.18021257 53_3	to,	clone 587401 3', mRNA sequence. (from Genbank)
	0.1409441	0.3939252	0.312358	U32 0.1802085 t	U32499_s_a t	D3 dopamine receptor mRNA
849 Lung	0.1407871	0.3938699	0.312355	0.18008693 R71205	at	EST: yi53g09.r1 Homo sapiens cDNA clone 143008 5' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);. (from Genbank)
850 Lung	0.1405638	0.3938529	0.312304	0.18005024 97 at	898	EST: zp74c05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 625928 3', mRNA seguence, (from Genhank)
	0.1405437		0.312213	0.17999251 D50312	ät	UKATP-1
852 Lung	0.1405437	0.3937709	0.312133	0.17990473 D50312		at-2 Potassium inwardly-rectifying channel, subfamily J, member 8
853 Lung	0.1404124	0.3937604	0.311989	HG880- 0.17979872 HT880 s at	380- 80 s at	Mucin 6, Gastric (Gb:L07517)
854 Lung	0.1400175	0.3937507	0.311905	RC_A 0.17965975 13 at	AA4026	RC_AA4026 EST: zu49c05,s1 Soares ovary tumor NbHOT Homo sapiens cDNA 13 at clone 741320 3' mRNA sequence (from Genbank)
Ti	0.1398231	1 1	0.311902	0.17961605 J04177	ä.	COL11A1 Collagen, type XI, alpha 1
856 Lung	0.13971	0.3936008	0.311875	0.17954832 D82	344 at-2	0.17954832 D82344 at-2 Paired mesoderm homeobox 2b
857 Lung	0.13971	0.3935396	0.311804	0.17941953 D82344 at	344_at	NBPhox
858 Lung	0.1396988	0.3935351	0.311684	0.17938818 t	43223_a	AA043223_a Homo sapiens clone 486790 diphosphoinositol polyphosphate t
859 Luna	0.1395714	0.3935319	0.311583	AA2 0.179275331	AA220236_a	EST: PMY0284 KG1-a Lambda Zap Express cDNA library Homo canions cDNA 5' mRNA sequence (from Ganhank)
	0 1205013	1		RC RC	A2333	September 2017 of the Control of the
	0.1333243	0.3833/78	0.311508	0.1792141 45	_at	666650 3', mKNA sequence. (from Genbank)
	0.1393928	0.3933545	0.311498	0.17915927 U67611	- 1	at-2 Mouse transaldolase gene mRNA, complete cds. (from Genbank)
862 Lung	0.1393928	0.3933477	0.311439	0.17913035 U67611	1	Mouse transaldolase gene mRNA
863 Lung	0.1391306	0.3931039	0.311411	AA3 0.17905445 t	AA305116_a t	EST176117 Colon carcinoma (Caco-2) cell line II Homo sapiens cDNA 5' end, mRNA sequence, (from Genbank)
864 Lung	0.138959	0.3930995	0.311372	0.17902942 U74324 at		Guanine nucleotide exchange factor mss4 mRNA
865 Lung	0.1386277	0.3930599	0.311349	RC_A 0.17896973 10_at	A5984	EST: ae48b06.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950099 3', mRNA sequence. (from Genbank)
866 Lung	0.1385029	0.3930414	0.31132	AA4 0.17883463 t	47876_a	AA447876_a EST: aa20c09.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t
867 Lung	0.1382243	0.3930365	0.311314	0.17876777 L23808_at		MMP12 Matrix metalloproteinase 12 (macrophage elastase)
868 Lung	0.1379621	0.3929079	0.311286	AA2 0.1786136 t	AA252752_a t	EST: zs26b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686299 5', mRNA sequence. (from Genbank)

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96011100	0 1378872	0.3928575	0.311257	0.17855059 Ko	10224 at	0.17855059 R86224 at Human IIIINA 101 NATO 110 SOLO, PORTO 110 SOLO, PORTO 110 S
870 Lund		0.3927889	0.311181	RC_ 0.17849697 31_8	AA2429 E	EST: zr26a02.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664490 3', mRNA sequence. (from Genbank)
	100000	0 2006300	0 341437	RC_A 0 17841657 92 at	A4245	FS1: ZV9 III IU.S1 SOGIES Rimining Companies 767203 31, mRNA sequence. (from Genbank)
871 Lung	0.1070000	0.3920302	0.011101	0 178379 H38727	77 at	Ribosomal protein L37
872 Lung	0.13/8245	0.392390	2,0			CONTRACTOR CONTRACTOR CONTRACTOR
					- \'	EST: ze44e02.r1 soares fellita Nz0+1 II/1 ionio separa de la company de
873 1 1100	0 1377806	0.3925767	0.311	0.17833771 W92283	at	contains Alu repetitive element; mRNA sequence. (from Genbank)
S Lai	3					EST: yi19a02.r1 Homo sapiens cDINA clotte Toacoo 5. (Il ott.)
874 Lung	0.1377016		0.310914	0.17829916 R63981 at		Germanny A DAIT And hydrocarbon recentor nuclear translocator
875 Lung	0.1373288	0.3921245	0.310836	0.17810999 MI09238 at	a	FCT: 744f10 s1 Soares NHHMPu S1 Homo sapiens cDNA clone
076	0 1373148	0.3920416	0.310819	0.17808872 07_at	AKSSO	666283 3', mRNA sequence. (from Genbank)
Crang						Zv01h10.r1 NCI_CGAP_GCB1 Homo saplens conversions to the conference of the conferenc
				<u> </u>	A419464_a	AA419464 a POLYPEPTIDE PRECURSOR (HUMAN);, mRNA sequence. (from
877 Lung	0.1372945	0.3919544	0.310804	0.17799254 t	1	Genbank)
0 200	0 1379899	0 3919135	0.310783	RC 0.17792772 80	_AA2554 at	682288 3', mRNA sequence. (from Genbank)
010	0.1370118	ı	0.340725	0.17783602	AF009426_a t	Clone 22 mRNA, alternative splice variant alpha-1
8/a rnuĝ	0.13/2110		2,010,0		3C AA2824	RC AA2824 EST: zs90e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
880 Lung	0.1366392			0.17775199 05 at	15 at	IMAGE:704770 3', mRNA sequence. (from Genbank)
881 Lung	0.13649	9 0.3918078	0.310491	0.17773938 033849	133849 at	Lympholia propracting converses (
-	0 1363/33	0 3917604	0.310473	0.1776064	RC_AA0053 08_at	
982 LUIIG	0.100040					
200	0.1363078	R 0.3917021	0.310403	0.17755325	RC_AA6209 98_at	
n coo				0.1774345	RC_AA3502	EST: EST57664 Infant brain Homo sapiens cDNA 3' end, mixiva sequence, (from Genbank)
884 Lung	0.1302718	0.0910904		2	RC_AA1349	RC_AA1349 EST: zo23g08.s1 Stratagene colon (#937204) Homo sapiens cDNA
885 Lung	0.136194	4 0.3915414	0.310321	0.17736258	68 at RC AA4365	clone 587774 3', mRNA sequence. (Iron Genbank) FST: zv08c11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
886 1 1100	0.1359219	9 0.3915151	0.31032	0.17730825	53 at	753044 3', mRNA sequence. (from Genbank)

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Docket	No.:	2825.2020-002
Title:	Geneti	ic Markers for Tumors
Invento	ors: Sri	dhar Ramaswamy, et al.

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		i	0 04000	HG2788- 0 17720716 HT2896 at		Calcyclin
887 Lung	0.1356629	- 5	0.310294	0.111231 101112030 dt	1	CX3C chemokine precursor, mRNA, alternatively spliced
888 Lung	0.1355367	7 0.3914444	0.3102	0.17772000	+	
						EST; zh51h04.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
080	0.13550	0 135506 0 3913298	0.310173	0.17714317 W78726_at	8726_at c	cDNA clone 415639 5, mrina sequence. (Illum Genbann)
600 Lui y	2			AK	287749 a Z	AA287749 a Zs51b11.r1 NCI_CGAP_GCB1 Homo sapiens cUNA clone
000	0 1354359	9 0.3911431	0.310171	0.17708886 t		IMAGE:700989 5', mRNA sequence. (from Genbank)
090 Lung	0.134941	1.	0.31009	0.17695856 L40401 at		(clone zap128) mRNA, 3' end of cds
09 I Lui ig	0.10404		0 310059	0 17691125 1 40401	C	Homo sapiens (clone zap128) mRNA, 3' end of cds
892 Lung	0.1043		200		4653	EST: aa23d09.s1 NCI CGAP GCB1 Homo sapiens cDNA clone
893 Lung	0.134924	24 0.3908235	0.309886	0.17685232 67	at	IMAGE:814097 3', mRNA sequence. (from Genbank)
						EST: 7x42e04 s1 Spares total fetus Nb2HF8 9w Homo sapiens cDNA
					0 0000000000000000000000000000000000000	Cons 780150 3' similar to TR:G641819 G641819 HHEB
		0 2007034	0 300850	0 17679831 14 at		HAL OHYDRIN EPOXIDASE B.;; mRNA sequence. (from Genbank)
894 Lung		0.0300/051	GCOCOCO.	RC	A4166	EST; zu08h02.s1 Soares testis NHT Homo sapiens cDNA clone
80511111	0.1347468	58 0.390618	0.309829	0.17666917 31	, at ,	731283 3', mRNA sequence. (from Genbank)
200		_		0X	X00695_s_a	
896 Luna	0.1346701	0.1 0.3905833	0.309774	0.17666431 t		INTERLEUKIN-2 PRECURSOR
				RG	RC_AA1564	EST; 2151f03.s1 Soares pregnant uterus inpution adplicate control
897 Lung		0.1345473 0.3905473	0.309742	0.17662485 50	at	clone 505469 3', mRNA sequence. (from Genbank)
898 Lung	0.1344081	81 0.3905444	0.309651	0.17650172 U82532_at		GDI-dissociation inhibitor Khoculgainina Illinina
		}			H89551_s_a	EST: yw28e07.r1 Homo sapiens cDNA done 2007.z 3 : (IIOIII
899 Lung	0.1343923	23 0.3905425	0.309636	0.17639622	, 00, 01	Genbank)
pail I loo	0 1343647	47 0 3905393	0.309552	0.17634879 t	4481201_a	AA481201 a EST: aas4612.11 NOT COAT COOL TOTAL SAPERS CONTROLLED IN AGE: 815158 5', mRNA sequence. (from Genbank)
200		1		0.1761804	RC_AA5999 54 at	Phosphatidylinositol glycan, class B
801 Luis			<u> </u>		X62654_rna	
902 Luna	0.1339174	74 0.390442	0.309467	0.17617229	at	ME491 gene extracted from H.sapiens gene for Me491/CD63 antigen
		0 000 0 044	0 300342	0 17615084	RC_AA0630	EST; zf67e06.s1 Soares pineal gland Nshr'o norno sapteus convo- clone 382018 3', mRNA sequence. (from Genbank)
903 Lung	0.1339070	1			AA451992_a	EST: zv75b06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
904 Lung	q 0.1337781	781 0.3903035	5 0.309254	0.17608719		clone 759443 5', mRNA sequence. (from Genbank)
		i			AA133029_a	TACCO mential cds
905 Lung	g 0.1337706	706 0.3902964	4 0.309218	0.17608485	7 8004 5	Homo Sapiers TACCZ protein (TACCZ) III. V. 3, partial conference and a conference refine N2h4HR Homo sapiens cDNA clone
908 1 100	0.1335578	578 0.3902825	5 0.309142	0.17591514	.C_AAU215 2_at	284032 3', mRNA sequence. (from Genbank)
1000	-					

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907 Lung	0.1335346	0.3902683	0.309127	0.17587863	RC_AA1499 87_at	Homo sapiens thymus specific serine peptidase mRNA complete cds
908 Lung	0.1334101	0.390258	0.309082	0.17573065	N75870_s_a t	Dual specificity phosphatase 1
909 Lung	0.1330162	0.3901953	0.309075	0.1757209	A287289_a	AA287289_a EST: zs49g10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
910 Lung	0.1329259	0.3901625	0.309031	0.17561547 t	U92314_s_a t	Hydroxysteroid sulfotransferase SHI T281a (HSST2) 22 DNA
911 Lung	0.1329259	0.3901141	0.308994	0.17554384	U92314_s_a	Sulfotransferase family 28 member 4
912 Lung	0.1327966	0.389808	0.308832		47269 at	Solicing factor, arginine/serine-rich 7 (35kD)
913 Lung	0.1326064	0.3897879	0.30876	0.17545015 L17075	17075_s_at	SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 s_at PRECURSOR
914 Lung	0.1325038	0.3897435	0.308648	0.17541745 H29683 at	29683 at	EST: ym61b06.r1 Homo sapiens cDNA clone 52750 5' similar to contains Alu repetitive element, contains KER repetitive element; (from Genbank)
915 Lung	0.1322415	0.3896492	0.308552	RC_A 0.17525758 05_at	A4615	EST: zx60b05.s1 Soares testis NHT Homo sapiens cDNA clone 795825 3', mRNA sequence. (from Genbank)
916 Lung	0.132051	0.389627	0.308516	0.1752138 L35546	,at	GLCLR Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), regulatory (30.8kD)
917 Lung	0.132051	0.3896247	0.308413	0.17515075 35546 at.2		Glutamate-cysteine ligase (gamma-glutamylcysteine synthetase),
918 Lung	0.1317424	0.1317424 0.3894547	0.308356			XG mRNA (clone PEP11)
919 Lung	0.1317297	0.3894403	0.308273	RC_A 0.17505275 99_at	A2905	EST: zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700416 3; mRNA sequence_(from Genhank)
920 Lung	0.1317241	0.3894375	0.308189	0.17495969 s	RC_D60354 s_at	Human mRNA for KIAA007 gene partial cds
921 Lung	0.13166	0.38941	0.308047	0.17494038 W60965_at		EST: zd30c02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342146 5', mRNA sequence, (from Genbank)
922 Lung	0.1313929	0.3893816	0.307999	RC_A 0.17481253 50_at		EST: zv17d09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753905 3' similar to contains element TAR1 TAR1 repetitive element ; mRNA sequence. (from Genbank)
923 Lung	0.1312947	0.3892777	0.307939	0.17476411 UE	50196_at-2	0.17476411 U50196_at-2 Adenosine kinase
924 Lung	0.1312947	0.3891819	0.307904	0.17476411 U50196	50196_at /	ADK Adenosine kinase
925 Lung	0.1309866	0.389154	0.307904	0.174739 H29723_at		EST: yp02a10.r1 Homo sapiens cDNA clone 186234 5'. (from Genbank)
926 Lung	0.1309821	0.1309821 0.3890771	0.307831	RC_A 0.17461346 66_at	A4007	Homo sapiens mRNA for KIAA0556 protein, partial cds

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

DOCKET NO.: 2825.2020-002 Title: Genetic Markers for Tumors

Inventors: Sridhar Ramaswamy, et al.

tages and the state of the stat	0.1306174 0.3890314 0.307767 0.1744603	0.1305526 0.3889823 0.307697 0.1744946991 at 0.1304886 0.3889799 0.307609 0.17444946 L76627 at AA313891 a	0.1303417 0.3888908 0.307532 0.17425461	0,1300526 0.3888381 0.307508 0.17422016	572_s	0.1297109 0.3886485 0.307426 0.17416929 71 at 0.17297109 0.3886485 0.307394 0.1741226 Y07867 at	0.1297049	0.3885271 0.307221 0.17402734 W27770 at AF000573_r	0.1295575 0.3884376 0.307131 0.17395227 na1_at RC_AA0349	5 at F002672_a	939 Lung 0.1291031 0.3883853 0.306979 0.1738844711 0.3883853 0.306979 0.4738844711 0.3883853 0.306979 0.4738844711 0.3883853 0.306979 0.4738874711 0.3883853 0.306979 0.4738874711 0.3883854 0.306979 0.4738874711 0.3883854 0.306979 0.475877 0.47677	0.3883485 0.306928 0.17382503 H50178 at 0.306929 0.17377426 U40223 at	0.1288946 0.3883451 0.30055	A4870	0.12876 0.3882018 0.306745 0.17367345 54 at	0.1287164 0.3881793 0.306732 0.17361404 J03909 at 0.1287164 0.3881793 0.306679 0.1735835 L17128 at	0.3061736 0.30667 0.17343584 U78313 at	0.1283728 0.3000130
	927 Lung	928 Lung 929 Lung	930 Lt	931	932/L	933	934	939	937	938	936	<u>4</u>	8	94	96	76	Ó	1

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947 Lung	0.1280852	0.3880158	0.306551	0.17336771 15_at	RC_AA2792 EST: zs83f06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 15_at IMAGE:704099 3', mRNA sequence. (from Genbank)
948 Lung	0.1276563	0.3880053	0.306549	RC_AA1914 0.17325982 95_at	
949 Lung	0.1276523	0.3879883	0.3065	AA130614_ 0.17317784 t	Zo10f02.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 567291 5' similar to TR:G1125026 G1125026 3-AA130614_a HYDROXYACYL COA DEHYDROGENASE.; mRNA sequence. t (from Genbank)
950 Lung	0.1275981	0.3879795	0.30647	0.17313856 D62633 F	EST: Human aorta cDNA 5'-end GEN-308H02, mRNA sequence. at (from Genbank)
951 Lung	0.1274128	0.3879569	0.306458	0.17309685 L34774_s_e	at Opioid-binding protein/cell adhesion molecule-like
952 Lung	0.1272099	0.3878615	0.306198	RC_AA0073	EST: zh98d02.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429315 3' similar to SW:POL1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN;, mRNA sequence.
953 Lung	0.1263195	_ii_	0.306185	0.17286539 X96698_at	D1075-like gene
954 Lung	0.1262246	0.3877869	0.306117	0.17275044 M62486 at	C4BPA Complement component 4-binding protein, alpha
955 Lung	0.1257587	0.3876841	0.306105	RC_AA4341 0.1726566 13 at	
956 Lung	0.1254499	0.3875594	0.306035	0.17260979 L10844 at	CDC42 Cell division cycle 42 (GTP-binding protein, 25kD)
957 Lung	0.1254446	0.3875257	0.306019	RC_A44856 0.17259628 55 at	· · · · · · · · · · · · · · · · · · ·
958 Lung	0.1254216	0.3874441	0.305979	RC_AA5983 0.17256227 97 at	
959 Lung	0.1254068	0.3874079	0.305966	0.17243433 f at	
960 Lung	0.1252746	1	0.305966		PSE-binding factor PTF gamma subjunit mRNA
961 Lung	0.1250318	0.3872659	0.305922		Ligase III, DNA, ATP-dependent
962 Lung	0.1249987	0.3872496	0.30588	0.17226854 t	BCL2 B-cell CLL/lymphoma 2
963 Lung	0.124497	0.3871949	0.305836	AA402109_a	a EST: zu55a06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741874 5' mRNA sequence (from Ganhank)
964 Lung	0.1244043	0.3871296	0.305697	0.17214946 M80647 at	THROMBOXANE-A SYNTHASE
965 Lung	0.124252	0.387122	0.305601	0.17208278 Z96810_at	DNA sequence from PAC 452H17 on chromosome X contains sodium and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. the state of the s

966 Lung	0.1242019	0.3871163	0.305554	0.17207249 KO	0629 f at F	0.17207249 K00629 f at Human kpni repeat mrna (cdna clone pcd-kpni-4), 3' end
967 Lung	0.1238909	0.3870255	0.305541	0.17202947 U62647 at	2647 at [Deoxyribonuclease I-like 2
000	0 1236748		0.305494	0.17199479 t	<u>U31929_s_a </u> t	DAX-1
969 Lund	0.1230902		0.305437		-	EST: zt70d02.r1 Soares testis NHT Homo sapiens cDNA clone 727683 5', mRNA sequence. (from Genbank)
070 Lind	0 1229971	1	0.305389	U210 0.17182809 1 at)51_rna	G protein-coupled receptor (GPR4) gene
971 Lung	0.1229522		0.305355	RC_A 0.17176127 58_at	A0401	EST: zk47b05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485937 3', mRNA sequence. (from Genbank)
972 l und	0.1226257	0.3867807	0.305329	RC 0.17171474 70	RC_AA0019 670_at	EST: zh83f07.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 427909 3', mRNA sequence. (from Genbank)
973 Luna	0.1224771	1	0.305187	RC_A 0.17170125 14_at	AA3480 at	RC_AA3480 EST: EST54433 Fetal heart II Homo sapiens cDNA 3' end, mRNA 0.17170125 14_at sequence. (from Genbank)
974 Luna	0.1224594	1	0.304926	AFFX- 0.17164434 5_st-2	BioB-	AFFX-BioB-5_st (miscellaneous control - 11k chips)
975 Lung	0.1224594	1	0,304843	AFF. 0.17153297 5_st	AFFX-BioB- 5_st	AFFX-BioB-5_st (endogenous control)
976 Lung	0.1223678	0.3863987	0.304826	0.17149651 t	\180854_a	AA180854_a EST: zp35h03.r1 Stratagene muscle 93/209 Homo sapiens CUNA to clone 611477 5', mRNA sequence. (from Genbank)
977 Luna	0,1223618	1	0.30478	RC_A 0.17141947 44_at	A5991	Myosin phosphatase, target subunit 1
978 Lung	0.1222019	!	0.304721	0.17141365 L19437_at		TALDO Transaldolase
979 Lung	0.1221612	0.3860507	0,304685	0.17136844 M34057	34057 at	LTBP1 Latent transforming growth factor beta binding protein 1
980 Luna	0.1221165	0.1221165 0.3859938	0.304685	0.17126703 t	4070545_a	AAU/0545_a Zm/Uc03.r1 Stratagene neuroepititellum (#957251) mino saprens t
981 Lung	0.1220644	0.1220644 0.3859637	0.304642	0.17120038 U62325 at		FE65-like protein (hFE65L) mRNA, partial cds
982 1100	0 1220164	0.3858567	0.304574	0.17111775 22 s at	647	EST: zx82d05.s1 Soares ovary tumor NbHO1 Homo sapiens cUNA clone 810249 3', mRNA sequence. (from Genbank)
983) 100	0.1219493		0.304524	0.171055 M57710 at	57710 at	LGALS3 Lectin, galactoside-binding, soluble, 3 (galectin 3) (NOTE: redefinition of symbol)
984 Lung	0.1217599	1		RC_A 0.17098396 65_at	C_AA4019	RC_AA4019 Homo sapiens growth suppressor related (DOC-1R) mRNA, complete 65_at cds
				エエ	HG4169- HT4439_s_a	
985 Lung	0.1216273			0.17090636		Syntaxin 1b
986 Lung	0.1215411	1 0.3856391	0.304342	0.17085183 X62078_at	62078 at	GM2A GM2 ganglioside activator protein

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AA453331 a clone 789362 51 similar to contains 1 11 1 reportition closures.	mRNA sentience (from Ganbont)	CW-1 mRNA	Ribosomal DNA complete repeating unit	RC_AA4571 EST: zx84f04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	AA316868 a EST: EST188529 HCC cell line (matastacis to liner is more) in 1.	Sapiens cDNA 5' and mRNA sociones (from Court of the Cour	0.17046939 L76687 at-2 Growth factor recenter bound emitting 4.4	Grand month	Avonal transfer	-	EST: zx54g10.r1 Soares fetal liver spleen 1NFLS S1 Homo saniens	AA203236_a cDNA clone 446370 5' similar to contains element PTR5 repetitive	element;, mRNA sequence, (from Genbank)			COLUMNITY OF ALITHOUGH SEDING. (Irom Genbank)	0.17011455 C17139 at (from Genbank)	RC_D60386 EST: Human fetal brain cDNA 3'-end GEN-103H09, mRNA sequence.	SMPD1 Sphingornyelin phosphodiesterase 1, acid lysosomal (acid	sphingomyelinase)
AA453331 a	-	0.17073461 D50663 at	1	RC_AA4571	AA316868 a	ا <u>ب</u>	L76687 at-2	0.17040393 76687 at		אפטטייט מו		AA203236_a		0.17030604 D25539 at	M91490_s_a		C17139 at	RC_D60386	7	
	0.17079692	0.17073461	0.17069243	RC_A 0.17062272 40 at		0.17052606	0.17046939	0.17040393	0 1703770B	200000		1	0.17034759	0.17030604	0.17018099±		0.17011455	0.1700299 at	1	U. 1099 / 482 M59916 at
*	0.30434	0.304246	0.304236	0.304202	1	0.304124	0.304115	0.3041	0.304031			0 00000	0.303897	0.30381	0.303802		0.303762	0.303699	7.69608.0	0.505057
	0.1214343 0.3854686	0.1213893 0.3854203	0.1212679 0.3854169	0.120995 0.3853394		0.1209776 0.3852518	0.1209395 0.3852305	0.1209395 0.3851693	0.1208849 0.3851602			0.1208708 0.3850204	18000000	0.385016	0.3849609		0.3848771	0.1205573 0.3848463	0 3848313	CI COLONIO
	0.1214343	0.1213893	0.1212679	0.120995		0.1209776	0.1209395	0.1209395	0.1208849			0.1208708	0 4200 00	0.1208458	0.1206311		0.1205743	0.1205573	0 1205492 0 3848313	20100=1
	987 Lung	988 Lung	989 Lung	990 Lung		aa.i Lung	992 Lung	993 Lung	994 Lung			9951 1100	000	aso ruild	997 Lung		998 Lung	999 Lung	000 Luna	6

FIG. 6W2

			-			-	
_	1.3723106 0.5039521	1.3723106		0.449323	RC_A 0.3534761 58_at	RC_AA0246 58_at	Ribosomal protein S19
N	2 Lymphoma 1.1656398 0.4679987	1,1656398		0.418099	0.33133417	382297_at	0.33133417 S82297_at BETA-2-MICROGLOBULIN PRECURSOR
	The state of the s				1	4A297912_a	AA297912_a EST: EST113641 T-cell lymphoma Homo sapiens cDNA 5' end,
ເນ	3 Lymphoma 1.1079978 0.4555078	1.1079978	0.4555078	0.404835	0.31944063	:	mRNA sequence. (from Genbank)
						3C_AA1218	RC_AA1218 Proteasome (prosome, macropain) subunit, beta type, 9 (large
4	4 Lymphoma	1.02126	0.446076	0.395554	0.31117448 79_s_at		multifunctional protease 2)
						U37546 s.a	
ťΩ	5 Lymphoma 0.9422403 0.4394731	0.9422403	0.4394731	0.388355	0.30497497		IAP homolog C (MIHC) mRNA
						U37546_s_a	
9	6 Lymphoma 0.9422403 0.4337181	0.9422403		0.384047	0.2999395 4-2	-2	Apoptosis inhibitor 1
						RC_AA4045	RC_AA4045 EST: zw38d02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
~	7 Lymphoma 0.9388786 0.4286351	0.9388786	0.4286351	0.380023	0.29578 12 at		clone 772323 3', mRNA sequence. (from Genbank)
			1	- (1	1	
သ	8 Lymphoma 0.9387285 0.4249089	0.9387285	0.4249089	0.37583	0.29255435 D8359/_at RP105	083597_at	RP105
ı							

FIG. 7A

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6	9 Lymphoma	0.9387285	0.4220441	0.372734	0.28904745)83597 at-2	0.28904745 D83597 at-2 Lymphocyte antigen 64 (mouse) homolog, radioprotective, 105kD
9	10 Lymphoma	0.9386553	0.419515	0.369998	0.28658897 62_at	RC_AA5212	RC_AA5212 EST: aa75e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 62_at IMAGE:826790 3', mRNA sequence. (from Genbank)
=	11 Lymphoma	0.9383826	0.4159639	0.367165	RC_AA4 0.28406295 87 s at	688	Synaptogyrin 2
12	12 Lymphoma	0.9362829	0.4131206	0.364741	0.2815551 t	s a	B-lymphocyte cell-surface antigen B1 (CD20)
33	13 Lymphoma	0.9303746	0.4113689	0.363488	0.27958748 X72755	at	Humig mRNA
4	Lymphoma	14 Lymphoma 0.9268587 0.4102988	0.4102988	0.361547	h 0 27747554 t	\A397670_a	EST: zt85h10.r1 Soares testis NHT Homo sapiens cDNA clone 729187 5' similar to TR:E243441 E243441 CHROMOSOME VII READING FRAME ORF YGR096W:;, mRNA sequence. (from Genhank)
15	Lymphoma	15 Lymphoma 0.9205939	0.4093482	0.360768	0.27558842 M89957_at	/89957_at	IGB Immunoglobulin-associated beta (B29)
9	Lymphoma	16 Lymphoma 0.9205939	0.4074558	0.358498	0.27373374 N	W89957 at-2	0.27373374 M89957 at-2 CD79B antigen (immunoglobulin-associated beta)
	17 Lymphoma	0.9166188	0.4050154	0.357199	0.27198726 t	X12530_s_a t	CD20 RECEPTOR
8	18 Lymphoma	0.8950695	0.4046188	0.355364	0.27013245 U77180	,at	EBI1-ligand chemokine
6	19 Lymphoma	0.8916236	0.4028494	0.35319	0.26860675 X07203_at		CD20 RECEPTOR
	20 Lymphoma	0.8882251	0.4017093	0.351473	0.26711926 U26174 at		GZMK Granzyme K (serine protease, granzyme 3)
<u></u>	21 Lymphoma	0.8726038	0.3992052	0.349987	0.26584104 40_s	A4642 at	EST: zx81a05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810128 3', mRNA sequence. (from Genbank)
- -	22 Lymphoma	0.8619036	0.3984305	0.348683	0.26451972 L	J03754 f at 1	0.26451972 U03754 f at Major histocompatibility complex, class I, A
	23 Lymphoma	0.8616518	0.3970168	0.347764	0.2633116	(02405 f at	0.2633116 K02405 f at CHAIN PRECURSOR
4	24 Lymphoma	0.8555751	0.3959627	0.346265	RC_A 0.2621845 20_at	A2336	EST: zr43d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666159 3', mRNA sequence. (from Genbank)
- 2	Lymphoma	25 Lymphoma 0.8492417	0.3948609	0.345184	0.26096663	.11015 s at l	0.26096663 L11015 s at Lymphotoxin beta (TNF superfamily, member 3)
9	-ymphoma	26 Lymphoma 0.8464394 0.3942199	0.3942199	0.343726	RC_AA 0.25982982 00_f_at	3C_AA4189 00_f_at	RC_AA4189 EST: zw01g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 00 f_at 768050 3', mRNA sequence. (from Genbank)

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				-		7.1.1	
27	27 Lymphoma	0.8429168	0.3928429	0.342734	AFFA- HSAC07/X 0.25865674 0351_5_at	0	AFFX-HSAC07/X00351_5_at (endogenous control)
						AFFX-	
28	28 Lymphoma	0.8429168	0.3918851	0.341933	0.25756884	HSAC07/X0 0.25756884 0351 5 at-2	No info for gene
			ı				
29	29 Lymphoma	0.8387807	0.3902384	0.341365	0.2561314		Homo sapiens mRNA for KIAA0746 protein, partial cds
30	Lymphoma	30 Lymphoma 0.8276051	0.389963	0.340044	A 0.25533625 t	F006083_a	Actin-related protein 3
						and the second s	Himan DNA cominance from clone 753D9 on chromosome Xc25_26 1
							Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-
31	Lymphoma	31 Lymphoma 0.8237535 0.3887247	0.3887247	0.339399	0.2545945	wz34791_a	Pro/X-Pro/Proline/Aminoacy/proline Aminopepudase) and a novel gene. Contains ESTs, STSs, GSSs and a gaaa repeat polymorphism
33	Ivmohoma	0.822552	0.3874336	0.338579	0.25371173.T80746 s		at Ferritin. light polypeptide
		_	1			21	
33	33 Lymphoma	0.8151091	0.3867773	0.337949	0.252441	,	Human MDA-7 (mda-7) mRNA, complete cds
70	conociana, I	04 i viriahomo 0 9445976	0.9853703	902250	RC_A	A4057	EST: zu66d12.s1 Soares testis NHT Homo sapiens cDNA clone
2	Lymbio	0.071	- 1	0.001200	77011020		FST: vf36a08.r1 Homo sapiens cDNA clone 128918 5'. (from
35	35 Lymphoma	0.8091871	0.3853414	0.336841	0.25094026 R10770_at		Genbank)
36	36 Lymphoma	0.8019967	0.3847336	0.335767	0.2501192 U66464	at t	Hematopoietic progenitor kinase (HPK1) mRNA
							,
37	37 Lymphoma	0.8019967	0.3836153	0.335362	0.24927327		Human hematopoietic progenitor kinase (HPK1) mRNA, complete cds
38	38 Lymphoma	0.8008153	0.3828973	0.33447	RC_A 0.2485061 90_at	A4004	EST; zu70a04.s1 Soares testis NHT Homo sapiens cDNA clone 743310 3', mRNA sequence. (from Genbank)
						AFFX-	
						HSAC07/X0	
133	Lymphoma	39 Lymphoma 0.8000225	0.3816113	0.334149	0.24769732	0351 M at-2	0.24769732 0351 M_at-2 No info for gene
3				000	0.0000		AFEV HCACOTIVADOR 1 M of (and annotation)
9	40 Lympnoma	C770008'0	0.3814/41	0.333399	U.24092120 U331 IN AL		AFFA-HOACUT/AUUSSI IN AL (EIIUUSEIIUUS COIIIIUI)
41	41 Lymphoma	0.7972664	0.380874	0.332567	0.24620968 47 at	47 at	687936 3', mRNA sequence. (from Genbank)
42	42 I vmnhoma		0.7929604 0.3798588	0.332131	0.24549004 R72037	R72037 at	EST: yj86c09.r1 Homo sapiens cDNA clone 155632 5'. (from Genhank)
14	Lyinhinding		0.01	0.002	2001011	2007	

0.24464384	M21121_s_a 0.24399655 t	H61295_s_a	FST: 71.02543 of 0.02543 of 0.02543	RC_AA4117 0.24247827 64_at	RC_AA4541 EST: zx46f10.s1 Soares testis NHT Homo sapiens cDNA clone 795307 31 mRNA sequence (from 5 april 5 clone con 5 clone con 5 clone	AA284380_s 0.2412768_at	0.24079382 X62466_at	0.24013416 M91391 at		0.0000000000000000000000000000000000000	1	0.23836167 44 at	RC_AA3423 0.23770358 55_s_at	AA336515_a	0.0000000000000000000000000000000000000	U.23074928 X80822 1 at Ribosomal protein L18a	9 0.23622586 W56046_at Homo sapiens mRNA for KIAA0748 profess and all all all all all all all all all al	0.23569952 X00274 at	0.2353530171 at	0.23485571 09 at	
0.24464384	0.24399655	0.2431649		RC_AA411 0.24247827 64_at	RC_AA454 0.24177948 59 at	0.2412768 at	0.24079382 X62466_at	0.24013416 M91391 at	0.23944487 t	0.0000000000000000000000000000000000000	N.23032232 M91196 at RC AA4240	0.23836167 44 at	RC_AA3423 0.23770358 55_s_at	VA336515			0.23622586 W56046 at	0.23569952 X00274 at	0.23535301 71 at	RC_AA4559 0.23485571 09_at	1136700 0 0
41 0.331334	99 0.330905	93 0.330266		17 0.329454	96 0.328968	0.328373	96 0.328049	93 0.327628	28 0.327199	0 328600		5 0.326162	2 0.325412	4 0.325068			1 0.324009	5 0.323585	5 0.323094	0.323017	
74 0.3792441	57 0.37865	33 0.37806		9 0.37747	0.3771496	3 0.3763106	1 0.37586	9 0.3755993	3 0.37528	5 0.3751609		0.3747905	5 0.3747272	0.374041	0.3738239	1	0.3737581	0.3729435	0.3709495	0.3707112	
a 0.7912974	a 0.79105	a 0.790649		0.789410	0.7892708	0.7890263	0.785218	0.7837459	0.7835063	0.783353		0.778577	0.7767535	0.7658663	0.7642185		0.7626857	0.7604024	0.7560449	0.7557885	
43 Lymphoma	44 Lymphoma 0.7910557 0.3786599	45 Lymphoma 0.7906493 0.3780693		46 Lymphoma 0.7894109 0.3774717	47 Lymphoma	48 Lymphoma	49 Lymphoma 0.7852181 0.3758696	50 Lymphoma	51 Lymphoma	52 Lymphoma 0.7833535	52 ymphome	2 Eymproma	54 Lymphoma	55 Lymphoma 0.7658663 0.3740414	56 Lymphoma		ov Lymphoma	58 Lymphoma	59 Lymphoma 0.7560449	60 Lymphoma	

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FIG. 7E

The first print print pears the mean pears to the pears of the pears o

62 Lymph	62 Lymphoma 0.7490465	465 0.3702929	9 0.32174	0.23369147 T67231 at	Succinate dehydrogenase complex, subunit D, integral membrane protein
63 Lymphoma	10ma 0.7488897	897 0.3698789	0.32		65
64 Lymph	64 Lymphoma 0.7479789	789 0.3698091	0.320927	C02143_s_a	
65 Lymphoma	loma 0.7438281		ļ	RC_AA4821 0.23229563 12 at	11 EST: zv43b10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756379 3* mRNA sequence (from Conhad)
66 Lymphoma	ioma 0.7400417	417 0.3696365		RC 0.2318304 13	_
67 Lymphoma	oma 0.7389721	721 0.3694383	0.318992	0	
68 Lутрћота	ота 0.7383922	922 0.3687783	0.318945		
69 Lymphoma	oma 0.7375007	0.3676483	0.318928	0.23051777 t	
70 Lymphoma	oma 0.7357451	151 0.3676318	0.318476	0.22993934 69 at	
71 Lymphoma	oma 0.7281507	507 0.367251	0.317995	0.22959355 89 at	
72 Lymphoma	oma 0.7273517	517 0.3669045	0.317629	0.22924097	AA095867_a EST: 16224.seq.F Fetal heart, Lambda ZAP Express Homo sapiens to CDNA 5', mRNA sequence. (from Genbank)
73 Lymphoma	0 72724	724 0 3664121	0.347964	M34996 s a	
			0.0	U.ZZ6646Z3 I RC AA4599	MHC cell surface glycoprotein (HLA-DQA) mRNA, 3'end 9 EST: 2x66c03 s1 Spares Intal Fatus Nh2HER Quir Home conjunctions
74 Lymphoma	oma 0.7252355	355 0.3655395	0.316948	0.22835961 61_at	
75 Lymphoma	oma 0.7243797	97 0.365009	0.31675	M13560_s 0.22800298 t	M13560_s_a PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 t
76 Lympho	oma 0.71972	76 Lymphoma 0.7197233 0.3646756	0.316547	0.22754906 W28944_at	EST: 54h12 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
77 Lymphoma	j	0.717179 0.3640513	0.316154	0.22705099 U22662_at	Nuclear orphan receptor LXR-alpha mRNA
78 Lymphoma	oma 0.7169247	47 0.3638963	0.345407	AA291334_01994334_	AA291334_a ENTRY III (HUMAN); contains Alu repetitive element;, mRNA
79 Lymphoma	oma 0.7155678		0.315193	0.22637036 37_at	Sequence: (non Senibalis) EST: aa44a02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 823754 3', mRNA sequence. (from Genhank)
80 Lympho	80 Lymphoma 0.7154263	63 0.3626657	0.314872	0.22598217 X61072 at	0.22598217 X61072_at-2 Human mRNA for T cell receptor, clone IGRA17

The control of the co

RC_AA1324 clone 588262 3' similar to contains OFR.t3 OFR repetitive element;, EST: zo28g12.s1 Stratagene colon (#937204) Homo sapiens cDNA RC_AA4217 EST: zu24b05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone AA431017_a EST: PMY0907 KG1-a Lambda Zap Express cDNA library Homo EST: zv01e07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone AA505198_a EST: aa58c03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone EST: zs94h08.s1 NCI CGAP GCB1 Homo sapiens cDNA clone EST: zr97d02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone EST: aa55f02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone EST: H. sapiens partial cDNA sequence; clone c-2ie11, mRNA AA383520_a EST: EST97097 Testis I Homo sapiens cDNA 5' end, mRNA IMAGE:746244 3', mRNA sequence. (from Genbank) IMAGE:825124 5', mRNA sequence. (from Genbank) IMAGE:6836193', mRNA sequence. (from Genbank) HYPOTHETICAL MYELOID CELL LINE PROTEIN 3 IMAGE:705183 3', mRNA sequence. (from Genbank) IMAGE:824859 3', mRNA sequence. (from Genbank) sapiens cDNA 5', mRNA sequence. (from Genbank) 0.22408882 Y11215 at-2 Src kinase-associated phosphoprotein of 55 kDa MYOCYTE-SPECIFIC ENHANCER FACTOR 2 738897 3', mRNA sequence. (from Genbank) mRNA sequence. (from Genbank) T cell receptor, clone IGRA17 sequence. (from Genbank) sequence. (from Genbank) CD53 CD53 antigen JAK binding protein SKAP55 protein CD19 antigen CD19 gene RC_AA4177 18_at RC_AA2153 0.22205266 83_at RC AA4888 RC AA2812 M84371_rna M84371_ma 0.22127011|D29642 at 0.22166076 M37033 at 0.21994573|F07806 at 0.22381018|X63380 at 0.22480145|U88326_at 0.22441822 Y11215_at 0.22549337 X61072_at 0.22086833 1 s at-2 0.22043738 | s at 0.22016425 15 at 0.22305155 09 at 0.22342251 98 at 0.22510928 78 at 0.21929313 18 0.21974152 0.22272788 0.22246407 0.308849 0.310419 0.310245 0.313013 0.312303 0.311203 0.31089 0.309563 0.309263 0.309017 0.31336 0.31275 0.31202 0.31183 0.311597 0.31127 0.314302 0.314074 0.313771 99|Lymphoma| 0.6918063| 0.3572623| 0.35943060.3581286 0.357708 87|Lymphoma| 0.7099217| 0.3610381| Lymphoma | 0.6936843 | 0.3580173 0.3623878 0.3619762 0.3617928 0.361472 0.3611044 0.3605840.3604647 92|Lymphoma| 0.7022232| 0.3601423| 0.698978 0.3597812 0.3594759 0.362527 0.36074 0.3609484 98|Lymphoma| 0.6927738| Lymphoma | 0.7096631 | 91 Lymphoma | 0.7072436 94|Lymphoma| 0.6976923| 95|Lymphoma| 0.6976923| 96|Lymphoma| 0.6940824| 82|Lymphoma| 0.7141152| 83 Lymphoma | 0.7134766 84 Lymphoma | 0.7129324 85 Lymphoma 0.7129324 86|Lymphoma| 0.7126781| 89|Lymphoma| 0.7088466| 90|Lymphoma| 0.7084061| 81 Lymphoma | 0.7154263 93 Lymphoma

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Docket No.:

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Invento	ors: Sri	dhar Ramaswamy, et al.

				1			
100	100 Lymphoma 0.6888455	0.6888455	0.3571636	0.308808	RC_A 0.21895884 12_at	A5987	EST: ae49d06.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950219 3', mRNA sequence. (from Genbank)
101	101 Lymphoma	0.6857551	0.3569513	0.308332	0.2185397	AA306911_a t	EST: EST178043 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)
102	102 Lymphoma	0.68516	0.3568401	0.308055	0.21811858 T81141	at	Yd24d03.r1 Homo sapiens cDNA clone 109157 5'. (from Genbank)
103	103 Lymphoma	0.6833432	0.3568399	0.307825	0.21779063 M26062_at		IL2RB Interleukin 2 receptor beta chain
104	104 Lymphoma	0.68047	0.356571	0.307504	0.2176248	0.2176248 U77942_at	Syntaxin 7
105	105 Lymphoma 0.6790842	0.6790842	0.356305	0.307406	RC_A 0.21729909 82_at	A4257	Homo sapiens mRNA for KIAA0874 protein, partial cds
106	106 Lymphoma 0.6786397	0.6786397	0.355918	0.307023	0.21709678	L02547_at-2	0.21709678 L02547_at-2 Cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD
107	107 Lymphoma	0.6786397	0.3555491	0.306949	0.21669526 L02547_at		CSTF1 Cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kD
108	108 Lymphoma	0.6782053	0.3554905	0.306665	0.21625909 M17733_at		Thymosin beta-4 mRNA
109	109 Lymphoma 0.6744419	0.6744419	0.3553441	0.306365	RC_A 0.21605416 23_at	A1734	EST: zp02d07.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595213 3', mRNA sequence. (from Genbank)
110	110 Lymphoma 0.6743678	0.6743678	0.3553281	0.30619	RC_AA4 0.215782 68_s_at	A4170 at	EST: zu13b04.s1 Soares testis NHT Homo sapiens cDNA clone 731695 3', mRNA sequence. (from Genbank)
11	111 Lymphoma 0.6742196 0.3548612	0.6742196	0.3548612	0.306033	M1 0.21552713 t-2	6336_s_a	CD2 antigen (p50), sheep red blood cell receptor
112	112 Lymphoma 0.6742196	0.6742196	0.3547999	0.305769	0.21527074 t	416336_s_a	CD2 CD2 antigen (p50), sheep red blood cell receptor
113	113 Lymphoma	0.6740577	0.354766	0.305437	0.21508488 N56493_at		EST: JJ9988F Homo sapiens cDNA clone JJ9988 5'. (from Genbank)
114	114 Lymphoma	0.6727566	0.3545109	0.305173	RC 0.21466826 37	_AA4637 _at	EST: aa07g07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 812604 3', mRNA sequence. (from Genbank)
115	115 Lymphoma	0.671299	0.3544803	0.304897	RC_A 0.21431512 88_at	A2113	EST: zq88c04.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 649062 3', mRNA sequence. (from Genbank)
116	116 Lymphoma	0.6700794	0.3540454	0.304614	0.21404636 IL2	at	No info for gene
117	117 Lymphoma 0.6651887 0.3536434	0.6651887	0.3536434	0.30452	0.21374978 H71130_at		Ys13d10.r1 Homo sapiens cDNA clone 214675 5'. (from Genbank)

The state of the s

at TTF mRNA for small G protein	0.21316981 Z35227_at-2 Ras homolog gene family, member H	0.21294783 M63262_at-2 Arachidonate 5-lipoxygenase-activating protein	at 5-lipoxygenase activating protein (FLAP) gene, exon 5	IT TYROSINE-PROTEIN KINASE ITK/TSK	0.2120807 L10717_at-2 (from Genbank)	RC_AA2119 EST: zq85a03.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 648364 3', mRNA sequence. (from Genbank)	AA091605_a Sparc/osteonectin, cwcv and kazal-like domains proteoglycan t	at CD37 CD37 antigen	76 EST: zu99g07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746172 3', mRNA sequence. (from Genbank)	 	1	Homo sapiens 5,10-methenyltetrahydrofolate synthetase mRNA, 0.2103295 L38928 at-2 complete cds	34 RNA guanylyltransferase and 5' phosphatase	AA127696_a EST: zk89d09.r1 Soares pregnant uterus NbHPU Homo sapiens t			
Z35227_at	Z35227_a	M63262_a	M63262_a	L10717_al	L10717_al	RC_AA21	AA091605 t	X14046_a	RC_AA4176 04 at	RC_AA5044 85 at		L38928 at	RC_AA2434 43_at	AA127696 t	H45382 at	RC_AA4241 71_at	X80822 a
0.21349148 Z35227_at	0.21316981	0.21294783	0.21268576 M63262_at	0.21245892 L10717_at	0.2120807	RC_A 0.21180731 09_at	0.21156687 t	0.21127483 X14046_at	RC_A 0.21110134 04 at	RC_A 0.21090299 85 at	0.21066643 L38928	0.2103295	RC_A 0.2101158 43 at	0.209809061	0.20949921 H45382	RC_A 0.20930217 71_at	0.20915093 X80822_at
0.304173	0.303992	0.303462	0.303305	0.30319	0.302925	0.30257	0.302472	0.302291	0.301832	0.301643	0.301447	0.301241	0.301194	0.301062	0.300933	0.300729	0.300447
0.3535279	0.3535053	0.3532871	0.353156	0.3531548	0.3529035	0.3527711	0.3524892	0.3521232	0.35183	0.3515028	0.3511734	0.3508883	0.3508499	0.3504031	0.3499805	0.3499138	0.648008 0.3495892
0.6646953		0.6639841	0.6639841	0.6630213	0.6630213	0.6608869	0.6594682	0.6590121	0.6584869	0.655122	0.6542777	0.6542777	0.6540586	0.6504417	0.6490832	0.6488603	0.648008
118 Lymphoma 0.6646953 0.3535279	119 Lymphoma 0.6646953	120 Lymphoma 0.6639841	121 Lymphoma	122 Lymphoma	123 Lymphoma	124 Lymphoma	125 Lymphoma	126 Lymphoma	127 Lymphoma	128 Lymphoma	129 Lymphoma	130 Lymphoma	131 Lymphoma		133 Lymphoma		135 Lymphoma
118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135

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GF3A 5_3 No info for gene	GF3A 5_3_	107_a EST: zr58b05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 667569 5', mRNA sequence. (from Genbank)	at Ly-9 mRNA	0.20820804 L42621_at-2 Lymphocyte antigen 9	RC_AA4548_EST: zx79h01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 74_at clone 810001 3', mRNA sequence. (from Genbank)	2_at. CTSH Cathepsin H	(4500 Homo sapiens clones 24718 and 24825 mRNA sequence		A4314 EST: zw70h05.s1 Soares testis NHT Homo sapiens cDNA clone 781593 3', mRNA sequence. (from Genbank)	at Homo sapiens mRNA for putative glucosyltransferase, partial cds		A2828 EST: zs91g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704880 3', mRNA sequence. (from Genbank)	8_at GABRR2 Gamma-aminobutyric acid (GABA) receptor, rho 2	0.20615818 M86868_at-2 Gamma-aminobutyric acid (GABA) receptor, rho 2	EST: ye11d01.r1 Homo sapiens cDNA clone 117409 5'. (from 5_at Genbank)	2_at CTSC Cathepsin C	AA464386_a EST: zx81f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA to clone 810169 5', mRNA sequence. (from Genbank)
AFFX- HUMISGF3A /M97935_3_ 0.20897247 at-2	AFFX- HUMISGF3A /M97935_3_ 0.20876388 at	AA228107_a 0.20863587 t	0.20838855 L42621	20820804 L42621	0.20800468 74_at	0.20780928 X16832_at.	RC_AA4500 0.20753191 92_at	AA456343_a 0.20736966 t	RC_AA4314 0.20700513 70_at	0.20686175 T95430	0.20672481 H84451_at	RC_AA2828 0.2064698 86_at	0.20625661 M86868_at	.20615818 M8686	0.20575918 T89815	0.20563205 X87212_at	AA464 0.20542054 t
0.300173 0	0.300137 0	0.299881 0	0.299642 0	0.299378 0	0.299244 0	0.299102 0	0.298944 0	0.29888 0	0.298694 0	0.298532 0	0.298457	0.297992	0.297976	0.297942	0.297942	0.297691	0.297532
0.3493336	0.3488649	0.3484443	0.3483919	0.3483879	0.3481848	0.3475847	0.3472823	0.3471331	0.3469061	0.3468661	0.3467815	0.3466618	0.3466069	0.3462975	0.3460721	0.3458356	0.3457728
0.647913	0.647913	138 Lymphoma 0.6457862 0.3484443	139 Lymphoma 0.6457266	0.6457266	0.6451268	0.6450587	143 Lymphoma 0.6445535	144 Lymphoma 0.6427078	0.6420125	0.6414065	0.6410974	148 Lymphoma 0.6409587	149 Lymphoma 0.6392438	150 Lymphoma 0.6392438	151 Lymphoma 0.6388556	152 Lymphoma 0.6377919	153 Lymphoma 0.6376922
136 Lymphoma	137 Lymphoma	Lymphorna	Lymphoma	140 Lymphoma	141 Lymphoma	142 Lymphoma	Lymphoma	Lymphoma	145 Lymphoma	146 Lymphoma	147 Lymphoma	Lymphoma	Lymphoma	Lymphoma	Lymphoma	Lymphoma	Lymphoma
136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153

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154	-ymphoma	154 Lymphoma 0.6367463	0.3457412	0.297307	0.20513533 76_	_AA2325 _at	EST: zr45d09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666353 3', mRNA sequence. (from Genbank)
155 1	-утрһота	155 Lymphoma 0.6362119	0.345283	0.29715	0.20476702 N23786	N23786_at	EST: yx35f11.r1 Homo sapiens cDNA clone 263757 5' similar to SP:S28583 S28583 RFBG PROTEIN - YERSINIA; (from Genbank)
156	156 Lymphoma	0.6356936	0.3448143	0.296967	0.20462623 V00478 s		at Actin, beta
157	157 Lymphoma	0.6348108	0.3447667	0.296798	0.20436633 C16652_at		KIAA0575 gene product
158	_ymphoma	158 Lymphoma 0.6334174	0.3445712	0.296551	0.20423472 t-2	0391_s_a	Interleukin 16 (lymphocyte chemoattractant factor)
159	159 Lymphoma	0.6334174	0.3445046	0.296512	0.20408845	M90391_s_a t	Putative IL-16 protein precursor, mRNA
160	160 Lymphoma	0.6323038	0.3437625	0.2963	0.2038871	AA090608_a t	AA090608_a EST: y0994.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)
161	161 Lymphoma	0.6322891	0.3434948	0.295897	0.203547	X93996_ma 1_at-2	H.sapiens mRNA for AFX protein
162	162 L.ymphoma	0.6322891	0.3434582	0.295745	X 0.20334846 1	X93996_rna 1_at	AFX protein
163	163 Lymphoma	0.6318573	0.343134	0.29562	0.20316143 X68149	X68149_at	BLR1 Burkitt lymphoma receptor 1, GTP-binding protein
164	164 Lymphoma	0.6317993	0.3429457	0.295356	0.2029678	RC_D59337 at	EST: Human fetal brain cDNA 3'-end GEN-017C09, mRNA sequence. (from Genbank)
165 1	165 Lymphoma	0.6316616	0.3428134	0.295166	0.20268214 18	RC_AA0444 18_at	EST: zk52g04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486486 3', mRNA sequence. (from Genbank)
166	166 Lymphoma	0.6299456	0.3420202	0.294892	0.20256962 W26322	W26322_at	Homo sapiens mRNA for KIAA0745 protein, partial cds
167	167 Lymphoma	0.6292235	0.3418647	0.294834	0.20239066 W28167 at	W28167 at	EST: 43a1 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
1681	-ymphoma		0.3418586	0.294624	0.20229895 76 s at	783	EST: zt08a12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712510 3'. mRNA sequence, (from Genbank)
1691	169 Lymphoma	0.6275017	0.3416064	0.294517	0.20202437 t	M63438_s_a t	GLUL Glutamate-ammonia ligase (glutamine synthase)
170	170 Lymphoma	0.6260822	0.3415106	0.29442	0.20180394 W03796	W03796_at	EST: za60c08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 296942 5', mRNA sequence. (from Genbank)
171	-ymphoma	171 Lymphoma 0.6259733	0.3413357	0.294323	RC_A 0.20164922 38 at	RC_AA5991 38 at	EST: ae52c11.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950516 3', mRNA sequence, (from Genbank)
172	утрнота	172 Lymphoma 0.6259022 0.3409944	0.3409944	0.294272	RC 0.20139566 26	RC_AA4568 26_at	EST: aa38f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815545 3', mRNA sequence. (from Genbank)

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17	173 Lymphoma	0.6239243	0.3409797	0.29411	RC 0.2012495827	3C_AA2798	RC_AA2798 EST: zs92f08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 27_at IMAGE:704967 3', mRNA sequence. (from Genbank)
17	174 Lymphoma	0.6238103	0.3407115	0.29403	RC_A 0.20105797 79_at	RC_AA4009 79_at	Homo sapiens mRNA encoding RAMP3
							EST: zw57b10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
					i-li-	RC AA4520	clone 774139 3' similar to SW:YHS2_YEAST P38829 HYPOTHETICAL 25.7 KD PROTFIN IN MSH1-ED14 INTEDGENIC
17	175 Lymphoma		0.6236455 0.3404308	0.293811	0.20084909 20 at	0 at	REGION: ;; mRNA sequence. (from Genbank)
17.	176 Lymphoma 0.6235814	0.6235814	0.3402013	0.293805	0.20071124 56_s_at	RC_AA4361 56_s_at	EST: zv22b10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754363 3', mRNA sequence. (from Genhank)
17.	177 Lymphoma	0.6234056	0.3400871	0.293326	RC 0 20041151 01	910	EST: aa52g12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824614 3' similar to TR:G1293732 G1293732 O3625P. ;;
178	178 Lymphoma		0.3400037	0.293177	0.20022374 t	A095041_a	AA095041_a EST: cp2556.seq.F Fetal heart, Lambda ZAP Express Homo sapiens to CDNA 5' mRNA sequence (from Canhank)
17.6	179 Lymphoma	0.620492	0.339471	0.293074	0.20008999 L00022_s		at IG EPSILON CHAIN C REGION
180	180 Lymphoma	0.6197528	0.3393022	0.292957	0.19990304 U15085 at		HLA-DMB Major histocompatibility complex class II DM hoto
<u>\$</u>	184 I vmohoma			000000000000000000000000000000000000000			EST: zd59e04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344958 5' similar to contains element MIR repetitive element
2	Lyinpiioiiia	0.0130/89	0.3392795	0.292582	0.1997247 W76097	ä,	mRNA sequence. (from Genbank)
182	182 Lymphoma	0.6179242	0.3392694	0.29256	0.19949141 R51954 at		EST: yj71g02.r1 Homo sapiens cDNA clone 154226 5'. (from Genbank)
183	183 Lymphoma	0.6176816	0.3391704	0.292396	0.19938862 t		MHC class II HLA-DP light chain mRNA
184	184 Lymphoma	0.6168518	0.3389453	0.292239	0.19923042 42_at	A2794	EST: zs84g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704208 31 mRNA sequence (from Canhark)
185	185 Lymphoma 0.6168244		0.3388142	0.292137	RC_A 0.1990895421_at	A4265	Nuclear autoantigen of 14 kDa
186	186 Lymphoma	0.616739	0.3387973	0.291794	0.19888093 M37766_at		CD48 CD48 antigen (B-cell membrane profein)
187	187 Lymphoma	0.6158703	0.3385952	0.291628	0.19873658 W60268_at		EST: zd29g01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342096 5', mRNA sequence. (from Genbank)
188	188 Lymphoma 0.6157668		0.3384735	0.29159	RC_AA2 0.198567 69 s at	533	EST: zr77b01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669385 3' similar to SW:YIAE_ECOL! P37666 PUTATIVE 2-HYDROXYACID DEHYDROGENASE IN BISC-CSPA INTERGENIC REGION: mRNA sequence (from General).
189	189 Lymphoma 0.6150584	0.6150584	0.338334	0.291581	RC_A 0.19841205 78_at	A4639	EST: zx86f03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810653.31 mRNA sequence (from Canhant)
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FIG 712

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Inventors: Sridhar Ramaswamy, et al. AA131252 a EST: zi31g02.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA RC AA4473 EST: zw87b08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: zc55c07.r1 Soares senescent fibroblasts NbHSF Homo sapiens EST: zc24d03.r1 Soares senescent fibroblasts NbHSF Homo sapiens clone 725897 3' similar to SW:ATF4_MOUSE Q06507 CYCLIC-AMP-RC_AA0051 cDNA clone 429050 3' similar to contains MER10.t3 MER10 repetitive EST: zh95e02.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens CYTOSOL AMINOPEPTIDASE;, mRNA sequence. (from Genbank) 0.1965617 53_at clone 723877 3', mRNA sequence. (from Genbank)
RC_AA2367 EST: zt29b02.s1 Soares ovary tumor NbHOT Homo saplens cDNA 0.1962034 68 s at clone 783927 3; mkink sequerice, (1962034 68 s at ab23e08.s1 Stratagene lung (#937210) Homo sapiens cDNA RC_AA4875 EST: ab23e08.s1 Stratagene lung (#937210) Homo sapiens cDNA RC_AA2355 EST: zt30f07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zt51f09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zv96d05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone repetitive element; contains element MER22 repetitive element; DEPENDENT TRANSCRIPTION FACTOR ATF-4 ; contains Alu AA418341_a 767625 5' similar to TR:G790473 G790473 GLYCINE RICH cDNA clone 326220 5' similar to SW:AMPL_BOVIN P00727 cDNA clone 323237 5', mRNA sequence. (from Genbank) clone 723723 3', mRNA sequence. (from Genbank) clone 503570 5', mRNA sequence. (from Genbank) 0.19727501 L41067_at-2 Nuclear factor of activated T-cells, cytoplasmic 4 PROTEIN: ;, mRNA sequence. (from Genbank) element;, mRNA sequence. (from Genbank) Endothelial differentiation-related factor 1 mRNA sequence. (from Genbank) Transcription factor NFATx mRNA Variably charged, Y chromosome KIAA0342 gene product HEM45 mRNA AA417129_a AB002340_a AA308998 a RC AA2923 0.196988 W42818 at 0.19679432 U88964 at ਜ਼ 0.1976103|L41067 at 0.19712873|W52821 0.19634266 02_at 0.19771034|35 at 0.19611338 63 at 0.19824977 28 at 0.19546083|t 0.19796516 0.19785275 0.19592279 0.19566914 0.289676 0.291436 0.291109 0.290568 0.289816 0.289296 0.291011 0.290138 0.289922 205 Lymphoma | 0.6010132 | 0.3351582 | 0.288657 0.29081 0.290698 0.290047 0.288951 0.288896 0.288708 0.614148 0.3378646 192 Lymphoma | 0.6124772 | 0.3377244 198 Lymphoma | 0.6056334 | 0.3365406 204 Lymphoma | 0.6014947 | 0.3354379 194 Lymphoma | 0.6104602 | 0.3376215 195 Lymphoma | 0.6104602 | 0.3375353 197 Lymphoma 0.6060559 0.3365648 199|Lymphoma | 0.6049919 | 0.3365244 200 Lymphoma | 0.6041677 | 0.3362633 0.602225 0.3354623 0.337978 0.337166 201 Lymphoma | 0.6035701 | 0.3358352 202 Lymphoma | 0.6022907 | 0.3356193 0.610876 0.3376651 196 Lymphoma | 0.6075186 190 Lymphoma | 0.6147595 191 Lymphoma 193 Lymphoma 203 Lymphoma

2825.2020-002

Title: Genetic Markers for Tumors

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0.599709

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208 Lymphoma 0.5991827

2825.2020-002 Docket No.: Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. EST: zx36e07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 340552 5' similar to PIR:S55053 S55053 Sm protein F - human AA463311_a EST: zx71d12.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: zd13e09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA EST: PTH078 HTCDL1 Homo sapiens cDNA 5/3', mRNA sequence. AA249434_a EST: j3922.seq.F Human fetal heart, Lambda ZAP Express Homo RC_AA2337 EST: zr47e07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 0.19427946 07_at 666564 3', mRNA sequence ffrom Genhanks EST: zr75d05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA4811 EST: aa34h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone EST: zr65f12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone AA263061_s EST: PMY0414 KG1-a Lambda Zap Express cDNA library Homo RC_AA2526 EST: zs14d03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog RC_D20846 EST: Human HL60 3'directed Mbol cDNA, HUMGS01827, clone clone 788580 3' similar to TR:G1255172 G1255172 MATERNAL 0.1946968 Z36531_at-2 H.sapiens mRNA for fibrinogen-like protein (pT49 protein) IMAGE:815205 3', mRNA sequence. (from Genbank) IMAGE:685157 3', mRNA sequence. (from Genbank) sapiens cDNA 5', mRNA sequence. (from Genbank) sapiens cDNA 5', mRNA sequence. (from Genbank) clone 796919 5', mRNA sequence. (from Genbank) TRANSCRIPT;, mRNA sequence. (from Genbank) Human mRNA for KIAA0309 gene, partial cds Homo sapiens clone 24649 mRNA sequence 668303 3', mRNA sequence. (from Genbank) 669225 3', mRNA sequence. (from Genbank) mp0825, mRNA sequence. (from Genbank) !;, mRNA sequence. (from Genbank) 0.1954222|D25278_at-2|KIAA0036 gene product FGL1 Fibrinogen-like 1 KIAA0036 gene (from Genbank) AA471278_a AB002307_a AA095959 a RC_AA2428 RC AA2326 RC AA4528 AA174152 f 0.19412436 W55958 at 0.19531766 D25278 at 0.19488768 Z36531 at 0.19348125|29 s at 0.19291164|86 i at 0.19445857 16 at 0.19404012 69 at 0.19259624 73 at 0.19504936 at 0.19319665 at 0.19276343 at 0.19457611 0.19515973|t 0.19387074 0.1936752t 0.19333233 0.285955 0.288268 0.288017 0.287906 0.287659 0.287261 215 Lymphoma 0.5962955 0.3340617 0.287076 0.286832 219|Lymphoma 0.5953296| 0.3332205| 0.286233| 0.285802 0.285705 0.285656 0.288444 0.28827 0.287581 0.286737 0.286269 0.287781 0.285801 217 Lymphoma | 0.5958921 | 0.3337846 | 216 Lymphoma 0.5962682 0.3338244 224 Lymphoma | 0.5908444 | 0.3324568 0.3346944 0.333382221 Lymphoma 0.5943639 0.3331268 223 Lymphoma 0.5929736 0.3326703 0.3351251 0.3349007 0.3348074 0.3346194 0.334581 213 Lymphoma | 0.5970908 | 0.3345466 220 Lymphoma 0.5944234 0.3331291 0.3350765 214 Lymphoma | 0.5963791 | 0.3343524 222 Lymphoma | 0.5939278 | 0.3328537

218 Lymphoma 0.5953891

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IMAGE:825206 3', mRNA sequence, (from Genbank)	EST: aa27b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814455 3', mRNA sequence. (from Genbank)	EST: ae48g12.s1 Stratagene lung carcinoma 937218 Homo sapiens	CDIVA CIOITE 930 I 02 3, INKINA Sequence. (Irom Genbank)	ILST: 2823605.31 INCL COAF GODT HOTTO Septems COMA CIONE IMAGE:686050 3', mRNA sequence. (from Genbank)	EST: zw99b11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 785085 3', mRNA sequence. (from Genbank)	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence.	(from Genbank)	Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	EST: zt49e08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA			clone 725903 5', mRNA sequence. (from Genbank)	EST: ze18c10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 359346 3', mRNA sequence. (from Genbank)	EST: yf36a10.r1 Homo sapiens cDNA clone 128922 5'. (from	FST: 2/23h12 s1 Spares NhHMPii S1 Homo sanians cDNA clone	754463 3', mRNA sequence. (from Genbank)	Human G protein-coupled receptor STRL33.1 (STRL33) mRNA,	complete cas	EST: zc32a07.r1 Soares senescent fibroblasts NbHSF Homo sapiens	CT: CETTON CT NOT COME CONTINUED CON	IMAGE:824510 3' similar to SW:YHS2_YEAST P38829	HYPOTHETICAL 25.7 KD PROTEIN IN MSH1-EPT1 INTERGENIC REGION: ,; mRNA sequence. (from Genbank)	Transcrintion factor 21	Lymphoid-specific SP100 homolog (LYSP100-A) mRNA	EST: zv37f09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755849 3', mRNA sequence. (from Genbank)	
- - - -	RC_AA4592 55_at	RC_AA5984	ר מ	54_at	RC_AA4763	26_at		D30851_at	M38193_rna 1_s_at	RC_AA3941	40_at	AA292417_a		RC_AA0105	40_at	D10268 of	RC AA4103	04_at	l	0/3331 at	0.10063637 W/6/89	1140400 at		RC_AA4905 22 at	W73859 at	U36500_at	RC_AA4963 74_at	
0.19248536 10_at	RC_A 0.19236875 55_at	RC 0.1022476.60	0.1322410	0.19209908 54_at		0.19189425 26_at		0.19179058 D30851	0.19164877	0,000,000	0.19146943 40 at		0.1913584 t		0.19117041 40	0.10104208 010266 21	0.10101.0	0.19090241 04_at	0.40078037	0.13010331	0.10063637	0.13000003		RC_A 0.19043598 22_at	0.1903317 W73859	0.19014046 U36500_at	RC 0.1900124 74	
0.285575	0.285233	0.085134		0.284957	-	0.284852	00,00	0.28468	0.28468		0.284494	6	0.28426		0.284246	0.283924	1000	0.283786	0.283705	0.202/00	0.283572	0.200012		0.283544	0.283496	0.283341	0.28316	
0.3324449	0.3324449	0.3300840	0.0022042	0.3322307		0.3321207		0.3320767	0.3320094	0.0040550	0.3319556		0.3318547		0.331796	0.3317198		0.3316788	0 331614	0.00.0	0.3314471			0.3314471	0.3314118	0.3313564	0.3307783	
0.5894775	0.5891589	0 5801118	0.000.0	0.5882627		0.5881668		0.5854048	0.5850233	0 5040040	0.5842519	1	0.5838729		0.5827766	0 5825497		0.5823731	0.581524	t-701.00:0	0.5810957	100010010		0.5796109	0.5790964	0.5790461	0.5780443	
225 Lymphoma 0.5894775	226 Lymphoma	227 vmphoma 0 5801118 0 33228/2	Lympholia	228 Lymphoma	-	229 Lymphoma	900	zso Lympnoma	231 Lymphoma	omodami	232 Lymproma 0.3842319	-	233 Lymphoma		234 Lymphoma	235 Lymphoma		236 Lymphoma	237 I vmnhoma	Ly morning	238 vmnhoma 0.5810957	Superior de la constante de la		239 Lymphoma 0.5796109	240 Lymphoma	241 Lymphoma	242 Lymphoma 0.5780443 0.3307783	
225	226	700	777	228	0	223	200	0€2	231	222	707	ç	233	Č	734	235		236	237	123	238			239	240	241	242	

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24.	3 Lymphome	a 0.5779285	243 Lymphoma 0.5779289 0.3303202	0.283016		0.18985632 U77664 at	RNaseP protein p38 (RPP38) mRNA
24,	4 Lymphoma	244 Lymphoma 0.5779289	0.3302951	0.283001	0.1897808 U77664	U77664_at-2	at-2 Human RNaseP protein p38 (RPP38) mRNA, complete cds
24;	Lymphoma	0.5773971	245 Lymphoma 0.5773971 0.3302223	0.282936	0.18964787	0.18964787 J05070 at	MMP2 Matrix metalloprofeinase 2 (nelatinase A. collaccina, to matrix metalloprofeinase 2 (nelatinase A. collaccina)
246	Lymphoma	246 Lymphoma 0.5759504	0.330207	0.282876	RC_A 0.18952262 72_at	RC_AA2521 72 at	EST: zr64d03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668165 31 mRNA sequence (from Conhant)
247	Lymphoma	0.5754765	247 Lymphoma 0.5754765 0.3301813	0.282529	0.18941422	RC_D59367 _at	EST: Human fetal brain cDNA 3'-end GEN-023H06, mRNA sequence. (from Genbank)
248	Lymphoma	248 Lymphoma 0.5747802	0.3301446	0.282478	RC_A 0.189284 78_at	RC_AA4321 78_at	EST: zw71g02.s1 Soares testis NHT Homo sapiens cDNA clone 781682 3', mRNA sequence (from Ganhank)
246	249 Lymphoma	0.5742781	0.3300333	0.282335	RC_A 0.18921274 49_at	RC_AA4054 49_at	EST: zw36a04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 772110 3', mRNA sequence (from Genhank)
250	Lymphoma	250 Lymphoma 0.5737209	0.3298904	0.2823	0.18912192 W03361	W03361_at	EST: za06g11.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone 291812.5', mRNA sequence (from Genhank)
251	251 Lymphoma		0.573499 0.3298328	0.282069	0.18901318	AA405119_a	EST: zu65c11.r1 Soares testis NHT Homo sapiens cDNA clone 742868 5' similar to TR:G1066392 G1066392 T(3;5)(Q25.1;P34) FUSION GENE NPM-MLF1 mRNA seruence (from Genthank)
252	Lymphoma	252 Lymphoma 0.5728199	0.3297132	0.282033	RC_A 0.18875816 24 at	RC_AA5987 24 at	RC_AA5987 EST: ae49f01.s1 Stratagene lung carcinoma 937218 Homo sapiens 24 at CDNA clone 950233 3' mRNA sequence (from Contact)
253	Lymphoma	253 Lymphoma 0.5720688 0.3295716	0.3295716	0.281966	0.18853574	RC_AA4279 20 at	RC_AA4279 EST: zw53d01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA contract from Contract Clone 773761 3' mRNA contract from Contract Clone 773761 3' mRNA contract from Contract Clone 773761 3' mRNA contract from Contract
254	Lутрhота	254 Lymphoma 0.5719351	0.3294361	0.281912	0.1884533 93 at	A2629	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit
255	255 Lymphoma	0.571813	0.3291288	0.281904	0.18835653	AA255638_a t	Thioredoxin-like 32kD
256	Lymphoma	256 Lymphoma 0.5717578 0.3290648	0.3290648	0.281579	0.18819246	AF000575_s at	AF000575_s Human clone HL9 monocyte inhibitory receptor precursor mRNA, at complete cds
257	Lymphoma	257 Lymphoma 0.5716004 0.3290647	0.3290647	0.281549	0.18809885 H26812 at		EST: yl63d06.r1 Homo sapiens cDNA clone 162923 5', (from Genbank)
258	Lymphoma	258 Lymphoma 0.5714207 0.3282786	0.3282786	0.281293	0.18795352 59_s_at	407	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3 (12kD, B12)
259	Lymphoma	259 Lymphoma 0.5712059	0.3281435	0.281256	0.18780105)	K15949_at-2	0.18780105 X15949_at-2 Interferon regulatory factor 2
260	Lymphoma	260 Lymphoma 0.5712059	0.3279782	0.281226	0.18766367 X15949	(15949_at	IRF2 Interferon regulatory factor 2
261	Lymphoma	261 Lymphoma 0.5705517 0.3279154	0.3279154	0.281109	0.1875422 N23801	at	EST: yx36b12.r1 Homo sapiens cDNA clone 263807 5'. (from Genbank)
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26	262 Lymphoma	0.569451	0.3278902	0.281022	0.187467551	AA424111_e t	AA424111_a EST: zv80e06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA to clone 759970 5' mRNA sequence (from Canhank)
26	263 Lymphoma	0.5688793	3 0.3278369	0.280947	X 0.1872783	X97267_rna 1_s_at	LPAP gene
26	264 Lymphoma, 0.5686818	0.5686818	0.3277679	0.280850	4 018711100		
26	265 Lymphoma	0.5663061			0.1870206	AA384220_a	
26	266 Lymphoma	0.5657781	0.3276105		0.1868456	AF006086_a	APD2/2 section Genbank)
26	267 Lymphoma	0.5650608	0.3275834	0.280325	0.18664779 W28798	W28798 at	EST: 52g10 Human retina cDNA randomly primed sublibrary Homo sabiens cDNA mRNA sequence (from Contact)
26	268 Lymphoma	0.5635439	0.3275833	0.280251	0.18659721 W28548 at	W28548 at	EST: 48d1 Human retina cDNA randomly primed sublibrary Homo
26(269 Lymphoma 0.5632062 0.3273261	0.5632062	0.3273261	0.280156	RC_A 0.1864481 09 at	RC_AA4589 09_at	EST: aa26e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
270	270 Lymphoma	0.5631544	0.3267421	0.279981	HG1872- 0.18632442 HT1907 at	HG1872- HT1907 at	Maior Histocompositivity, Control of the Control of
271	271 Lymphoma	0.5631071	0.3267267	0.279891	0.18621527 07 at	A5045	EST: aa60g07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
272	272 Lymphoma	0.5615543	0.3267019	0.279781	0.18598068 D82712 at)82712 at	ST. similar to none mDMA comment.
273	273 Lymphoma 0.5614649	0.5614649	0.3266508	0.279691	0.185870291	æ,	Homo capiano mDNA for NOTA 1
274	274 Lymphoma 0.5610402	0.5610402	0.3264535	0.279555	0.18581972 t	√69245_s_a	M69245_s_a Human pregnancy-specific beta-1 glycoprotein (PSG) mRNA, tomplete cds. (from Genbank)
275	275 Lymphoma	0.5609091	0.3263791	0.279481	0.1856473 R55902 at		Ya92d05 r1 Homo conjens chan decentation
276	276 Lymphoma	0.5597442	0.3261644	0.279422	0.18547653 59 at	A2837	EST: 2s48b05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700689.3' mRNA sequence from Carbart
277	277 Lymphoma (0.5596944	0.3261329	0.279363	O.18535453 t	A263146_a	AA263146_a EST: PMY0511 KG1-a Lambda Zap Express cDNA library Homo
278	278 Lymphoma 0.5590776 0.3260188).5590776	0.3260188	0.279128	0.18519531 t	A431398_a	AA431398_a 782135 5' similar to WP:M01F1.6 CE01034;, mRNA sequence. (from Genbank)
279	279 Lymphoma (0.5573739	0.3257908	0.279059	0.18508475 X17206	at	PTB Ribosomal protein L26
280	280 Lymphoma C	0.5573096	0.3256352	0.279051	0.18497077 U43586 at	1	Kinase suppressor of ras-1 (KSR1) mRNA, partial cds

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0.18484868 U43586_at-2 Kinase suppressor of ras	Peroxisomal biogenesis factor 11B	H. sapiens putatively transcribed partial sequence; UK-HGMP sequence ID AAAALMI; single read, mRNA sequence. (from Genbank)	Homo sapiens chromosome 9, P1 clone 11659	EST: zl47g02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725522 3', mRNA sequence. (from Genbank)	Modulator recognition factor I (MRF-1) mRNA, 3' end	0.18410148 M62324_at-2 Human modulator recognition factor I (MRF-1) mRNA, 3' end	CD8 antigen, alpha polypeptide (p32)	RC_AA4864_EST; ab36f11.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 842925 3', mRNA sequence. (from Genbank)		AA092898_a EST: m0386.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t	EST: zv21d10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754291 3', mRNA sequence. (from Genbank)			Epstein-Barr virus-induced protein mRNA	KIAA0480 gene product	AA279359_a EST: zs84d01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR
68 U43586_at-2	0.1847214 H44262_at	0.18465897 Z19751 at	AA314466_a 33_t	RC_AA3978 03 25_at	0.18423972 M62324_at	48 M62324_at-2	M26315_cds 0.18400207 2_s_at	RC_AA4864 0.18387945 44_at	0.18381476 04 at	AA092898_a	RC_AA4794 0.18358295 98 at	RC_AA0454 0.183454 81_at	RC_AA4586 24 44_at	0.18323193 U19261_at	0.18313983 R34531 at	AA279359_a	0.18288116 X62744 at
0.184848	0.18472	0.184658	0.18452433 t	RC 0.1843503 25	0.184239	0.184101	0.184002	0.183879	0.183814	0.18368623 t	0.183582	0.1834	RC_A 0.18342124 44_at	0.183231	0.183139	0.18298216 t	0.182881
0.278842	0.278809	0.278721	0.278661	0.278435	0.27,8231	0.278214	0.278047	0.277864	0.277701	0.277548	0.277424	0.277262	0.277146	0.277144	0.27699	0.276752	0.276724
0.3255421	0.3253575	0.3251653	0.3250759	0.3249639	0.3248133	0.3247504	0.3245162	0.3244596	0.3244254	0.3242706	0.3241949	0.3240677	0.3239683	0.3238952	0.3238064	0.323739	0.3235079
0.5573096 0.3255421	0.5573081	0.556936	0.5567452	0.5565508	0.5547744	0.5547744	0.5547602	0.5543321	0.5541011	0.5535236	0.5532835	0.5528798	294 Lymphoma 0.5501466 0.3239683	295 Lymphoma 0.5494753 0.3238952	296 Lymphoma 0.5492095 0.3238064	0.547767	298 Lymphoma 0.5453966 0.3235079
281 Lymphoma	282 Lymphoma	283 Lymphoma	284 Lymphoma	285 Lymphoma	286 Lymphoma	287 Lymphoma	288 Lymphoma	289 Lymphoma	290 Lymphoma	291 Lymphoma	292 Lymphoma	293 Lymphoma 0.5528798	-ymphoma	_ymphoma	-ymphoma	297 Lymphoma	-ymphoma
281	282	283	284	285	286	287	288	289	290	291	292	293	294 1	295	296 1	297	298

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors then the state of

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. AA082926_a|RETINOBLASTOMA BINDING PROTEIN 1;, mRNA sequence. (from AA247275_a EST: csg0884.seq.F Human fetal heart, Lambda ZAP Express Homo RC_AA6205 |EST: ae60h08.s1 Stratagene lung carcínoma 937218 Homo sapiens EST: ze30d05.s1 Soares retina N2b4HR Homo sapiens cDNA clone EST: zn07f11.r1 Stratagene hNT neuron (#937233) Homo sapiens 0.18249594 85_at 687804_3', mRNA sequence (from Conback) AA249385_a EST: j2332.seq.F Human fetal heart, Lambda ZAP Express Homo EST; zt75a11.s1 Soares testis NHT Homo sapiens cDNA clone AA400632_s EST: zu70f01.r1 Soares testis NHT Homo sapiens cDNA clone HLA-DPB1 Major histocompatibility complex, class II, DP beta 1 cDNA clone 546765 5' similar to SW:RBB1_HUMAN P29374 EST: yi37a05.r1 Homo sapiens cDNA clone 141392 5'. (from RC_AA4356 |728156 3' similar to contains Alu repetitive element;, mRNA CHRNB3 Cholinergic receptor, nicotinic, beta polypeptide 3 cDNA clone 951327 3', mRNA sequence. (from Genbank) Homo sapiens mRNA for KIAA0914 protein, complete cds sapiens cDNA 5', mRNA sequence. (from Genbank) sapiens cDNA 5', mRNA sequence. (from Genbank) HLA-DOB MHC class II protein HLA-DO beta chain 0.18240331 U62438_at-2 Cholinergic receptor, nicotinic, beta polypeptide 3 Protein tyrosine phosphatase, non-receptor type 7 Homo sapiens mRNA for LAK-4p, complete cds 687804 3', mRNA sequence. (from Genbank) 743353 5', mRNA sequence. (from Genbank) 360489 3', mRNA sequence. (from Genbank) Interleukin 13 receptor, alpha 1 sequence. (from Genbank) Genbank) Genbank) AA478704_a M64322_s_a RC_AA2792 0.18187208|X03066_at RC AA0157 0.18233201 U62438 at 0.18199782|R68846_at 0.18120287 M83664_at Ħ, 0.1809123 W27440 0.18269542 64 at 0.18214327 94 at 0.18156908 98_at 0.18130067|51 at 0.18175481 at 0.1828068 0.18255728 0.18144517 0.18125017 0.18104085 0.27633 0.276223 0.276086 0.275978 0.275975 0.27637 0.276121 0.275671 0.275545 0.275461 0.275363 0.275177 0.274999 0.274977 0.27479 0.27474 0.274633 301 Lymphoma | 0.5441038 | 0.3231901 299|Lymphoma| 0.5449806| 0.3234495| 300[Lymphoma| 0.5448306| 0.3232553| 0.54387 0.3231352 303|Lymphoma| 0.5428686| 0.3231352| 0.3231124 0.542415 | 0.3230177 0.3228915 0.322812 0.541371 | 0.3227011 0.3227486 0.3225508 310|Lymphoma| 0.5413337| 0.3226111| 0.540953 0.3223176 315|Lymphoma| 0.5403914| 0.3221422| 0.322289 314 Lymphoma | 0.5405091 | 0.3222151 304|Lymphoma| 0.5428686| 306|Lymphoma| 0.5419941| 0.541656307|Lymphoma| 0.5417521 0.5410871 313|Lymphoma| 0.5408223| 302 Lymphoma 305 Lymphoma 308 Lymphoma 309|Lymphoma| 311|Lymphoma 312 Lymphoma

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	RC_AA2321 EST: zr25c10.s1 Stratagene NT2 neuronal precursor 937230 Homo 316 Lymphoma 0.5399377 0.3219896 0.274563 0.18077035 87_at sapiens cDNA clone 664434 3', mRNA sequence. (from Genbank)	obey 20 0.5395976 0.3219346 0.274349 0.18063405 84 at 753344 3', mRNA sequence. (from Genbank)	0.5392029 0.3219346 0.274267 0.18061343 t	AA136382_s EST: zn89a06.r1 Stratagene lung carcinoma 937218 Homo sapiens 0.5390996 0.3219073 0.274168 0.180454 at converse converse (from Canbank)	0.274093 0.18042484 54 at	0.5380406 0.3216421 0.274008 0.18024616 M55267 at-2	homa 0.5380406 0.3213662 0.273923 0.18019971 M55267 at 2A PROTEIN)	323 Lymphoma 0.5377693 0.3212344 0.273556 0.18003485 99_at cDNA clone 501429 3', mRNA sequence. (from Genbank)	324 Lymphoma 0.5374493 0.3211493 0.2735 0.17995387 55_at Dihydropyrimidinase-like 2	ohoma 0.5370858 0.3211397 0.273392 0.17981735 U56814_at-2 Deoxyribonuclease I-like 3	homa 0.5370858 0.3210295 0.273257 0.17974319 U56814_at DNase1-Like III protein (DNAS1L3) mRNA	homa 0.536853 0.3207765 0.273078 0.17961916 M98539 at Prostaglandin D2 synthase gene	328 Lymphoma 0.5361224 0.3206471 0.273057 0.1795327 M12759_at-2 Human Ig J chain gene	329 Lymphoma 0.5361224 0.3206168 0.273045 0.17935115 M12759 at IMMUNOGLOBULIN J CHAIN	homa 0.535921 0.3205697 0.272735 0.1793149 H10321 at Genbank)	homa 0.535593 0.3205252 0.27261 0.17920817 04_at 897623 3', mRNA sequence. (from Genbank)	332 Lymphoma 0.5352778 0.3205205 0.272604 0.17910056 H72388 at Genbank)	homa 0.5347686 0.3203815 0.272567 0.17908262 t Homo sapiens GA17 protein mRNA, complete cds	334 vmnhoma 0 5335506 0 320185 0 272547 0 17899667 D82422 at EST. similar to none mDNA common version of the common ve
	Lymphoma 0.53	317 Lymphoma 0.53	318 Lymphoma 0.53	Lymphoma 0.53	320 Lymphoma 0.53	321 Lymphoma 0.53	322 Lymphoma 0.53	Lymphoma 0.53	Lymphoma 0.53	325 Lymphoma 0.53	326 Lymphoma 0.53	327 Lymphoma 0.5	Lymphoma 0.53	Lymphoma 0.53	330 Lymphoma 0.5	331 Lymphoma 0.5	Lymphoma 0.53	333 Lymphoma 0.53	vmphoma 0 53

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	EST: zx04f03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785501 3', mRNA sequence. (from Genbank)	EST: zr57a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	667480 3', mRNA sequence. (from Genbank)	at Acidic epididymal alycoprotein-like 1		Human membrane-associated lectin type-C mRNA	Human Hpast (HPAST) mRNA, complete cds	Actin-related protein 2	EST: zc01e01.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321048 5', mRNA sequence. (from Genbank)	RPS25 Ribosomal protein S25	EST: zo97h05.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 594873 3', mRNA sequence. (from Genbank)	EST: zw17a10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 769530 3', mRNA sequence. (from Genbank)	at Major Histocompatibility Complex, Class li Beta W52	EST: yj36g07.r1 Homo sapiens cDNA clone 150876 5'. (from Genbank)	1	-			Ribosomal protein S18	
0.110033000 12 at	RC_AA4492 67_at	RC_AA2278	84_at			02_at	AA151328_a t	AF006082_a	W56875_at	0.17801118 M64716 at	RC_AA1717 36_at	RC_AA4262 61_at	HG3576- HT3779 f al	H02675 at	RC_AA2810 74 at	AA424307_a t	AA174149_a	RC_AA0113 10_s_at	X69150_at	
	RC_A 0.17875114 67_at		0.17861034 84_at	0.17850007 \$80310 s		0.17845714 02 at	ρ 0.1783834 t	0.17822467 t	0.17812067 W56875_	0.17801118	RC_A 0.17791574 36_at	RC_A 0.17785768 61_at	HG3576- 0.17770077 HT3779 f	0.17762926 H02675 at	RC_A 0.17750302 74 at	0.17743471	A 0 177240221	RC_AAC 0.17718893 10_s_at	0.17705253 X69150_at	
21.1.0	0.27233	L	0.272285	0.272271		0.272122	0.272017	0.271951	0.271693	0.271625	0.271611	0.271569	0.271514	0.271474	0.271442	0.271328	0.271254	0.27125	0.271226	
0.020.00	0.3201314	1	0.3200808	0.3199861	ŧ .	0.3199687	0.3198687	0.3197521	0.3196618	0.3193594	0.3193445	0.3193396	0.3193243	0.3191913	0.3190549	0.3189265	0.3189065	1 1	0.3187657	
0.0004010	0.5333529		0.532409	0.5308081		339 Lymphoma 0.5300815	340 Lymphoma 0.5298708 0.3198687	0.5298174	0.5294091	0.5290833	0.5272148	0.5264043	0.5254951	347 Lymphoma 0.5251394	0.5242806	0.5240557	0.5237947		0.5231271	
335 Lymphoma	336 Lymphoma		337 Lymphoma	338 Lymphoma		Lymphoma	Lymphoma	341 Lymphoma	342 Lymphoma	343 Lymphoma	344 Lymphoma	345 Lymphoma	346 Lymphoma 0.5254951	Lymphoma	348 Lymphoma	349 Lymphoma	350 Lymphoma	351 Lymphoma	352 Lymphoma 0.5231271	
335	336	100	337	338		339	340	341	342	343	344	345	346	347	348	349	350	351	352	

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ednence.	lomo sapiens	rom					omo sapiens		no sapiens	\ clone	spo e				DNA clone	4 clone	ıry Homo	ss Homo
D31544_s_a EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)	AA247989_a K8033.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)	EST: yi96b06.r1 Homo sapiens cDNA clone 147059 5'. (from Genbank)	Butyrophilin (BTF2) mRNA	0.17641424 U90550_at-2 Human butyrophilin (BTF2) mRNA, complete cds	M-phase phosphoprotein, mpp5	0.1762672 X98261_at-2 H.sapiens mRNA for M-phase phosphoprotein, mpp5	EST: zc49f01.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 325657 5', mRNA sequence. (from Genbank)	Arp2/3 protein complex subunit p16	AA090695_a EST: y1365.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence, (from Genbank)	AA453381_a EST: zx47e08.r1 Soares testis NHT Homo sapiens cDNA clone t 795398 5', mRNA sequence. (from Genbank)	Homo sapiens cyclophilin-33A (CYP-33) mRNA, complete cds	Liver mRNA for interferon-gamma inducing factor(IGIF)	0.17554952 D49950_at-2 Interleukin 18 (interferon-aamma-inducina factor)	Ubiquitin-conjugating enzyme E21.6	RC_AA0470 EST: zf50b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone 34 at 380349 3', mRNA segmence. (from Genbank)	EST: zt02b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711935 3', mRNA sequence (from Genhank)	EST: 16a4 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genbank)	AA248994_a EST: I2187.seq.F Human fetal heart, Lambda ZAP Express Homo t sapiens cDNA 5'. mRNA sequence (from Genhank)
D31544_s_a t	AA247989_a t	R80333_at	U90550_at	U90550_at-2	0.1763235 X98261_at	X98261_at-2	W52638_at	AF006088_a t	AA090695_a t	AA453381_a t	RC_AA4764 50_at		D49950_at-2	RC_AA4127 00 at	RC_AA0470 34_at	A2821		4A248994_a
0.17685358 t	0.17671913	0.17669219 R80333	0.17656825 U90550	0.17641424	0.1763235	0.1762672	0.17608501 W52638_at	0.17606878	0.175965491	0.17582078	RC_A 0.1757397 50_at	0.17565858 D49950_at	0.17554952	RC_A 0.17545503 00 at	RC_A 0.17532094 34 at	RC 0.17525198 47	0.17516522 W26898 at	0.17503932
0.271061	0.27105	0.270919	0.270632	0.27061	0.270411	0.270101	0.269929	0.269903	0.269903	0.269778	0.269759	0.26974	0.269683	0.269651	0.269485	0.269302	0.269223	0.269117
0.3186295	0.3186067	0.3185857	0.318229	0.3182206	0.3181455	0.3179763	0.3177496	0.3176373	0.3176319	0.3175233	0.3174847	0.3171968	0.3167492	0.316647	0.3166144	0.3165132	0.3164794	0.3164333
0.5231077	0.5230388	0.5224261	0.5222992	0.5222992	0.5222184	0.5222184	0.5219629	0.5215229	0.521315	0.5206098	0.5204284	0.5199574	0.5199574	0.519936	0.5196908	0.5188556		0.5178661
353 Lymphoma	354 Lymphoma	355 Lymphoma	356 Lymphoma 0.5222992	357 Lymphoma	358 Lymphoma 0.5222184 0.3181455	359 Lymphoma 0.5222184	360 Lymphoma	361 Lymphoma	362 Lymphoma	363 Lymphoma	364 Lymphoma 0.5204284	365 Lymphoma 0.5199574 0.3171968	366 Lymphoma 0.5199574	367 Lymphoma	368 Lymphoma	369 Lymphoma	370 Lymphoma 0.5183544	371 Lymphoma 0.5178661
353	354	355	356	357	358	359	360	361	362	363	364	365	3661	3671	3681	1698	3701	371

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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372	372 Lymphoma	0.517763	0.3163402	0.268918	AFFX- HUMIS ////////////////////////////////////	GF3A 5_M	No info for gene
373	373 Lymphoma	0.517763	0.3162571	0.268878	AFF) HUM ///W97 0.17484179 B_at	<- IISGF3A 935_M	AFFX-HUMISGF3A/M97935_MB_at (endogenous control)
374	Lymphoma	374 Lymphoma 0.5177347	0.316151	0.268846	0.17476134	J00105_s_at	0.17476134 J00105_s_at BETA-2-MICROGLOBULIN PRECURSOR
375	Lymphoma	375 Lymphoma 0.5174834	0.3161171	0.26868	RC 0.17462955 87_	RC_AA0258 87_at	RC_AA0258 EST: ze86h12.s1 Soares fetal heart NbHH19W Homo sapiens cDNA 87_at clone 365927 3', mRNA sequence. (from Genbank)
376	376 Lymphoma	0.5172433	0.3160481	0.268629	0.17458479	M33600_f_at	0.17458479 M33600_f_at HLA-DRB1 Major histocompatibility complex, class II, DR beta 5
377	377 Lymphoma	0.5170456	0.3160433	0.268579	RC_A 0.17443602 20 at	RC_AA4767 20 at	RC_AA4767 EST: zw92g06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 20 at clone 784474 3', mRNA sequence. (from Genbank)
378	378 Lymphoma	0.5165935	0.3157479	0.268451	RC 0.17432834 05	AA2355 at	EST: zt35f12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 724367 3', mRNA sequence. (from Genbank)
379	Lymphoma	379 Lymphoma 0.5161895 0.3156834	0.3156834	0.268346	0.17418513	RC_D59362 at	EST: Human fetal brain cDNA 3'-end GEN-023A02, mRNA sequence. (from Genbank)
380	Lymphoma	380 Lymphoma 0.5157975	0.315461	0.268291	0.174101551	AA148094_a t	Homo sapiens CC3 (CC3) mRNA, complete cds
381	381 Lymphoma	0.5156616	0.3154143	0.26819	RC_A 0.17407674 70_at	RC_AA6209 70_at	Syntaxin 7
382	382 Lymphorna	0.5155967	0.3153643	0.268183	0.17390539	AA091085_a t	Homo sapiens PAC clone DJ0905J08 from 7p12-p14
383	383 Lymphoma	0.5146776	0.3153214	0.26811	0.17380425 X62078_at	X62078_at	GM2A GM2 ganglioside activator protein
384	Lymphoma	384 Lymphoma 0.5143648 0.3150509	0.3150509	0.268018	0.1736784 H69440_at	H69440_at	EST: yr88c02.r1 Homo sapiens cDNA clone 212354 5' similar to SP:C18F10.7 CE00784; (from Genbank)
385	Lymphoma	385 Lymphoma 0.5140838	0.3149224	0.267843	0.17359237	X04011_at-2	0.17359237 X04011_at-2 Cytochrome b-245, beta polypeptide (chronic granulomatous disease)
386	Lymphoma	386 Lymphoma 0.5140838	0.3147598	0.267796	0.1735137 X04011_at	X04011_at	CYBB Chronic granulomatous disease
387	387 Lymphoma	0.513625	0.3147093	0.267731	0.173426021	AA426168_a t	Homo sapiens mRNA for KIAA0805 protein, partial cds
388	Lymphoma	388 Lymphoma 0.5134165	0.3147078	0.267596	0.17331235 M28170	M28170_at	CD19 CD19 antigen
389	Lymphoma	0.5131865	389 Lymphoma 0.5131865 0.3146439	0.26745	0.17324805 H23893	H23893_at	Yn71g12.r1 Homo sapiens cDNA clone 173926 5' similar to contains Alu repetitive element;. (from Genbank)

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MacMarcks mRNA	EST: zv98g08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 767870 3', mRNA sequence. (from Genbank)	BING4	AA262458_a EST: zs16h04.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone t		EST: zw94g05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784664 3', mRNA sequence (from Genhank)			EST: zr34g09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665344 3', mRNA sequence. (from Genbank)	EST: zp03d01.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595297 3', mRNA sequence. (from Genbank)	EST: yp05f06.r1 Homo sapiens cDNA clone 186563 5'. (from Genbank)	EST: zv79f11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759885 3', mRNA sequence. (from Genbank)	Ribosomal protein S27 (metallopanstimulin 1)	Yu05d11.r1 Homo sapiens cDNA clone 232917 5'. (from Genbank)	at-2 Holocytochrome c synthase (cytochrome c heme-lyase)	Putative holocytochrome c-type synthetase mRNA	RC_AA2435 EST: zr67h10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 74_at 668515.3', mRNA sequence. (from Genbank)	HLA-E MHC class I antigen HLA-E	AB000221_a Small inducible cytokine subfamily A (Cys-Cys), member 18, t pulmonary and activation-regulated
X89109_s_a	RC_AA4188 78_at	RC_D20483 i_at	AA262458_e t	AA313677_a t	RC_AA4433 34 at	RC_AA4826 20_at	RC_AA2511 29 at	RC_AA1952 29_s_at	RC_AA1739 72_at	H43250_at	RC_AA4238 92_at	U57847_s_a t	H72650_at	U36787_at-2	J36787 at	RC_AA2435 74_at	X56841_at	AB000221_a
0.1731813	0.1730083 78	0.17292859	0.17286152	0.17281915 t	RC_A 0.1727098 34 at	0.17264234 20 at	RC_A 0.17254676 29 at	RC_AA1 0.1724321 29_s_at	RC_A 0.17234933 72_at	0.17218779 H43250_at	RC_A 0.17206582 92_at	0.17200131	0.17181213 H72650 at	0.17167278 U36787	0.17162815 U36787 at	RC_A 0.17152633 74_at	0.17150238 X56841	0.17133912
0.267448	0.267411	0.267219	0.266892	0.266783	0.266657	0.266551	0.266505	0.266485	0.266339	0.266292	0.266267	0.2662	0.266173	0.26584	0.265783	0.265779	0.265722	0.265683
0.314557	0.3144499	0.314287	0.3142125	0.3139595	0.3139546	0.3139471	0.3137436	0.3136233	0.3135579	0.3135192	0.3135053	0.3134845	0.3134545	0.3134458	0.3134357	0.3133913	0.3132858	0.3131756
0.5125923	0.5120077	0.5118421	0.5115662	0.5110772	0.5106558	0.5106116	0.5102195	0.5097103	0.5096799		0.5086533	0.5085723	0.5082719	0.5080409	0.5080409	0.5080199	0.507296	0.5071035
390 Lymphoma	391 Lymphoma	392 Lymphoma	393 Lymphoma	394 Lymphoma	395 Lymphoma	396 Lymphoma	397 Lymphoma 0.5102195	398 Lymphoma	399 Lymphoma 0.5096799	400 Lymphoma 0.5094477	401 Lymphoma 0,5086533	402 Lymphoma	403 Lymphoma	404 Lymphoma	405 Lymphoma	406 Lymphoma	407 Lymphoma	408 Lymphoma 0.5071035 0.3131756
ř	8	3	ř	33	8	33	38	36	33	40	8	40	4	40	8	40	40	40

Docket No.: 2825.2020-002

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31256 0.265678 0.17120236 17 s at Forkhead (Drosophila) homolog 1 (rhabdomyosarcoma)	0.265662 0.17119241 t	0.26561 0.17110251 Z20462_at	28771 0.265535 0.17105994 L01087_at PRKCQ Protein kinase C-theta	12776 0.265431 0.1709616 L01087_at-2 Protein kinase C, theta	0.26536 0.17082238	0.265319 0.17077254	25323 0.26526 0.17066024 t-2 Nuclear cap binding protein, 80kD	25193 0.265255 0.1705426 D30758_at KIAA0050 gene	24014 0.265055 0.1704065 D30758 at-2 KIAA0050 gene product	0.265036 0.1703332 83_at	0.264821 0.17023356 53_at	0.264781 0.1701263 HT3391 at	19158 0.264639 0.16999939 t AA406435_a EST: zv12d12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753431 5', mRNA sequence. (from Genbank)	18224 0.264565 0.16993955 D50840_at	18178 0.264382 0.16980603 D50840 at-2 UDP-glucose ceramide glucosyltransferase	0.264362	0.264213 0.16961645 02 at	
0.3131256 0.2			0.3128771 0.2	0.312776 0.2		0.3126153 0.2	0.3125323 0.	0.3125193 0.2	0.3124014 0.2	0.3123792 0.2	0.3122508 0.2		0.3119158 0.2	0.3118224 0.2	0.3118178 0.2	0.3118013 0.2	0.3115675 0.2	1
409 Lymphoma 0.5063697	1	0.5057313	0.5054904	a 0.5054904	414 Lymphoma 0.5050198 0.3127317	415 Lymphoma 0.5046549	0.5046549	0.504543	0.504543	0.504483	0.5041115	421 Lymphoma 0.5040442 0.3119722	0.5030366	0.5027992	0.5027992	0.502516	0.5022289	
Lymphoma	410 Lymphoma	Lymphoma	412 Lymphoma	413 Lymphoma	1 Lymphome	5 Lymphome	416 Lymphoma	417 Lymphoma	418 Lymphoma	419 Lymphoma	420 Lymphoma	Lymphome	422 Lymphoma	423 Lymphoma	424 Lymphoma	425 Lymphoma	426 Lymphoma	,

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0 Homo	ns cDNA element ;,		sapiens	None				ins cDNA			nic		clone equence.		apiens) BETA
EST: zr26d11.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664533 3', mRNA sequence. (from Genbank)	EST: zd92a04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356910 5' similar to contains element LTR3 repetitive element ;; mRNA sequence. (from Genbank)	RPS16 Ribosomal protein S16	AA007264_a EST: zh97e06.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens t	EST: zr80f08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682023 3', mRNA sequence, (from Genbank)	EST: yj49f04.r1 Homo sapiens cDNA clone 152095 5'. (from Genbank)	Homo sapiens mRNA for KIAA0639 protein partial cds	Homo sapiens mRNA for pre-mRNA cleavage factor I subunit	EST: zv65g11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 758564 3', mRNA sequence, (from Genbank)	Novel centrosomal protein RanBPM	BZip protein B-ATF mRNA	NCF1 47 kD autosomal chronic granulomatous disease profesion	EST: yn54h07.r1 Homo sapiens cDNA clone 172285 5'. (from Genbank)	EST: zr71c02.s1 Soares NhHMPu S1 Homo sapiens cDNA done 668834 3' similar to TR:G969170 G969170 PX19.;; mRNA sequence. (from Genbank)	Pituitary tumor-transforming 1	EST: zq77c12.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 647638 3', mRNA sequence, (from Genbank)	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(W1.1) BETA
A2431	W92678_at	M60854_at	AA007264_a t	RC_AA2563 26_at	H04627_at	RC_AA3985 52_at	RC_AA4365 0.16700849 70 at	A4018	AA291444_a t	0.1668405 U15460_at	0.1666771 M55067 at		629	A4300	A2060	to
RC_A 0.16763712 73_at	0.16757235 W92678	0.1673887 M60854	0.1673447	RC 0.1672572 26	0.16713656 H04627_at	0.16709335	RC_A 0.16700849 70 at	RC_A 0.16696228 09_at	0.16687767 t	0.1668405	0.1666771	0.16657688 H19562 at	RC_AAZ 0.1664923 69 f_at	RC_A 0.16638966 32_at	RC_A 0.1663082 23 at	0 16624503 Xn3068 £
0.262329	0.262319	0.26227	0.26227	0.262239	0.262112	0.262067	0.262043	0.261998	0.261953	0.261703	0.261677	0.26163	0.2615	0.26147	0.261467	0.261306
0.3099369	0.3099326	0.3099232	0.3099209	0.3098009	0.3096889	0.309602	0.3095457	0.3094899	0.3094322	0.3094218	0.309218	0.3092141	0.3091564	0.3091098	0.3090815	0.3090539
0.4937576	0.4937521	0.4933912	0.4931738	0.4931697	0.4924473	0.4923333	0.4918718	0.4915474	0.4913811	0.4911034	0.4905382	0.4903538	0.4899899	0.4893799		464 Lymphoma 0.4884109 0.3090539
448 Lymphoma	449 Lymphoma 0.4937521	450 Lymphoma 0.4933912	451 Lymphoma 0.4931738 0.3099209	452 Lymphoma 0.4931697	453 Lymphoma	454 Lymphoma	455 Lymphoma	456 Lymphoma 0.4915474	457 Lymphoma 0.4913811	458 Lymphoma 0.4911034 0.3094218	459 Lymphoma 0.4905382	460 Lymphoma	461 Lymphoma	462 Lymphoma	463 Lymphoma 0.4884768	-ymphoma
448	449	450	451	452	453	454	455	456	457	458	459	460	461	462 1	463 [464

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

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46	465 Lymphoma 0.4880095 0.3089931	a 0.488009	5 0.308993	1 0.261044	RC_A 0.16616985 07_at	RC_AA4901 5 07_at	
46	466 Lymphoma 0.4876634 0.3089661	a 0.487663 ²	4 0.308966	1 0.260952		0.16607879 W79409_at	Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
46	467 Lymphoma 0.4876027 0.3089148	a 0.4876027	7 0.3089148	8 0.260943	AFF) 0,16598448 5 at	AFFX-BioC-	×
468	468 vmphomo	407000				AFFX-BioC-	AFFA-Bloc-5 at (endogenous control)
ř	o Lymprome	0.4876027	0.3088642	2 0.260745	0.16594674 5 at-2	15 at-2	AFFX-BioC-5 at (miscellaneous control 11k aking)
46(469 Lymphoma	а 0.487177	0.3088585	5 0.260678		0.1657831 X17093 at	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F ALPHA CHAIN PRECURSOR
470	470 Lymphoma 0.4868153	0.4868153	0.3088575	0.260678		RC_AA2929	
471	471 Lymphoma 0.4863762	0.4863762	0.3088156	0.260618	0	RC_AA2997 89 at	EST: EST12356 Uterus tumor I Homo sapiens cDNA 3' end, mRNA sequence (from Garback)
472	472 Lymphoma 0.4860996 0.3087816	0.4860996	0.3087816	0.260354	X0310 0.16551088 2_at	X03100_cds 2_at	X03100_cds HLA-SB alpha gene (class II antigen) extracted from Human HLA-2_at SB(DP) alpha gene
473	473 Lymphoma	0.4852366	0.4852366 0.3087606	0.260329	X01038 0.16539599 1_s_at	X01038_rna 1_s_at	Fetal gene for apolipoprofein Al pressures
474	474 Lymphoma 0.4851981	0.4851981	0.3086963	0.260327	0.165265	ta	Anti-one in the contract of th
475	475 Lymphoma 0.4847626	0.4847626	0.3086499	0.08000	0.46500404)259	Autr-colorectal carcinoma heavy chain
347			}		0.10322494 05 t at	U5_f at	Homo sapiens TNF-inducible protein CG12-1 mRNA, complete cds
4/0	470 Lymphoma	0.484688	0.3086315	0.260204	0.1651336 S76992_at		VAV2 Vav 2 oncogene
477	477 Lymphoma	- 1	0.484688 0.3084959	0.260192	0.16508189	S76992 at-2	0.16508189 S76992 at-2 Vav 2 oncorana
478	478 Lymphoma	0.4834751	0.3084716	0.260188	0.1650337 t	AA234259_a	AA234259_a Zr71c08.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone
479	479 Lymphoma 0.4827471		0.3082822	0.260032	0.16487533 53	_AA2368 at	EST: zs01b04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
480	480 Lymphoma	0.4826184	0.3082234	0.259715	0.16482487 90 at	A0437	EST: zk59f12.s1 Soares pregnant uterus NbHPU Homo sapiens CDNA clone 487151 31 mPM/ 000000000000000000000000000000000000
481	481 Lymphoma 0.4820257		0.3081968	0.259626	0.16475107 W73663 at		EST: zd55e07.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344580 51 mRNA sociames (from Contract)
482 1	482 Lymphoma 0.4818273		0.3079852	0.259513	0.164626751	AA310510_a	AA310510_a Human mRNA expressed in HC/HCC livers and MolT-4 proliferating to cells, partial sequence
483	483 Lymphoma 0.4811449 0.3079478	0.4811449	0.3079478	0.259374	0.16458634 H21219 at		RAB6, member RAS oncogene family

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484	484 Lymphoma	0.4810958	0.3077937	0.259318	0.16445291	AA248079_a t	AA248079_a EST: cp2131.seq.F Human fetal heart, Lambda ZAP Express Homo t sapiens cDNA 5', mRNA sequence. (from Genbank)
485	485 Lymphoma	0.480833	0.3077875	0.259285	RC_A 0.16439046 80_at	A2359	EST: zs05e09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684328 3', mRNA sequence. (from Genbank)
486	486 Lymphoma	0.4806607	0.3076404	0.259227	RC_A 0.16425137 83 at	A4001	EST: zu64d03.s1 Soares testis NHT Homo sapiens cDNA clone 742757 3' mRNA sequence. (from Genhank)
487	Lymphoma	487 Lymphoma 0.4800119 0.3076221	0.3076221	0.259079	0.16419928 t	4A055361_a	EST: zf20a04.r1 Soares fetal heart NbHHH19W Homo sapiens cDNA clone 377454 5', mRNA sequence (from Genhank)
488	Lymphoma	488 Lymphoma 0.4799957	0.3075579	0.259018	0.16415285 t	A340215_a	EST: EST45566 Fetal brain III Homo sapiens cDNA 5' end, mRNA sequence. (from Genhank)
489	489 vmohoma	0.4798849	0.3075244	0.258976	0.46406704	/26004_s_a	
490	490 Lymphoma	0.4796203		0.2589	0.16401476 t	\A091296_a	CNZ Complement component (30/Epstein Barr virus) receptor 2 Phosphatidylinositol divisor class E
491	491 Lymphoma	0.4795759	0.3075014	0.258892	0.16398475 t	AB000114_a	Osteomodulin
492	Lymphoma	0.4795759	492 Lymphoma 0.4795759 0.3073728	0.258844	AB 0.16388205 ₁ -2	000114_a	Osteomodulin
493	493 Lymphoma	0.47956	0.3073222	0.258716	RC_A 0.16381769 05 at	A4013	EST: zu68c01.s1 Soares testis NHT Homo sapiens cDNA clone 743136 3', mRNA sequence, (from Genhank)
494	494 Lymphoma	0.4793671	0.3072074	0.258555	AH HI M 0.16363816 at	FX- JMGAPDH 33197_5_	AFFX-HUMGAPDH/M33197_5_at (endogenous control)
495	Lymphoma	495 Lymphoma 0.4793671	0.3071489	0.258479	AFF HUN //M3: 0.16356792 at-2	X- ////////////////////////////////////	Glyceraldehyde-3-phosphate dehydrogenase
4961	Lymphoma	496 Lymphoma 0.4786223	0.3071241	0.258464	0.16346438	AA135452_a t	CGG triplet repeat binding protein 1
497	Lymphoma	497 Lymphoma 0.4780626	0.3071182	0.258365	0.16345115 R25043	at	Yg41h10.r1 Homo sapiens cDNA clone 35408 5'. (from Genbank)
4981	498 Lymphoma	0.4777667	0.3070644	0.258306	0.1633898	0.1633898 H62426_at	Ribosomal protein S25
4991	499 Lymphoma	0.477442	0.3068466	0.258276	RC 0.16332293 57		Ribosomal protein, mitochondrial, S12
2001	-ymphoma	500 Lymphoma 0.4773842	0.3068204	0.258203	0.16318329 U38864		at-2 Human zinc-finger protein C2H2-150 mRNA, complete cds
501	-ymphoma	501 Lymphoma 0.4773842 0.3067706	0.3067706	0.258188	0.16313538 U38864_at		Zinc-finger protein G2H2-150 mRNA

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RC_AA4258 EST: zv48d10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 36_at clone 756883 3', mRNA sequence, (from Genbank)	AA417126_a EST: zu13c10.r1 Soares testis NHT Homo sapiens cDNA clone t 731730 5', mRNA sequence. (from Genbank)	H.sapiens mRNA for NADH dehydrogenase	EST: zw62d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774631 3', mRNA sequence. (from Genbank)	Manic fringe (Drosophila) homolog	EST: zu05e01.s1 Soares testis NHT Homo sapiens cDNA clone 730968 3', mRNA sequence. (from Genbank)	EEF1A1 Translation elongation factor 1-albha-1	EST: ze07h05.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358329 5' similar to PIR:A56724 A56724 cni protein - fruit fly ;, mRNA sequence. (from Genbank)	Manic fringe (Drosophila) homolog	EST: zl88c05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511688 3' similar to contains Alu repetitive element; contains element 1.1 repetitive element 1.2 mRNA segments	EST: zu70g04.s1 Soares testis NHT Homo sapiens cDNA clone 743382 3', mRNA sequence. (from Genbank)	Homo sapiens mRNA for transducin (beta) like 1 protein	EST: ym25f01.r1 Homo sapiens cDNA clone 48919 5'. (from Genbank)	WD protein IR10 mRNA	0.16209228 U57057_at-2 WD repeat domain 2	RC_AA0630 EST: zf67e06.s1 Soares pineal gland N3HPG Homo sapiens cDNA 70_at clone 382018 3', mRNA sequence. (from Genbank)	LMP2 gene extracted from H.sapiens genes TAP1, TAP2, LMP2, LMP7 and DOB	EST: zs45f10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700459 3', mRNA sequence. (from Genbank)
RC_AA4258 36_at	AA417126_a t	000_rna	A4418		A4165		at	AA484997_a t	A1211	A4005	0.1622346 W44973_at	at	at	J57057_at-2 \V	3C_AA0630 E	.01_cds	_AA2906 at
RC_A 0.16302575 36_at	0.16296189	X819 0.16290188 1 at	RC_A 0.16287763 02_at	0.16273604 U94352_at	RC_A 0.16269724 51_at	0.16258064 Z12962_at	0.16243859 W95793	0.16239354	RC_A 0.16233556 23_at	RC_A 0.16227311 12_at	0.1622346	0.16215807 H14879	0.16209751 U57057	0.16209228	RC 0.16198546 70	X664 0.16190626 1 at	0.16184361 30
0.258163	0.258093	0.257976	0.257816	0.257751	0.257747	0.257399	0.257342	0.257298	0.257207	0.257201	0.257162	0.257131	0.257117	0.257078	0.25704	0.256812	0.256775
0.3063737	0.3062795	0.3061908	0.3061358	0.3061316	0.3060992	0.3060649	0.3060094	0.3059767	0.3058469	0.3056891	0.3055018	0.3053692	0.3053502	0.3052999	0.3052734	0.472722 0.3050946	0.3050545
0.4773721	0.4772288	0.4764133	0.4763579	0.4757499	0.4756461	0.475554	0.4752049	0.4752024		0.4743813	0.4740894	0.4738022	0.4734473	0.4734473		0.472722	0.4724755
502 Lymphoma	503 Lymphoma	504 Lymphoma	505 Lymphoma 0.4763579	506 Lymphoma 0.4757499 0.3061316	507 Lymphoma	508 Lymphoma	509 Lymphoma	510 Lymphoma 0.4752024	511 Lymphoma 0.4748591	512 Lymphoma 0.4743813	513 Lymphoma	514 Lymphoma	515 Lymphoma	516 Lymphorna	517 Lymphorna 0.4730473	518 Lymphoma	519 Lymphoma 0.4724755 0.3050545
502	503	504	502	506	202	508	509	510	511	512	513	514	515	516 1	5171	5181	5191

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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RC_AA4114 EST: zv30g06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 65_at clone 755194 3', mRNA sequence. (from Genbank)	EST: yf53e11.r1 Homo sapiens cDNA clone 25730 5'. (from Genbank)	EST: ze32f10.r1 Soares retina N2b4HR Homo sapiens cDNA clone	Human Chromosome 16 BAC clone CIT987SK-A-735G6	EST: yw72c02.r1 Homo sapiens cDNA clone 257762 5'. (from Genhank)	EST: zu46d07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741037.3' mRNA seguence. (from Genbank)	EST: zd40h08.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343167 5' similar to SW:SARA_MOUSE P36536 GTP-BINDING PROTEIN SARA. [1];, mRNA sequence. (from Genbank)	Human ribosomal protein L35 mRNA, complete cds	EST: zu56g05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 742040 3', mRNA sequence. (from Genbank)	RC_AA4466 EST: zw85h03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 18 at clone 783797.31 mRNA sequence. (from Genbank)	Aa38d10.r1 NCI CGAP GCB1 Homo sapiens cDNA clone		Homo canians and protain thingsfarase mRNA complate ode	Historiens 8.2kDa differentiation factor mRNA	AA410480_a EST: zv23b05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	EST: EST65911 Jurkat T-cells I Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)	V-abl Abelson murine leukemia viral oncogene homolog 1::Human U07563_cds ABL gene, exon 1b and intron 1b, and putative M8604 Met protein 1 at-2	U07563_cds ABL gene, exon 1b and intron 1b, and putative M8604 Met protein 1_at (M8604 Met) gene
3C_AA4114 35_at	67134 R12040_at	A016186_a	A362594_s	İ	4	23068 W67213_at	14485 T50262 at	RC_AA4028 14 at	RC_AA4466	5	AA456895_a	RC_AA4499	X79563 at	AA410480_a	RC_AA3572 04 s at	U07563_cds 1_at-2	U07563_cds 1_at
RC_A 0.16173892 65_at	0.16167134	0 161556171	0.16150951	0 16140717 N41849 at	RC_A 0 16127142 16 at	0.16123068	0.16114485	03706	98247		0.16091307	O 16080336 QO	0.16073586 X79563	0 16064318	0.16056718 04	U0756 0.1605216 1 at-2	0.16043113 1_at
0.256713	0.256713	0.25680	0.256599	0.256365	0.256313	0.256158	0.256032	0.256024	0.255882		0.255845	0.055.705	0.255766	0.255628	0.255609	0.255588	0.255501
0.3050371	0.3050129	0 304000	0.3049868	0.304973	0.3049176	0.3049164	0.3048878	0.3048064			0.3047031	0 304610	0.3046067	0.3045258	0.3044692	0.3044614	0.3043981
0.4724245	0.4722337	7740347	0.4716279	0.471304	0.4709064		0.4685468	0.4681419			0.4680113	0.4676941	0.4676563	0.4674477	0.4671531	0.4670663	0.4670663
520 Lymphoma	521 Lymphoma			524 Lymphoma			527 Lymphoma		529 l vmphoma 0 4680364		530 Lymphoma 0.4680113	531 Lymphoma	532 Lymphoma	533 ymphoma 0.4674477	534 Lymphoma 0.4671531	535 Lymphoma 0.4670663 0.3044614	536 Lymphoma 0.4670663 0.3043981
5201	5211	500	523	5241	525	5261	5271	528 1	529.1	2	530	534	532	533	534	535	536

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556	556 Lymphoma	0.4622544	0.30286	0.25432	RC 0.15895781 52	RC_AA6100 52_at	EST: at 1010 0.ST Sources testis NHTL Homo sapiens CDNA clone 1032057 3' similar to TR:G168081 G168081 UNIDENTIFIED GENE.;, mRNA sequence. (from Genbank)
557	557 Lymphoma	0.4622276	0.3028352	0.254316	0.1588391	0.1588391 W00405_at	Apg12 (autophagy, yeast) homolog
558	558 Lymphoma	0.462168	0.3026753	0.254244	RC_AA< 0.15874623 68_r_at	RC_AA4170 68_r_at	EST: zu13b04.s1 Soares testis NHT Homo sapiens cDNA clone 731695 3', mRNA sequence. (from Genbank)
559	559 Lymphoma 0.4620487	0.4620487	0.3025678	0.254161	0.15859039 H10482_at	H10482_at	EST: yl90d12.r1 Homo sapiens cDNA clone 45664 5'. (from Genhank)
999	560 Lymphoma 0.4617675	0.4617675	0.3025008	0.254106	RC_A 0.15850651 02_at	RC_AA4315 02 at	Homo saniens lok mRNA for protein kinase complete cds
190	561 Lymphoma	0.4615154	0.3024307	0.254045	RC_A 0.15845156 66 at	RC_AA2830 66 at	RC_AA2830 EST: zs91h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 66 at IMAGE:704887 3', mRNA sequence. (from Genbank)
199	562 Lymphoma	0.4614739	0.3024224	0.253987	0.158368	C01687_s_a t	F1Fo-ATPase synthase f subunit
99	563 Lymphoma	0.4612488	0.3024081	0.253954	0.15828967 19	RC_AA2588 19 s at	EST: zs32f05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686913 31 mRNA sequence (from Genhank)
964	564 Lymphoma 0.4611935 0.3023944	0.4611935	0.3023944	0.253871	RC_A 0.15823747 17 at	RC_AA4634 17_at	EST: zx71g06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796954 3', mRNA sequence (from Genhank)
965	565 Lymphoma		0.4611105 0.3022851	0.253803	RC_A 0.15815136 87_at	RC_AA2625 87 at	EST: zs22d03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685925.31 mRNA sequence (from Ganhank)
199	566 Lymphoma 0.4608573	0.4608573	0.3022542	0.253783	RC_A 0.1580616 17 at	RC_AA2624 17 at	EST: zs16g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685394 3', mRNA sequence (from Genhank)
1 /9	567 Lymphoma 0.4607934	0.4607934	0.3020549	0.253771	0.15796278 N78018 at	V78018 at	EST: yv71a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 248148 5' similar to gb:M18533 DYSTROPHIN (HUMAN): mRNA sequence (from Genhank)
189	568 Lymphoma 0.4605532	0.4605532	0.3019942	0.253771	RC_AAZ 0.15791476 73 s at	RC_AA4364 73_s_at	EST: zv08e08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753062 3', mRNA sequence. (from Genbank)
169	569 Lymphoma 0.4604169	0.4604169	0.3019727	0.253767	0.1578807 H06532	H06532_at	Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
101	570 Lymphoma	0.460272	0.3018751	0.253747	0.15775098 D82797	at.	EST: similar to none, mRNA sequence. (from Genbank)
711	571 Lymphoma	0.4601813	0.3018087	0.253723	0.1576673	X00351 f at	0.1576673 X00351 f at ACTB Actin. beta
72.1	572 Lymphoma 0.4599361	0.4599361	0.301758	0.253718	0.1575614 1_at	U05259_rna 1_at	MB-1 gene
73 [573 Lymphoma 0.4595795	0.4595795	0.3015964	0.253689	0.15753362 t	AA234657_a t	Zr75g08.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 669278 5', mRNA sequence. (from Genbank)
74 [574 Lymphoma 0.4593212 0.3015783	0.4593212	0.3015783	0.253636	0.1574842 00	AA0187	EST: ze54e06.s1 Soares retina N2b4HR Homo sapiens cDNA clone

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G/C	575 Lymphoma 0.4590846	0.4590846	0.3015646	0.253564	0.15740599 W15618_at	N15618_at	EST: zb05f07.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 301189 5', mRNA sequence. (from Genbank)
576	576 Lymphoma	0.4585275	0.3015617	0.253552	0.15732065 N41987	N41987_at	EST: yw69b06.r1 Homo sapiens cDNA clone 257459 5'. (from Genbank)
277	577 Lymphoma 0.4583989	0.4583989	0.3013871	0.253539	0.15720116 U48263_at	J48263_at	Pre-pro-orphanin FQ (OFQ) mRNA
578	578 Lymphoma	0.4583989	0.3013657	0.253271	0.15715349	J48263_at-2	0.15715349 U48263_at-2 Prepronociceptin
579	579 Lymphoma 0.4582757 0.3012805	0.4582757	0.3012805	0.25323	0.15709794	\A075599_a	EST: zm88c03.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544996 5' similar to SW:Ni2M_BOVIN Q02369 AA075599_a NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT;, mRNA t sequence. (from Genbank)
580	580 Lymphoma 0.4579643	0.4579643	0.3012222	0.253155	0.15700534 t	4A047055_a	AA047055_a EST: zf50g10.r1 Soares retina N2b4HR Homo sapiens cDNA clone t 380418 5, mRNA sequence. (from Genbank)
581	581 Lymphoma 0.4577725	0.4577725	0.3012019	0.253119	0.15694085 M20902 at		APOC1 Apolipoprotein Cl
582	582 Lymphoma 0.4577502	0.4577502	0.3010995	0.253085	0.15688698 FAS_at		No description for gene: FAS at
583	583 Lymphoma	0.4575031	0.3010762	0.253055	RC_A 0.15682718 19_at	A4657	EST: aa32f07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814981 3', mRNA sequence. (from Genbank)
584	584 Lymphoma 0.4572826	0.4572826	0.3009313	0.252965	RC_AA4 0.15676369 40_s_at	RC_AA4500 40_s_at	ADP-ribosylation factor-like 2
585	585 Lymphoma 0.4565934 0.3006821	0.4565934	0.3006821	0.252884	RC_A 0.15669736 08_at	A070	EST: zm69d06.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 530891 3', mRNA sequence. (from Genbank)
586	586 Lymphoma 0.4565233	0.4565233	0.3006407	0.252845	0.1566089 t	A203548	a Homo sapiens F1FO-type ATPase subunit d mRNA, nuclear gene encoding mitochondrial protein, complete cds
587	587 Lymphoma 0.4555549	0.4555549	0.3005857	0.252754	0.15649772 R06629 at	306629 at	Adducin 2 (beta)
588	588 Lymphoma	0.4553219	0.3005146	0.252725	0.15638246 86	60	EST: zf66c03.s1 Soares retina N2b4HR Homo sapiens cDNA clone 381892 3', mRNA sequence. (from Genbank)
589	589 Lymphoma	0.454982	0.3004212	0.25272	AFFX- HSAC07/X0 0.15629882 0351 3 at-2		No info for gene
290	590 Lymphoma	0.454982	0.3003941	0.252598	AFFX- HSAC07/X 0.15623137 0351 3 at		AFFX-HSAC07/X00351 3 at (endogenous control)
591	591 Lymphoma 0.4547807 0.3003687	0.4547807	0.3003687	0.252461	RC_A 0.15606539 40_at	6	EST: zs01d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683917 3', mRNA sequence. (from Genbank)

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AA083339_a EST: zn31d10.r1 Stratagene endothelial cell 937223 Homo sapiens t cDNA clone 549043 5', mRNA sequence. (from Genbank)	EST: aa54g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824804 3', mRNA sequence. (from Genbank)	EST: zd83f05.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 347265 5' similar to SW:SYB2_XENLA P47193 SYNAPTOBREVIN 2;, mRNA sequence, (from Genbank)	EST: yv52a12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 246334 5', mRNA sequence. (from Genbank)	EST: 19b2 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)	EST: yi60f07.r1 Homo sapiens cDNA clone 143653 5'. (from Genbank)	Messenger RNA for human leukocyte (alpha) interferon. (from Genbank)	EST: zn97h02.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 566163 3', mRNA sequence. (from Genbank)	Homo sapiens chromosome 19, cosmid F22329	Homo sapiens Dim1p homolog (hdim1+) mRNA, complete cds	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)	KIAA0331 gene product	Src-like adapter protein mRNA	AA256771_a EST: zs22h09.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t IMAGE:685985 5', mRNA sequence. (from Genbank)	EST: za76b09.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 298457 5' similar to contains element MER22 repetitive element, mRNA sequence. (from Genbank)	Cathepsin Z	Complement component (3b/4b) receptor 1, including Knops blood at group system	AA410353_s 753339 5' similar to TR:G457883 G457883 ZINC FINGER PROTEIN. at ;; mRNA sequence. (from Genbank)
AA083339_a	A4890			äţ	क्रं	0.15562275 J00214 f at	A1369	at	AA460128_a t		A4529	at	AA256771_a		AA131127_a t	s at	AA410353_s
0.15604697	RC_A 0.15596607 74_at	0.15582645 W80846 at	0.15579109 N74749_at	0.15573561 W26989	0.15569472 R76066	0.15562275	RC_A 0.15556777 40 at	0.15546615 R11267	0.15536627	0.15531231 D31184 at	RC_A 0.15523967 13 at	0.15514946 D89077	0.15511785 t	0.15504779 W04732 at	0.15493405	0.15490547 Y00816	0.15486063
0.252402	0.252225	0.252159	0.252001	0.251814	0.251798	0.251791	0.251616	0.251604	0.251546	0.251464	0.251396	0.251394	0.251307	0.251282	0.251256	0.251252	0.25124
0.300294	0.300242	0.3001426	0.3000544	0.3000216	0.3000007	0.2999614	0.299957	0.2999365	0.2999177	0.2998219	0.2995821	0.2995773	0.2995476	0.299465	0.2994247	0.2993525	0.2993226
0.4545412	0.4541784	0.454119	0.4540041	0.4538769	0.4537107	0.4534683	0.4533986	0.4533417	0.4531421	0.4525061	0.4524671	0.4523326	0.4522882	0.4520637	0.4518604	0.4518507	0.4517575
592 Lymphoma 0,4545412	593 Lymphoma	594 Lymphoma	595 Lymphoma	596 Lymphoma	597 Lymphoma	598 Lymphoma	599 Lymphoma 0.4533986	600 Lymphoma 0.4533417	601 Lymphoma	602 Lymphoma	603 Lymphoma	604 Lymphoma 0.4523326	605 Lymphoma	606 Lymphoma 0.4520637	607 Lymphoma	608 Lymphoma	609 Lymphoma 0.4517575 0.2993226
592	593	594	595	596	597	598	599	900	601	602	603	604	605	909	607	809	609

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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RC_AA4559 EST: aa14f10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 21_at 813259 3', mRNA sequence. (from Genbank)	Zv01h10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746275 5' similar to gb:J04422 ISLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN);, mRNA sequence. (from Genbank)	IRF4 Interferon regulatory factor 4	EYA1A gene	Peroxisomal farnesylated protein	MHC CLASS II TRANSACTIVATOR CIITA	EST: zp23h11.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 610341 3', mRNA sequence, (from Genbank)	FUCA1 Fucosidase, alpha-L- 1, tissue	EST: aa28h02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814611 3', mRNA sequence. (from Genbank)	EST: zp63e07.s1 Stratagene endothelial cell 937223 Homo sapiens	EDIVA CIONE 024300 3, INNIVA SEQUENCE. (ITOM GENDANK) EST: zr75d08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669231 3', mRNA sequence. (from Genbank)	35a7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genbank)	EST: yi84a04.r1 Homo sapiens cDNA clone 145902 5' similar to contains Alu repetitive element; contains PTR7 repetitive element;	(Irom Genbank) EST: zv31e09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755272 31 mRNA sequence (from Genbank)	EST: zs15e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685276 5', mRNA sequence, (from Genhank)	EST: af61g05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 1046552 31 mRNA sequence (from Genhank)	EST: zs85b03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704237 3', mRNA sequence. (from Genbank)
RC_AA4559 21_at	AA419464_a t	U52682_at	Y10260 at	RC_AA1264 29 at	X74301_s_a t	RC_AA1761 64_r_at	M29877 at	RC_AA4809 91_s_at	RC_AA1819	RC_AA2322 39 at	at		RC_AA4963 47 at	AA243523_a t	AA6211 s at	A2793
RC_A 0.15479703 21_at	0.1546873 [1	0.15462057 U52682	0.15459685 Y10260 at	RC_A 0.15447827 29 at	0.15439142	RC_AA 0.15434413 64 r at	0.15431316 M29877 at	0.15423946 91	RC 15418112 11	0.1541626 39 at	0.15409301 W27603	0.45404.202	0.15398791 47 at	0.15392728	0.15386732 62	RC_A 0.15379548 37_at
0.251191	0.251131	0.251126	0.251114	0.251107	0.251094	0.250897	0.250895	0.250874	0.250818	0.250762	0.250631	0.05084	0.250563	0.250494	0.25044	0.250314
0.2992886	0.2991815	0.2991568	0.2990216	0.2990108	0.2989451	0.2986669	0.2985756	0.2985225	0.2984801		0.2984419	0.208413	0.2981668	0.2980929	0.2980479	0.2980459
0.4517442	0.4516966	0.4515642	0.4510315	0.4510014	0.4509181	0.4508372	0.4505091	0.4504607	0.4502895	0.4499491	0.4496515	0.4494863	0.4493459	0.4490154	0.4489474	0.4489304
610 Lymphoma	611 Lymphoma	612 Lymphoma	613 Lymphoma 0.4510315	614 Lymphoma 0.4510014	615 Lymphoma 0.4509181	616 Lymphoma 0.4508372	617 Lymphoma	618 Lymphoma	619 Lymphoma 0.4502895	620 Lymphoma	621 Lymphoma	622 Vmphoma		624 Lymphoma	625 Lymphoma	626 Lymphoma 0.4489304
610	611	612	613	614	615	616	617	618	6191	620	6211	622	623	624 [625 [626 [

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RC D60438 EST: Human fetal brain cDNA 3'-end GEN-108H04, mRNA sequence. EST: ze64e11.r1 Soares refina N2b4HR Homo sapiens cDNA clone EST: zo19g09.s1 Stratagene colon (#937204) Homo sapiens cDNA AA187579_a EST: zp66d11.r1 Stratagene endothelial cell 937223 Homo sapiens RC_AA4031 | Homo sapiens U-snRNP-associated cyclophilin (USA-CyP) mRNA, AA477288_a EST: zu43f11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: ab16f05.s1 Stratagene lung (#937210) Homo sapiens cDNA RC AA1802 EST: zp35f01.s1 Stratagene muscle 937209 Homo sapiens cDNA Za35g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA AA020927_a 363788 5' similar to contains L1.t2 L1 repetitive element ;, mRNA EST: zk14d05.s1 Soares pregnant uterus NbHPU Homo sapiens 0.1530418 54 s at sequence. (from Geninaliny RC_AA4892 EST: aa57g04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone RC_AA4892 EST: aa57g04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone AA458602_a EST: aa12f12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA4172 EST: zu07h02.s1 Soares testis NHT Homo sapiens cDNA clone RC_AA0316 element; contains element PTR7 repetitive element;, mRNA cDNA clone 625173 5', mRNA sequence. (from Genbank) cDNA clone 470505 3' similar to contains Alu repetitive clone 294584 5', mRNA sequence. (from Genbank) clone 840993 3', mRNA sequence. (from Genbank) clone 587392 3', mRNA sequence. (from Genbank) clone 740781 5', mRNA sequence. (from Genbank) clone 611449 3', mRNA sequence. (from Genbank) 731187 3', mRNA sequence. (from Genbank) 813071 5', mRNA sequence. (from Genbank) Homo sapiens gene for NBS1, complete cds Chemokine receptor X (CKRX) mRNA Cytochrome c oxidase subunit IV Receptor protein 4-1BB mRNA sequence. (from Genbank) Chemokine receptor (from Genbank) complete cds RC_AA1303 0.15341356 49 at RC_AA4865 0.15352747 79 at U03397 s a AF014958_a AF014958_a 0.1526989 50 at 0.15366735 W01881 at 0.15314652 T75086 at 0.15283406 65 s at 0.15298344|33 at 0.15311949 16 at 0.15249592 08 at 0.15265991 t-2 0.15253052 t 0.15289684|t 0.15276879 0.15370917 0.15328460.15321128 0.15261038 0.250266 0.2501 0.250099 0.250083 0.249556 0.250026 0.249792 0.249278 0.248956 0.248956 0.249881 0.249541 0.249482 0.249387 0.249229 0.249193 0.249364 0.249161 641 Lymphoma | 0.4456227 | 0.2971341 629 Lymphoma | 0.4477941 | 0.2978599 630 Lymphoma | 0.4477818 | 0.2977402 0.297553 635 Lymphoma | 0.4465935 | 0.2973303 0.2972894 639 Lymphoma | 0.4459289 | 0.2972048 644 Lymphoma | 0.4453964 | 0.2969199 627 Lymphoma | 0.4485151 | 0.2979618 0.297669 632 Lymphoma | 0.4476775 | 0.2975923 633 Lymphoma | 0.4476775 | 0.2975807 636 Lymphoma | 0.4463517 | 0.2973099 637 Lymphoma | 0.4462955 | 0.2972961 640 Lymphoma | 0.4456292 | 0.2971727 | 642|Lymphoma | 0.4456227 | 0.2971186 643 Lymphoma | 0.4455442 | 0.2971025 628|Lymphoma| 0.4482572| 0.2979597| 638|Lymphoma| 0.4461644| 631 Lymphoma | 0.4476848 | 634|Lymphoma| 0.4469234|

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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0.296896	0.248831	0.15242894 28	28 at	28 at clone 838500 3', mRNA sequence, (from Genbank)
0	0.248751	0.15239221	C15910_s_a t	C15910_s_a NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, t
0	0.24875		AA452724_a	TFAR19 novel apoptosis-related gene
0	0.24866	RC_A 0.15213473 20_at	A2790	EST: zs83a12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704062 3', mRNA sequence. (from Genbank)
0.24	0.248507	0.15208687 L44544_at		BUB3 (budding uninhibited by benzimidazoles 3, yeast) homolog
0.24	0.248433	0.15201409	F006084_a	Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA
0.248411	3411	0.15197447 t	AA095039_a t	AA095039_a Cp2534.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)
0.248346	3346	0.151897241	A092376_a	15 kDa selenoprofein
0 248326	3326	0 15187089 96	SC_AA4117	Homo eanione clone 24631 mBNA comingo
0.248185	185	0.151834951	01677_s_a	Glyceraldehyde-3-phosphate dehydrogenase
	-		AA05044E 2	EST: 2/95a03.r1 Stratagene corneal stroma (#937222) Homo sapiens
0.248173	73	0.15168144 t	t	mRNA sequence. (from Genbank)
0.248138	38	0.15165226 38	_AA4307 at	EST: zw32c02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770978 3', mRNA sequence, (from Genbank)
0.248062	32	0.15158977	AA4259 at	EST: zv48g04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756918 3', mRNA sequence. (from Genbank)
0.248032	32	0.15151133	60479	EST: Human fetal brain cDNA 3'-end GEN-111H01, mRNA sequence. (from Genbank)
0.2478	897	0.1514648		AA093977_a EST: cl1504.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t
0.247884	884	0.15137158 L40395_at		(clone S20iii15) mRNA, 3' end of cds
0.247	824	0.15133484 L40395		at-2 Homo sapiens clone 23689 mRNA, complete cds
0.24	0.247783	RC_A 0.15126473 52_at	RC_AA1026 52_at	RC_AA1026 EST: zn73b01.s1 Stratagene NT2 neuronal precursor 937230 Homo 52 at sapiens cDNA clone 563785 3', mRNA sequence. (from Genbank)
0.2	0.24775	RC 0.15120895 58_	A2927	EST: zt56a01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726312 3', mRNA sequence. (from Genbank)

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EST: yi45a03.r1 Homo sapiens cDNA clone 142156 5'. (from Genbank)	H.sapiens MTCP1 gene, exons 2A to 7 (and joined mRNA)::H.sapiens MTCP1 gene, exons 2A to 7 (and joined mRNA)	EST: zr79g09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681952 3', mRNA sequence. (from Genbank)	Peroxisomal acyl-CoA thioesterase	EST: yr50b10.r1 Homo sapiens cDNA clone 208699 5'. (from Genbank)	EST: zv61g10.s1 Soares testis NHT Homo sapiens cDNA clone 758178 3', mRNA sequence. (from Genbank)	EST: EST51569 Gall bladder II Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)		Homo sapiens mRNA in the region near the btk gene involved in a-	mRNA in the region near the btk gene involved in a-gamma- globulinemia	EST: Human fetal brain cDNA 5'-end GEN-143D03, mRNA sequence. (from Genbank)	EST: zv75e06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759490 5', mRNA sequence, (from Genbank)	Homo sapiens GTPase-activating protein (SIPA1) mRNA, complete cds	EST: ze07c05.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358280 5', mRNA sequence, (from Genhank)	AA285293_a EST: PMY0799 KG1-a Lambda Zap Express cDNA library Homo	0.15032057 L23134 s at Homo sapiens metase (MET-1) mRNA complete cds	Polymyositis/scleroderma autoantigen 1 (75kD)	MYBL1 V-myb avian myeloblastosis viral oncogene homolog-like 1	KIAA0476 gene product
R69700_at	Z24459_rna 1_at	RC_AA2561 27_at	X86032 at	H61002 at	RC_AA4422 53_at	AA345469_s at	AA133244_a t	L20773 at-2		D60964_at	AA452004_a t	A0646	ä	AA285293_a	L23134 s at	AA424282_a t	at at	at
0.15109718 R69700	2244 0.15101692 1_at	RC_A 0.1509908 27_at	0.1509598 X86032	0.15087526 H61002 at	RC_A 0.1508415 53_at	0.15079863	0.15072393	0.1506941 L20773	0.1506632 L20773	0.15062588 D60964_at	0.15059908 t	RC_A 0.1504958 56_at	0.15043089 W95746	0.1503335	0.15032057	0.15028028 t	0.15013526 X66087	0.15001209 R50692
0.247695	0.247579	0.247536	0.247483	0.247431	0.247379	0.247261	0.24719	0.247138	0.247079	0.247033	0.246976	0.24692	0.24686	0.246847	0.246751	0.246686	0.24658	0.246528
0.2959104	0.2959042	0.2958241	0.2958203	0.2958139	0.2958035	0.2957078	0.2955936	0.2955197	0.295517	0.2954117	0.2953101	0.2951872	0.2950925	0.2950745	0.2950379	0.2950192	0.2950003	0.2949428
0.4414763	0.4407121	0.4405855	0.440322	0.4399855	0.4394719	0.4394041	0.4389496	0.4389198	0.4389198	0.4387516	0.4385256	0.4381341	0.4376817	0.4374224	0.4373139	0.4372422	0.4372161	0.4371688
664 Lymphoma	665 Lymphoma 0.4407121	666 Lymphoma	667 Lymphoma	668 Lymphoma 0.4399855	669 Lymphoma	670 Lymphoma	671 Lymphoma	672 Lymphoma	673 Lymphoma	674 Lymphoma	675 Lymphoma 0.4385256 0.2953101	676 Lymphoma	677 Lymphoma	678 Lymphoma 0.4374224	679 Lymphoma	680 Lymphoma	681 Lутрнота	682 Lymphoma 0.4371688 0.2949428
999	665	999	299	668	699	670	671	672	673	674	675	9/9	229	879	679	680	681	682

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Eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)	AA442400_a Homo sapiens hepatitis B virus X interacting protein (XIP) mRNA, toomplete cds	at-2 Human melanoma antigen p15 mRNA, complete cds	Velanoma antigen p15 mRNA	EST: zw49d02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773379.37 mRNA sequence (from Genhank)	AA431277_a EST: zw78h07.r1 Soares testis NHT Homo sapiens cDNA clone the Table 1782365 5', mRNA sequence. (from Genbank)	Non-histone chromosome protein 2 (S. cerevisiae)-like 1	EST: zx89a01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810888 3', mRNA sequence. (from Genbank)	Hexosaminidase B (beta polypeptide)	EST: zx29g12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 787942 3', mRNA sequence. (from Genbank)	Homo sapiens chromosome 19, cosmid R30783	EST: zs27c02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686402 3', mRNA sequence. (from Genbank)	EST: zl07b03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491597 5', mRNA sequence. (from Genbank)	KIAA0084 gene, partial cds	EST: zs27c12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686422 31, mRNA sequence, (from Genbank)	EST: EST62091 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)	AA255577_a EST: zs31b05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t	Zc32a12.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323998 5', mRNA sequence, (from Genbank)	AA236843_s EST: zr76h09.r1 Soares NhHMPu \$1 Homo sapiens cDNA clone at 669377 5', mRNA sequence, (from Genbank)	RC_AA4499 Homo sapiens mRNA for glycoprotein-associated amino acid
	AA42400_a l	U19796_at-2 }	0.14976731 U19796_at	A4257	AA431277_a E	0.1495977 W26716 at N	A4592		522	AA215299_s _at	A2528	AA150364_a t		A2527	AA353903_s at		0.14883077 W46245 at 0	AA236843_s E	RC_AA4499 14_at
R(0.14997393 51	0.14992474	0.1498426 U19796	0.14976731	RC_A 0.14972058 53 at	0.14963236 t	0.1495977	RC_A 0.14951788 77_at	0.14944656 F15210 at	0.14940268 80 s at	0.1493359	RC_A 0.149275 08_at	0.14922553	0.14915347 D42043 at	RC_A 0.14901197 62 at	0.14895856	0.14893648	0.14883077	0.14881602	RC_A 0.14881334 14_at
0.246478	0.246472	0.246402	0.246383	0.24634	0.246251	0.24621	0.246022	0.245988	0.245956	0.245932	0.245879	0.24579	0.245703	0.24563	0.24556	0.245535	0.245511	0.245375	0.245291
0.2949082	0.2948245	0.2946966	0.2946158	0.2945809	0.2945532	0.2944861	0.294481	0.2943329	0.294324	0.2942882	0.2942571	0.2942571	0.2941678	0.2941446	0.294122	0.2940624	0.2939774	0.2939622	0.2939196
0.4371084	0.4368806	0.4363753	0.4363753	0.4358464	0.4358135	0.4356911	0.4352945	0.4351078	0.4350218	0.4350001	0.4348142	0.4347649	0.4346931	0.4345636	0.4344814	0.4344083	0.4342016	0.4338027	0.4336802
683 Lymphoma	684 Lymphoma	685 Lymphoma	686 Lymphoma 0.4363753	687 Lymphoma 0.4358464	688 Lymphoma	689 Lymphoma 0.4356911	690 Lymphoma	691 Lymphoma 0.4351078	692 Lymphoma 0.4350218	693 Lymphoma 0.4350001	694 Lymphoma	695 Lymphoma	696 Lymphoma	697 Lymphoma 0.4345636	698 Lymphoma 0.4344814	699 Lymphoma	700 Lymphoma 0.4342016	701 Lymphoma	702 Lymphoma 0.4336802 0.2939196
683	684	685	989	289	889	689	069	691	692	693	694	695	1969	1 269	1869	1 669	7001	701	702

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0.43362	0.293872	0.245223		0.14873835 U53225 at	SNX1 Sorting nexin 1
(0)	0.4333586 0.2938301	0.245159	0.1486321	AA133359_a t	EST: zl17d12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502199 5', mRNA sequence. (from Genbank)
~~	0.4332978 0.2937678	0.245135	0.14851177 H66211	H66211 at	EST: yu16h09.r1 Homo sapiens cDNA clone 234017 5'. (from Genbank)
	706 Lymphoma 0,4332056 0,2937457	0.245033	0.14845335 t	AA165234_a t	Immunoglobulin (CD79A) binding protein 1
	0.4331406 0.2937169	0.244939	0.14845173 t	VA401547_a	EST: zu62a05.r1 Soares testis NHT Homo sapiens cDNA clone 742544 5', mRNA sequence. (from Genbank)
	0.432953 0.2936913	0.244912	0.14838 t	AA085059_a t	AA085059_a clone 547369 5' similar to gb:M26880 UBIQUITIN (HUMAN);, mRNA sequence. (from Genbank)
	709 Lymphoma 0.4329484 0.2936382	0.244832	0.14832777	AA121287_a t	EST: zn76e04.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 564126 5' similar to SW:PYRG_HUMAN P17812 CTP SYNTHASE:, mRNA sequence. (from Genbank)
	0.4327512 0.2936022	0.244781	RC 0.14825161 57	RC_AA5211 57_at	EST: aa73c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826578 3', mRNA sequence, (from Genbank)
(1)	0.4320673 0.2935704	0.244676	0.14817566 R90942 at	R90942 at	EST: yp92b03.r1 Homo sapiens cDNA clone 194861 5'. (from Genbank)
ω	0.4320228 0.2935645	0.244651	RC 0.14811444 74	_AA4304 at	EST: zw23a12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770110 3', mRNA sequence. (from Genbank)
	0.4319933 0.2934007	0.244644	0.14804092 S43646_at	S43646_at	KERATIN, TYPE II CYTOSKELETAL 2 EPIDERMAL
	0.4319933 0.2933278	0.244586	0.14791767		Cytokeratin 2 [human, epidermis, mRNA, 2427 nt]. (from Genbank)
	715 Lymphoma 0.4317215 0.2932816	0.244568	0.1478633	AA488505_a t	Human placenta (Diff33) mRNA, complete cds
(0)	716 Lymphoma 0.4315046 0.2932765	0.244543	RC 0.1478398 37	_AA4564 _at	EST: zx34h08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788415 3, mRNA sequence. (from Genbank)
CO (0.4313668 0.2932565	0.244392	0.14781494 W86706 at		EST: zh63d02.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 416739 5', mRNA sequence. (from Genbank)
	0.4312815 0.2930411	0.24433	Z149 0.14777303 1_at	182_ma	MHC-encoded proteasome subunit gene LAMP7-E1 gene (proteasome subunit LMP7) extracted from H.sapiens gene for major histocompatibility complex encoded proteasome subunit LMP7
	719 Lymphoma 0.4311701 0.2928774	0.244297	[0.147754191	049824_s_a	HLA-B null allele mRNA

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AA464043_s EST: zx86c06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA at clone 810634 5; mRNA sequence, (from Genbank)	EST: zu12b06.r1 Soares testis NHT Homo sapiens cDNA clone 731603 5', mRNA sequence, (from Genbank)		0.14752695 H03686 i at Human GAP SH3 binding profein mRNA complete cds	AA249538_a EST: jj6896.seq.F Human fetal heart, Lambda ZAP Express Homo		EST: zr81c12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682102 3', mRNA sequence. (from Genbank)	0.1473097 L13203_at-2 Human HNF-3/fork-head homolog-3 HFH-3 mRNA, complete cds	HNF-3/fork-head homolog-3 HFH-3 mRNA			BLM Bloom syndrome	Homo sapiens mRNA for KIAA0914 profein complete cds	Carboxypeptidase D	EST: zf22b01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 377641 3', mRNA sequence. (from Genhank)	EST: zx68f11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796653 31 mRNA sequence (from Genhank)	EST: zv14d10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	AA430008_a EST: zw65a08.r1 Soares testis NHT Homo sapiens cDNA clone t	RC_AA1820 EST: zp62f10.s1 Stratagene endothelial cell 937223 Homo sapiens 01_r_at cDNA clone 624811 3', mRNA sequence. (from Genbank)
	AA405278_a t	RC_AA2920 86_s_at	H03686 i at	AA249538_a t	AA471293_a t	RC_AA2562 73 at	L13203_at-2	L13203 at	RC_AA0344 07_at	A0535	U39817 at	W26845 at	RÇ_AA4586 55 at	A0559	A4605	A4787	4A430008_a	RC_AA1820
0.14765108	0.14761382	RC_AA2 0.14761147 86_s_at	0.14752695	0.147470221	0.1473862 t	RC_A 0.14737943 73 at	0.1473097	0.14712197 L13203 at	0.14706735	RC_A 0.14705315 08_at	0.14695461 U39817	0.14686866 W26845 at	RC_A 0.14680415 55 at	RC_A 0.14672771 92 at	0.14664954 51	0.14662546 27 at	0.146597921	RC_AA
0.244247	0.244222		0.244122	0.244118	0.244079	0.243975	0.243972	0.243843	0.243794	0.24379	0.243559	0.243538	0.243504	0.243442	0.24338	0.243291	0.243187	0.243148
0.292809	0.2927926	0.2927353	0.2927232	0.2927053	0.2926831	0.2926294	0.292627	0.2926255	0.2925414	0.2923915	0.2921976	0.2920614	0.2919997	0.2919738	0.2919165	0.2918973	0.2918845	0.2918436
0.4306343	0.4304687	0.4304529	0.4304477	0.4304226	0.4303733	0.4302757	0.4300166	0.4300166	0.4298033	0.4296877	0.4293944	0.4293805	0.4290007 0.2919997	0.4287318	0.4285827	0.4284406		0.4280496
720 Lymphoma	721 Lymphoma	722 Lymphoma 0.4304529	723 Lymphoma 0.4304477	724 Lymphoma 0.4304226 0.2927053 0.2441	725 Lymphoma 0.4303733	726 Lymphoma 0.4302757	727 Lymphoma 0.4300166	728 Lymphoma 0,4300166	729 Lymphoma 0.4298033	730 Lymphoma 0.4296877	731 Lymphoma 0.4293944 0.2921976	732 Lymphoma 0.4293805 0.2920614	733 Lymphoma	734 Lymphoma	735 Lymphoma 0.4285827 0.2919165	736 Lymphoma 0.4284406	737 Lymphoma 0.4281119	738 Lymphoma 0.4280496 0.2918436
720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738 1

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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756	Lymphoma	756 Lymphoma 0.4256564	0.2908675	0.242114	0.14542271 at	W67291_s_ at	EST: zd43b10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343387 5' mRNA sequence (from Genhank)
757	Lymphoma	757 Lymphoma 0,4252334	0.2908505	0.242047	0.14537668 U90546	U90546_at	Butyrophilin (BTF4) mRNA
758	Lymphoma	758 Lymphoma 0.4252334	0.2908505	0.242044	0.1453367	U90546 at-2	0.1453367 U90546 at-2 Human butvronhilin (RTE4) mRNA complete cds
759	Lymphoma	759 Lymphoma 0.4251561	0.2908083	0.242003	0.14530474 44 at	RC_AA4057 44 at	RC_AA4057 EST: zu66f10.s1 Soares testis NHT Homo sapiens cDNA clone 44 at 742987 3' mRNA sequence (from Genhank)
760	Lymphoma	760 Lymphoma 0.4249699	0.2907927	0.241995	0.1452068 t	AA248589_a t	
761	761 Lymphoma	0.4248904	0.2907927	0.241982	0.1451136 t	AC002306_a	AC002306_a Endothelial differentiation, lysophosphatidic acid G-protein-coupled to receptor, 4
762	762 Lymphoma	0.424794	0.2907823	0.241956	RC_A 0.14505336 96 at	RC_AA0635 96_at	EST: ze87c06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 365962 3' similar to SW:NC5R_RAT P20070 NADH-CYTOCHROME B5 REDUCTASE;, mRNA sequence. (from Genhank)
763	Lymphoma	763 Lymphoma 0.4246376		0.241774	0.14501981	X16869_s_a t	Eukarvotic translation elongation factor 1 alpha 1
764	Lymphoma	764 Lymphoma 0.4244974	0.2906598	0.241689		HG3549- HT3751 at	Wilm'S Tumor-Related Protein
765	765 Lymphoma	0.424458	0.2906428	0.241644	0.1449409	0.1449409 N71232_at	EST: yw36g09.r1 Homo sapiens cDNA clone 254368 5'. (from Genbank)
992	766 Lymphoma	0.4244561	0.2906348	0.241643	0.14484346 t	AA282978_a t	
797	767 Lymphoma	0.424376	0.2905532	0.241643	0.14478923 W67189 at	W67189 at	EST: zd43g04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 343446 5', mRNA sequence, (from Genhank)
768	768 Lymphoma	0.4243576	0.2905335	0.24164	RC 0.14476319 29	_AA4241 at	EST: zv81a02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 760010 3', mRNA secuence (from Genhank)
169/	769 Lymphoma	0.424309	0.424309 0.2905223	0.241635	RC_AA 0.14471485 31_r_at	1066	
770	770 Lymphoma	0.4243012	0.2905117	0.241613	0.1446056	0.1446056 M97936_at	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1-ALPHA/BETA
7711	771 Lymphoma	0.4239892	0.2905027	0.241569	RC_A 0.144558162 at	A0052	Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker p182691 and STS.
772	772 Lymphoma 0.4239311	0.4239311	0.290491	0.241561	RC_A 0.1445135972_at	A4592	EST: aa27d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814479 3', mRNA sequence. (from Genbank)

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Lymphome	а 0.4235869	773 Lymphoma 0.4235869 0.2904481	0.241504	X699 0.14442864 1_at	X69908_rna 1_at	form H.sapiens gene for mitochondrial ATP synthase gene extracted from H.sapiens gene for mitochondrial ATP synthase c subunit (P2 form)
Lymphome	774 Lymphoma 0.4235869	0.2903478	0.241283		X69908_rna 1_at-2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
775 Lymphoma	0.422996	0.2903135	0.241242		RC_AA4124 83_at	Homo sapiens clone 24448 unknown mRNA, partial cds
776 Lymphoma 0.4228248 0.2902254	0.4228248	0.2902254	0.24122	RC 0.14428823,47	RC_AA5991 47_at	EST: ae52d08.s1 Stratagene lung carcinoma 937218 Homo sapiens CDNA clone 950511.3, mRNA secuence (frame Carling Carling)
777 Lymphoma 0.4227898	0.4227898	0.2902139	0.241212	RC_A 0.14422473 87_at	RC_AA3995 87_at	EST: zt93d01.s1 Soares testis NHT Homo sapiens cDNA clone 729889 31 mRNA sequence (from Casteria)
778 Lymphoma 0.4226742	0.4226742	0.2901701	0.241167	0.14408697 85 at	A4599	EST: zx66e07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
779 Lymphoma 0.4226716	0.4226716	0.2901141	0.241148	0.14404237	RC_D25755 s_at	EST: Human colon 3'directed Mbol cDNA, HUMGS04122, clone cm1358, mRNA sequence (from Conhort)
780 Lymphoma 0.4225621	0.4225621	0.290049	0.24114	0.14395627	AA070671_a t	Oxidase (cytochrome c) assembly 1-like
781 Lymphoma 0.4225078 0.2896486	0.4225078	0.2896486	0.241115	0.14393078 U10485	at	[Vmphoid-restricted mombranes
782 Lymphoma	0.4224639	0.2895004	0.241089	0.14389074	AA316868_a t	AA316868_a EST: EST188529 HCC cell line (matastasis to liver in mouse) II Homo
783 Lymphoma	0.4223548	0.2894458	0.240873	0.14381664	OT.	EST: zk70c11.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488180 5'. mRNA seguence (from Corbot).
784 Lymphoma 0.4222235	0.4222235	0.2893836	0.240873	0.14375687 57	2_AA4963 at	Homo sapiens SKR1Hs mRNA complete add
785 Lymphoma 0.4219461	0.4219461	0,2893681	0.240862	0.143713281	A215938_a	Himan RNA polymers of III such and American
786 Lymphoma 0.4217372 0.2893335	0.4217372	0.2893335	0.2408	RC_A 0.14364707 94_at	A0403	EST: zf05h02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 376083.31 mRNA sequence of from Conf.
787 Lymphoma	0.4213867	0.2892698	0.240652	0.14358312 t	1617_a	Cell division evols 2 G4 to 8 and C2 to 1.
788 Lymphoma	0.421381	0.289134	0.240601	0.14354391 25_at	A4908	EST: aa49g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
789 Lymphoma 0.4207785	0.4207785	0.289023	0.240551	0.14344981 52 at	A4525	Acyl-Coenzyme A oxidase 3. pristanovl
790 Lymphoma 0.4207745	0.4207745	0.289023	0.240503	0.1433373 U14970_at		RPS5 Ribosomal protein S5
791 Lymphoma 0.4206601 0.2889941	0.4206601	0.2889941	0.24044	RC_A 0.1432843 14 at	A5992	EST: ag34c05.s1 Jia bone marrow stroma Homo sapiens cDNA clone
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EST: zd52b01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344233 5', mRNA sequence. (from Genbank)	Homo sapiens mRNA for KIAA0625 protein, partial cds	Tropomyosin 4	EST: aa30c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814764 3', mRNA sequence, (from Genbank)	EST: EST177101 Jurkat T-cells VI Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)	EST: aa35c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815238 3', mRNA sequence. (from Genbank)	Lactate dehydrogenase B	RC_AA4002 EST: zu63a07.s1 Soares testis NHT Homo sapiens cDNA clone 59 at 742644 3', mRNA sequence. (from Genhank)	NBK apoptotic inducer protein	AA460047_a EST: zx66b11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA tolone 796413 5' mRNA sequence. (from Genbank)	AA418230_a EST: zv97h11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t 767781 5', mRNA sequence. (from Genbank)	EST: zh82b09.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	CDNA CIONE 427 09 5, INNNA Sequence. (IIOM Genbank) EST: zs80g10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703842 3'. mRNA sequence. (from Genhank)	EST: zn12d03.r1 Stratagene hNT neuron (#937233) Homo sapiens AA085232_a cDNA clone 547205 5' similar to SW:ASF1_YEAST P32447 ANTI-t SILENCING PROTEIN 1 mRNA sequence (from Genhank)	EST: yr13d05.r1 Homo sapiens cDNA clone 205161 5' similar to contains Alu repetitive element; contains L1 repetitive element;. (from Genbank)	EST: zl66d11.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509589 3' similar to gb:M25108 IIII ALU CLASS F WARNING ENTRY IIII (HUMAN);contains Alu repetitive element;, mRNA sequence. (from Genbank)	EST: 54b7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
0.14325349 W70167_at		AA085463_a t	_AA4549 at	AA306121_a t	_AA4812 at	0.14283907 R78991 at	RC_AA4002 59_at	X89986_s_a t			AA001296_s	788	A085232_a	160661 at)455	at
0.14325349	RC 0.14317684 47	0.14310572	0.14305925 37	0.14296068	0.14290671 68	0.14283907	RC 0.14280191 59	0.14277191	0.14270519	0.14267641	0.44260337	0.1425292 38 s at	Δ Δ 0.14249793 t	0.14244393 H60661	RC_A 0.14242479 96_at	0.14236675 W28953
0.240434	0.240425	0.24034	0.24034	0.240307	0.240294	0.240249	0.240211	0.240117	0.240068	0.240048	0.230037	0.239797	0.239785	0.239723	0.239621	0.239591
0.2889794	0.2889621	0.2888152		0.288769	0.2887644	0.2887623	0.2887376	0.2887183	0.2886976	0.2886471	0 2885638		0.2885008	0.2884841	0.2884431	0.2884104
0.4200393	0.4198139	0.4198082	0.4196206	0.4195114	0.4194267	0.4194259	0.4189566	0.4187936	0.4187437	0.4184738	0.4178011	0.4177361	0.4176488	0.4174737	0.4172906 0.2884431	0.417079
792 Lymphoma 0.4200393	793 Lymphoma	794 Lymphoma 0.4198082	795 Lymphoma 0.4196206	796 Lymphoma	797 Lymphoma	798 Lymphoma	799 Lymphoma	800 Lymphoma 0.4187936	801 Lymphoma 0.4187437	802 Lymphoma	803 vmnhoma 0.4178011	804 Lymphoma	805 Lymphoma 0.4176488 0.2885008	806 Lymphoma	807 Lymphoma	808 Lymphoma
792	793	794	795	796	797	798	799	800	801	802	803	804	902	908	807	808

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809 Lymphoma	а 0.4168455	0.2882794	0.239568	0.14225444	AA242923_a t	AA242923_a EST: zr64g07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t 668220 5', mRNA sequence. (from Genhank)
810 Lymphoma	a 0.4167173	0.2882639	0.239508	0.14221868		AA406000_a EST: zu56g05.r1 Soares ovary tumor NbHOT Homo sapiens cDNA to clone 742040 5', mRNA sequence. (from Genbank)
811 Lymphoma	9 0.4165246	0.2881549	0.239393	0.14212856t	AA441970_a t	KIAA0494 gene product
812 Lymphoma	a 0.4164667	0.2880923	0.239345	RC_A 0.1420498 45_at	RC_AA0226 45_at	EST: ze71b02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364395 3', mRNA sequence. (from Genbank)
813 Lymphoma 0.4163246	0.4163246	0,2880853	0.239333	0.1419693 t	AA187045_a t	AA187045_a EST: zp58a07.r1 Stratagene endothelial cell 937223 Homo sapiens t
814 Lymphoma 0.4160707	0.4160707	0.2880386	0.239328	RC_A 0.14192979 10_at	RC_AA2511 10_at	EST: zs03g05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684152 3', mRNA sequence. (from Genbank)
815 Lymphoma, 0.4160548	0.4160548	0.2879706	0.239321	0.14188004 D82558	D82558_at	Novel centrosomal protein RanBPM
816 Lymphoma	0.4159915	0.2879281	0.239317	0.14184445	M36542_s_a t	POU2F2 POU domain, class 2, transcription factor 2
817 Lymphoma	0.4157058	0.2877627	0.239255	0.14176275 U29680_at	U29680_at	Bcl-2 related (Bfl-1) mRNA
818 Lymphoma	0.4155923	0.2876655	0.239254	RC_A 0.14171952 63_at	RC_AA0340 63_at	RC_AA0340 EST: zi05g06.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens 63_at cDNA clone 429946 3', mRNA sequence. (from Genbank)
819 Lymphoma	0.4155859	0.2876593	0.239213	0.14166424 W88449_at		EST: zh69h03.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417365 5', mRNA sequence. (from Genbank)
820 Lymphoma	0.4155579	0.2876409	0.239172	0.141605691	\A429706_a	Thioredoxin-like, 32kD
821 Lymphoma	0.4155415	0.2876009	0.239045	0.14157908 W74106	at	EST: zd03e05.r1 Pancreatic Islet Homo sapiens cDNA clone 339584 5' similar to PIR:S52698 S52698 hypothetical protein YD9346.02c - yeast;, mRNA sequence, (from Genbank)
822 Lymphoma	0.4154697	0.2874641	0.239017	0.14151977 M28827 at		CD1C CD1c anticien (flymocyte antican)
823 Lymphoma	0.41528	0.2874085	0.238962	RC_A 0.14146945 69_at	3C_AA4104 39_at	RC_AA4104 EST: zv15g11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 69_at 753764 3', mRNA sequence, (from Genbank)
824 Lymphoma 0.4151618 0.2873928	0.4151618	0.2873928	0.238954	AFF HUN //M3: 0.14144704 at-2	X- MGAPDH 3197_M_	Glyceraldehyde-3-phosphate dehydrogenase

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· · · · · · · · · · · · · · · · · · ·						AFFX- HUMGAPDH /M33197 M	
825 Lymphoma	phoma	0.4151618	0.2873797	0.23875	0.14137994		AFFX-HUMGAPDH/M33197 M at (endogenous control)
826 Lymphoma	phoma	0.4148818	0.2872924	0.238745	0.14131454	R60523_s_a	EST: yh13f11.r1 Homo sapiens cDNA clone 42955 5' (from Genhank)
827 Lym	phoma	0.4146522	827 Lymphoma 0.4146522 0.2872174	0.238696	RC_A 0.14123037 08_at	RC_AA6090 08_at	+
828 Lymp	phoma	828 Lymphoma 0.4145601	0.2871712	0.238668	0.14120658 t	AA227366_a t	AA227366_a EST: zr17h05.r1 Stratagene NT2 neuronal precursor 937230 Homo
829 Lymp	phoma	829 Lymphoma 0.4144475	0.2870675	0.238628	0.1410762 W28968	W28968 at	EST: 54d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genhank)
830 Lymp	ohoma	830 Lymphoma 0.4142996	0.2870529	0.238613	0.14102367	0.14102367 R36553_at	EST: yg35a04.r9 Homo sapiens cDNA clone 34269 5'. (from Genbank)
831 Lymp	choma	831 Lymphoma 0.4141701	0.2869847	0.238547	0.14098641	AA096343_a t	
832 Lymp	ohoma	0.4136955	832 Lymphoma 0.4136955 0.2869802	0.23854	0.1409714 W79850	W79850 at	EST; zd75e07,r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346500 5', mRNA sequence (from Genhank)
833 Lymphoma	homa	0.4136472	0.2868038	0.238487	0.14093909 t	R39398_s_a t	EST: yh95d06.r1 Homo sapiens cDNA clone 137483 5'. (from Genbank)
834 Lymphoma	homa	0.4133438	0.2867934	0.238481	0.14088072	X83490_s_a t	Fas/Apo-1 (clone pCRTM11-Fasdelta(3.4))
835 Lymp	homa	835 Lymphoma 0.4132124	0.286692	0.238422	0.14081809 H71514_at	H71514_at	EST: ys11c12.r1 Homo sapiens cDNA clone 214486 5'. (from Genbank)
836 Lутрнота		0.4131587	0.286541	0.23822	0.14072691	AB002378_a t	KIAA0380 gene product
837 Lymp	homa	837 Lymphoma 0.4129566 0.2865333	0.2865333	0.238217	0.14069253 L42452 at		Pyruvate dehydrogenase kinase isoenzyme 3 (PDK3) mRNA
838 Lymphoma	homa	0.4129262	0.2864811	0.238165	0.14065503 t	vA084932_a	Golgi SNAP receptor complex member 2
839 Lymp	homa	839 Lymphoma 0.4125276	0.2862485	0.238119	0.14055859 Z21206_at		EST: H. sapiens putatively transcribed partial sequence; UK-HGMP sequence ID AAADSOA; single read, mRNA sequence. (from Genbank)
840 Lympi	homa	840 Lymphoma 0.4125085	0.2860758	0.238096	RC_A 0.14054541 40_at	A4549	EST: aa30c12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814774 3', mRNA sequence. (from Genbank)
841 Lymphoma	homa	0.412377	0.2859515	0.238069	HG3928- 0.14034931 HT4198_at		Surfacant Protein Sp-A1 Delta
842 Lympł	homa (842 Lymphoma 0.4121418	0.28571	0.237991	RC_A 0.14031689 96_at	A2807	EST: zs97b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711545 3', mRNA sequence, (from Genhank)
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843|Lymphoma| 0.4120804| 0.2855041|

844 Lymphoma | 0.4120712 | 0.2854623

845|Lymphoma| 0.4119494| 0.2854359|

0.41169 0.2854274

846 Lymphoma

847 Lymphoma | 0.4115815 | 0.2854227

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. AA496240_a Zx70g11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone EST: zx44a10.s1 Soares total fetus Nb2HF8 9w Homo sapičas cDNA | RC_AA1433 | EST: zo37h02.s1 Stratagene endothelial cell 937223 Homo sapiens 0.14008354 | 29_at | cDNA clone 589107 3', mRNA sequence. (from Genbank) RC_AA4113 EST: zv28c04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 0.14013141 51_at clone 754950 3'. mRNA sequence. (from Genhank) Eukaryotic translation elongation factor 1 delta (guanine nucleotide EST: aa07d06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone C00449_s_a EST: HUMGS0006582, Human Gene Signature, 3'-directed cDNA RC_AA4264 EST: zv05g05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone AA313414_s EST: EST185312 Colon carcinoma (HCC) cell line Homo sapiens RC_AA4516 |clone 789306 3' similar to contains Alu repetitive element;, mRNA EST: zug8h10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone EST: yi02f09.r1 Homo sapiens cDNA clone 138089 5'. (from Homo sapiens chondroadherin gene, 5'flanking region and IMAGE:746083 3', mRNA sequence. (from Genbank) TNF receptor associated factor 5 mRNA, partial cds Homo sapiens chromosome 19, cosmid R26529 Homo sapiens RCL (Rcl) mRNA, complete cds cDNA 5' end, mRNA sequence. (from Genbank) 812555 3', mRNA sequence. (from Genbank) sequence, mRNA sequence. (from Genbank) 796868 5', mRNA sequence. (from Genbank) Chondroadherin gene, 5'flanking region and 752792 3', mRNA sequence. (from Genbank) 0.1394939 U69108_at-2 TNF receptor-associated factor 5 sequence. (from Genbank) 0.13940953 T63174_s_at KIAA0331 gene product exchange protein) HGF activator Genbank) 0.13977322 12_at RC_AA4825 J96769_rna D14012_s_a U96769_ma AA422159 a 0.13957484 U69108_at aţ 0.13985819 D79276_at 0.13934493 R53779 0.1403027 72 s at 0.13968277 | 1_at-2 0.1397306|97 at 0.14025|04 at 0.13961701 1 at aţ 0.13941887 at 0.1399293|t0.1400208 t 0.13995393t 0.14017548 0.14016822 0.237258 0.237154 0.237192 0.237292 0.237292 0.237269 0.23727 0.237452 0.237428 0.237314 0.237805 0.237791 0.237574 0.237467 0.237597 0.237697 0.237966 0.237836 0.23781

861|Lymphoma| 0.4094939| 0.2846888|

0.2847643

860|Lymphoma| 0.4095159|

855|Lymphoma| 0.4097138| 0.2851044|

856|Lymphorna| 0.4097138| 0.2850598|

857 Lymphoma | 0.4096688 | 0.2850225 |

0.2849141

858 Lymphoma | 0.4096688

0.2848564

859|Lymphoma| 0.4096609|

853|Lymphoma| 0.4098373| 0.2851324|

852|Lymphoma| 0.4103429| 0.2851472|

849|Lymphoma| 0.4108565| 0.2853418|

848|Lymphoma| 0.4112842| 0.2853947|

850|Lymphoma| 0.4107183| 0.2852789|

851 Lymphoma | 0.4104554 | 0.2852541

854|Lymphoma| 0.4098248| 0.2851318|

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EST: 49b12 Human retina cDNA randomly primed sublibrary Homo	EST: EST97722 Thyroid Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)	AA203147_a cDNA clone 446601 5' similar to contains element MSR1 repetitive	EST: ag24h03.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1090517 3', mRNA sequence, (from Genhank)	EST: yd97g10.r1 Homo sapiens cDNA clone 116226 5. (from Genbank)	IFNAR2 gene (interferon receptor) extracted from Homo sapiens (clone Q-20D3) interferon recentor (IENAD2)	Interferon (alpha heta and omoció) and occión (alpha heta and occión)	EST: 19866.seq.F Fetal heart, Lambda ZAP Express Homo sapiens	EST: zp14c07.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 609420 5', mRNA sequence. (from Genhank)	Ilmon principal to	EST: PMY0265 KG1-a Lambda Zap Express cDNA library Homo	EST: zk93h01.r1 Soares pregnant uterus NbHPU Homo sapiens	Human Hnast (HDAcT) mbMA	EST: zx39c03.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788836 5', mRNA sequence (from Conhack)	Human DNA-PK interaction protein (VID) with	Subpressor of varianation 3.0 (December 1)	TDE C DESCRIPTION OF THE STATE	EST: zu52c05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	EST: zr75d05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669225 3', mRNA sequence. (from Genbank)
3928783 W28610 at	AA384184_s at	AA203147_a	RC_AA5999 45_at	T89072 at	43_cds	spo_s	465_a	AA179892_a	ŧ	20 a	AA136326_s E	AA2817 s at		U83236_s_a t	996	to	011	326
0.13928783	0.13925263	0.13917442	RC_A 0.1390786 45_at	0.1390025 T89072	0.1389976 1_at	L4224; 0.13891426 1 at-2	0.13888681	0.13886471 t	0.13886172 195822	0.13878341 [0.13873152	RC 0.13867393 69	A 0.13859299 t	0.13855603 t	0.13854893 85 s at	0.1384677 Y00062	840868	0.1383982 86
0.237112	0.237011	0.236943	0.236896	0.236837	0.23681	0.236726	0.236676	0.236661	0.236536	0.236506	0.236463	0.236443	0.236342	0.236298	0.236294	0.236233	0.236232	
0.2845846	0.2845556	0.2844135	0.2843816	0.2842468	0.2841432	868 Lymphoma 0.4089276 0.2841425	0.4089205 0.2838673	0.2838481	0.2837812	0.2837696	0.2836947	0.2836187	0.2835748	0.2835184	0.2834147	0.2834021	3.2833477	
0.4092678	0.4091986	864 Lymphoma 0.4091433	0.4090335	0.4089425	867 Lymphoma 0.4089276	0.4089276	0.4089205	0.4088943	0.4086964	0.4086098	0.4084718	0.4082187	0.4081785		877 Lymphoma 0.4080448 0.2834147	0.4080438	879 Lymphoma 0.4076591 0.2833477	880 Lymphoma 0.4074731 0.2832753
862 Lymphoma	863 Lymphoma	Lymphoma	865 Lymphoma	866 Lymphoma	Lymphoma	Lymphoma	869 Lymphoma	870 Lymphoma	871 Lymphoma	872 Lymphoma	873 Lymphoma 0.4084718	874 Lymphoma 0.4082187	875 Lymphoma	876 Lymphoma 0.4081028	Vmphoma (878 Lymphoma 0.4080438	/mphoma (/mphoma (
862	863	864	865	866	867	868	869	8701	8711	8721	873 [874 L	875 L	876 L	877 L	878 L	879 L)	880 L)

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

881 L	утрнота	881 Lymphoma 0.4072835	0.2832347	0.236158	0.13830787 54_at	RC_AA1914 54_at	FGF intracellular binding protein
882 L	882 Lymphoma	0.4072093	0.2832301	0.236076	0.138218 U91616	U91616 at	l kappa B epsilon (IkBe) mRNA
883 🖳	883 Lymphoma	0.4071499	0.2832288	0.236045	RC_A 0.13816349 49 at	RC_AA4362 49 at	EST: zv24g07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754620 3', mRNA sequence. (from Genbank)
884 L	ymphoma	884 Lymphoma 0.4068977	0.283072	0.236033	RC_A 0.13807723 81_at	A4602	EST: zx51a04.s1 Soares testis NHT Homo sapiens cDNA clone 795726 3, mRNA sequence. (from Genbank)
885 L)	утрнота	885 Lymphoma 0.4068012	0.283055	0.236003	0.13805269	0.13805269 U31556 at	E2F5 E2F transcription factor 5, p130-binding
886 L)	ymphoma	0.4067893	886 Lymphoma 0.4067893 0.2830429	0.235995	RC_A 0.13800958 34 at	RC_AA6100 34_at	EST: af18f07.s1 Soares testis NHT Homo sapiens cDNA clone 1032037 3', mRNA sequence, (from Genbank)
887 Ly	887 Lymphoma		0.406656 0.2829691	0.235986	0.13799176	D82348 at-2	0.13799176 D82348 at-2 ribon ucleotide transformylase/inosinicase, complete cds
888 L)	888 Lутрнота	0.406656	0.2829594	0.235956	0.13792677 D82348 at	D82348 at	5-aminoimidazole-4-carboxamide-1-beta-D-ribonucleoti de transformylase/inosinicase
889 L)	889 Lymphoma	0.4065511	0.2828924	0.235848	RC_A 0.13782714 92 at	RC_AA0162 92_at	EST: ze38c02.s1 Soares retina N2b4HR Homo sapiens cDNA clone 361250 3', mRNA sequence. (from Genbank)
890 L)	890 Lymphoma	0.4058655	0.2828535	0.235789	RC_A 0.13779864 65_at	A4019	Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds
891 Ly	891 Lymphoma	0.4057701	0.2827185	0.235711	0.13771069 D42046		at-2 DNA2 (DNA replication helicase, yeast, homolog)-like
892 Ly	/mphoma	0.4057701	892 Lymphoma 0.4057701 0.2827081	0.235694	0.13767102 D42046_at	D42046_at	KIAA0083 gene, partial cds
893 Ly	трнота	0.4057397	893 Lymphoma 0.4057397 0.2826949	0.235647	0.13763493 Z21081 at	Z21081_at	EST: H. sapiens putatively transcribed partial sequence; UK-HGMP sequence ID AAADMBX; single read, mRNA sequence. (from Genbank)
894 Ly	mphoma	894 Lymphoma 0.4055338	0.2826607	0.235589	RC_A 0.13760754 96 at	A4358	EST: zt80e12.s1 Soares testis NHT Homo sapiens cDNA clone 728686 3', mRNA sequence. (from Genbank)
895 Ly	895 Lymphoma	0.4052647	0.2826536	0.235563	RC_A 0.13753949 75 at	A4546	EST: zx76a07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809652 3', mRNA sequence, (from Genbank)
896 Ly	трнота	896 Lymphoma 0.4052604	0.2825769	0.235504	0.13747247 t	AA216017_a t	AA216017_a EST: hp0234.seq.F Fetal heart, Lambda ZAP Express Homo sapiens t cDNA 5', mRNA sequence. (from Genbank)
897 Ly	897 Lymphoma	0.4051957	0.2825212	0.235426	0.13743249 U14972_at	U14972_at	Ribosomal protein S10 mRNA
898 Ly	трнота	898 Lymphoma 0.4050985 0.2824197	0.2824197	0.235419	0.13732928	AA147144_a	Zo32c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone AA147144_a 588586 5' similar to WP:C14B1.4 CE00901 GUANINE NUCLEOTIDE t BINDING PROTEIN ;, mRNA sequence. (from Genbank)

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RC_AA4063 EST: zv10e03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 88_at · 753244 3', mRNA sequence. (from Genbank)	Homo sapiens mRNA encoding rat C4.4-like protein	EST: zl8zd04.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511111 3' mRNA segmence. (from Genhank)	EST: yq53b01.r1 Homo sapiens cDNA clone 199465 5'. (from Genbank)	AA307748_s sapiens cDNA 5' end similar to similar to M. musculus hypothetical at protein (GB:L12982), mRNA sequence. (from Genbank)	AA234663_a EST: zs39a07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t 687540 5, mRNA sequence, (from Genbank)	EST: zw61a09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774520 3', mRNA sequence. (from Genbank)	EST: zt62f06.s1 Soares testis NHT Homo sapiens cDNA clone 726947 3', mRNA sequence. (from Genbank)	Eukaryotic translation elongation factor 1 alpha 1	RAB interacting factor	Guanine nucleotide exchange factor mss4 mRNA	0.1368021 t Inhibitor of growth 1	EST: ze58g08.s1 Soares retina N2b4HR Homo sapiens cDNA clone 363230 3', mRNA sequence. (from Genbank)		EST: EST61676 Activated T-cells XX Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)		AA251957_a EST: zs09f10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t	0.1364388 U11292_at-2 Human Ki nuclear autoantigen mRNA, complete cds
RC_AA4063 88_at	RC_AA4598 0.1372813 97_at	RC_AA0882 28 at	R97442_s_a t		AA234663_a t	RC_AA4301 06_at	RC_AA3984 69_at	0.13696958 W00799_at	S78873_s_at 2	S78873 s at	AF001954_a	RC_AA0188 77_at	Z36714_at	AA353516_a t	RC_AA1654 00_at	AA251957_a t	U11292_at-2
0.13731675 88_at	0.1372813	RC_A 0.13722795 28 at	0.13717978 t	0.13716073	0.13710143 t	RC 0.13705318 06	RC 0.13703439 69	0.13696958	0.136934012	0.1368451	0.1368021	RC_A 0.13676618 77_at	0.13666014 Z36714_at	0.13660644	RC_A/ 0.13655232 00_at	0.13649873	0.1364388
0.235391	0.235302	0.235297	0.23524	0.235199	0.235143	0.235105	0.235092	0.234962	0.234912	0.234879	0.234874	0.234822	0.234802	0.234685	0.234613	0.234606	0.234553
0.2823569	0.4049054 0.2823419	0.282216	0.404775 0.2822019	0.2821743	0.2821442	0.2821316	0.2820864	0.2820782	0.282078	0.2818099	0.2816954	0.2816323	0.2815677	0.2815564	0.2814837	0.2814697	0.2813993
0.4050809		0.4048		0.4043019	0.4040363	0.4037999	0.4037317	0.4035078	0.4033656	0.4033656	0.4033484	0.4032017	0.4029064	0.4027987	0.4027576	0.4026642 0.2814697	0.4025022
899 Lymphoma 0.4050809	900 Lymphoma	901 Lymphoma	902 Lymphoma	903 Lymphoma 0.4043019 0.2821743	904 Lymphoma	905 Lymphoma	906 Lymphoma 0.4037317	907 Lymphoma 0.4035078	908 Lymphoma 0.4033656	909 Lymphoma 0.4033656 0.2818099	910 Lymphoma 0.4033484 0.2816954	911 Lymphoma 0.4032017 0.2816323	912 Lymphoma	913 Lymphoma	914 Lymphorna 0.4027576	915 Lymphoma	916 Lymphoma 0.4025022 0.2813993
899	006	901	902	903	904	905	906	206	806	606	910	911	912	913	914	915	916

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917 Lyr	917 Lymphoma	0.4025022	0.2813419	0.234455	0.13639612 U11292_at	U11292_at	Ki nuclear autoantigen mRNA
918 Lyn	918 Lymphoma	0.4024472	0.2813035	0.234452	0.13637477 C00032_at	C00032 at	EST: HUMGS0003377, Human Gene Signature, 3'-directed cDNA sequence, (from Genbank)
919 Lyn	919 Lymphoma	0.4023716	0.2812597	0.234396	ρ 0.13633724 t	AA019475_a t	AA019475_a EST: ze57c01.r1 Soares retina N2b4HR Homo sapiens cDNA clone t 363072 5', mRNA sequence. (from Genbank)
920 Lyn	прнота	0.4022352	920 Lymphoma 0.4022352 0.2812515	0.23436	RC 0.1362845 05	RC_AA2242 05 at	EST: zr15f03.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 663485 3, mRNA semience (from Genhank)
921 Lyn	921 Lymphoma	0.4020522	0.2812256	0.23436	0.13624829 t	AA012864_a t	AA012864_a Ze34d10.r1 Soares retina N2b4HR Homo sapiens cDNA clone t 360883 5', mRNA sequence, (from Genhank)
922 Lyn	922 Lymphoma	0.401877	0.2811643	0.234357	0.13616103 62 at	A4292	EST: zv50a08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 757046 3', mRNA sequence. (from Genbank)
923 Lyn	923 Lymphoma	0.401781	0.2811466	0.234223	RC_A 0.1361004 53_at	RC_AA4634 53_at	EST: zx98b12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 811775 3', mRNA sequence. (from Genbank)
924 Lyn	прһота	924 Lymphoma 0.4016997	0.2811163	0.234196	0.13606927	U16811_s_a t	Bak protein mRNA
925 Lyn	прнота	925 Lymphoma 0.4016997 0.2810746	0.2810746	0.234146	U1 0.13603964 t-2	U16811_s_a t-2	BCL2-antagonist/killer 1
926 Lyn	926 Lymphoma	0.4014557	0.4014557 0.2810539	0.234146	0.13593347 U89995_at		DNA binding protein FKHL15 (FKHL15) mRNA
927 Lyn	927 Lymphoma	0.4014557	0.2809632	0.234122	0.13593347	U89995_at-2	0.13593347 U89995_at-2 Forkhead (Drosophila)-like 15
928 Lyn	928 Lymphoma	0.4014535	0.2809392	0.234089	0.13585812 W28839	क्र	KIAA0043 gene product
929 Lyn	929 Lymphoma	0.4014302	0.2808832	0.234022	0.13573688 U77413_at	U77413_at	O-linked GlcNAc transferase mRNA
930 Lyrr	phoma	930 Lymphoma 0.4011119	0.2808319	0.234011	0.13565734		Homo sapiens mRNA for ADP ribosylation factor-like LAK, complete cds
931 Lyrr	прнота	931 Lymphoma 0.4008947	0.280736	0.234011	0.13558364	A278286_a	M-phase phosphoprotein 1
932 Lym	phoma	932 Lymphoma 0.4007486	0.2807001	0.233981	0.13553727 t	\A232156_a	Insulin-like growth factor 2 (somatomedin A)
933 Lут	933 Lymphoma	0.4006888	0.2806735	0.233959	RC_A 0.13552909 58_at	A6001	EST: ae50e09.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950344 3', mRNA sequence, (from Genbank)
934 Lymphoma	phoma	0.4003771	0.2804357	0.233951	0.1354233 X06617	क्रं	RPS11 Ribosomal protein S11
935 Lym	phoma	935 Lymphoma 0.4003564 0.2804298	0.2804298	0.233859	RC_A 0.1353919477_at	A4525	EST: zx35h11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788517 3', mRNA sequence. (from Genbank)

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936	936 Lymphoma	0.4002082	0.2804287	0.233838	RC 0.13536817 87	2_AA4592 _at	Myosin IXB
937	Lymphoma	937 Lymphoma 0.4001874	0.2803443	0.233835	RC_A 0.13529858 75_at	A5985	EST: ae35e11.s1 Gessler Wilms tumor Homo sapiens cDNA clone 897836 3', mRNA sequence. (from Genbank)
938	Lymphoma	938 Lymphoma 0.4000722 0.2803019	0.2803019	0.233791	0.1352478	X16260_s_a t	ITIH3 Pre-alpha (globulin) inhibitor, H3 polypeptide
939	Lymphoma	939 Lymphoma 0.4000722 0.2802941	0.2802941	0.233791	X1 0.13523708 t-2	X16260_s_a t-2	Inter-alpha (globulin) inhibitor, H1 polypeptide
940	Lymphoma	940 Lymphoma 0.4000463	0.2802793	0.233544	0.13517725 U82979_at		Immunoglobulin-like transcript-3 mRNA
941	941 Lymphoma	0.4000253	0.2802396	0.233499	0.13512638	AA020941_a t	AA020941_a EST: ze64c11.r1 Soares retina N2b4HR Homo sapiens cDNA clone t 363764 5', mRNA sequence. (from Genbank)
942	942 Lymphoma	0.3998492	0.2801414	0.233363	0.13509157 52	_AA5995 s_at	EST: ag08a06.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1069714 3', mRNA sequence. (from Genbank)
943	943 Lymphoma	0.3992499	0.2801414	0.233343	0.13508603 U73514_at	U73514_at	Short-chain alcohol dehydrogenase (XH98G2) mRNA
944	944 Lymphoma	0.3988138	0.2800792	0.233291	0.13505258	RC_AA4600 0.13505258 24 at	Semaphorin W
945	Lymphoma	945 Lymphoma 0.3987513 0.2800788	0.2800788	0.233278	RC_A 0.13502967 24_at	RC_AA2788 24_at	EST: zs78f04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703615 3', mRNA sequence. (from Genbank)
946	946 Lymphoma	0.3986904	0.2800648	0.233261	0.13502523 H78550_at	H78550_at	EST: yu13g03.r1 Homo sapiens cDNA clone 233716 5'. (from Genbank)
947	947 Lymphoma	0.3986233	0.2800198	0.233189	0.13494551	AF004709_a t	Protein kinase mitogen- activated 13
948	948 Lymphoma	0.3980054	0.2799504	0.233178	0.13492592	AA453130_a t	Homo sapiens mRNA for KIP2, complete cds
949	949 Lymphoma	0.3978993	0.2798556	0.23311	0.13483009 L12723_at	L12723_at	HSPA4 Heat shock 70kD protein 4
950	950 Lymphoma	0.3973691	0.3973691 0.2798534	0.23309	0.13474678 U77735_at		Pim-2 protooncogene homolog pim-2h mRNA
951	951 Lymphoma	0.3971289	0.2798316	0.233016	0.13471194	M94891_s_a t	Pregnancy specific beta-1-dlycoprotein 4
952	952 Lymphoma	0.3969451	0.2797855	0.233016	0.134675	0.134675 C00463_at	EST: HUMGS0007162, Human Gene Signature, 3'-directed cDNA sequence, (from Genbank)
953	953 Lymphoma	0.3968857	0.2797609	0.232927	0.13462697	α.	EST: PMY0132 KG1-a Lambda Zap Express cDNA library Homo sapiens cDNA 5', mRNA sequence. (from Genbank)
954	954 Lymphoma	0.3968269	0.2797566	0.232905	0.13462697	AA092596_a t	Bone morphogenetic protein 6
955	Lymphoma	955 Lymphoma 0.3963356	0.2797099	0.232849	0.13457035 t	AA047791_a t	AA047791_a EST: zf99d06.r1 Soares retina N2b4HR Homo sapiens cDNA clone t 380267 5', mRNA sequence. (from Genbank)

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EST: zw85e11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 783788 5' similar to SW:KAD3_BOVIN P08760 GTP:AMP AA476639_a PHOSPHOTRANSFERASE MITOCHONDRIAL; mRNA sequence. (from Genbank)	AFFX-HUMGAPDH/M33197 5 st (endogenous control)	Glyceraldehyde-3-phosphate dehydrogenase	EST: ae48d08.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950127 3', mRNA sequence. (from Genbank)	Homo sapiens clone DT1P1B6 mRNA CAG reneat region	Homo sapiens TRIAD1 type I mRNA, complete cds	Human BAC clone RG385F02 from 7p15	0.13408658 U81787_at-2 Human Wnt10B mRNA, complete cds	Wnt10B mRNA	EST: zs91d09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704849 3' similar to SW:DNA2_YEAST P38859 DNA REPLICATION HELICASE DNA2.;, mRNA sequence. (from Genbank)	Secretory carrier membrane profein 2	EST: zv57b03.s1 Soares testis NHT Homo sapiens cDNA clone 757709 3. mRNA sequence (from Genhank)	EST: zs47h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700679 3', mRNA sequence (from Genhank)	EST: zv18e04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754014 3', mRNA sequence. (from Genhank)	EST: yx88d07.r1 Homo sapiens cDNA clone 268813 5'. (from Genbank)
AA476639_a t	AFFX- HUMGAPDH /M33197_5_ st	AFFX- HUMGAPDH //M33197_5_ st-2	RC_AA5984 29_at	aţ	_	RC_AA2238 74_at	U81787_at-2	U81787_at	A2828	\F005038_a	_AA4366 at	A2839	A4789	at
0.13455406	AH HI <i>IN</i> 0.13443808 st	AFF HUN //M3: 0.13433419 st-2	0.13429257	0.13425575 H57717	0.13423847	RC_A 0.1341851774_at	0.13408658	0.13406663 U81787	RC_A 0.13402016[03] at	0.13400687 t	0.13393493 46	RC A 0.13387349 34 at	RC 0.13384195 68	0.13380262 N36626
0.232846	0.232833	0.232737	0.232737	0.232718	0.232561	0.23243	0.232418	0.232416	0.232415	0.232333	0.232291	0.232183	0.232046	0.232021
0.2796523	0.3959785 0.2796224	0.279617	0.2796168	0.2794914	0.2794905	0.2794116	0.2793925	0.2793503	0.2793139	0.2793093	0.2792737	0.278925	0.2788715	0.2788384
0.3962916		0.3959785	0.3959328	0.3956305	0.3956126	0.3955412	0.3954591	0.3954591	0.3953896	0.3950799	0.3947507	0.3947169	0.3947042	0.3946702
956 Lymphoma	957 Lymphoma	958 Lymphoma	959 Lymphoma	960 Lymphoma	961 Lymphoma	962 Lymphoma	963 Lymphoma 0.3954591	964 Lymphoma 0.3954591	965 Lymphoma	966 Lymphoma	967 Lymphoma	968 Lymphoma	969 Lymphoma	970 Lymphoma
956	957	958	959	960	961	962	963	964	965	996	296	896	696	970

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971	971 Lymphoma	0.3944314	0.2787418	0.231942	RC_AA: 0.13376594 31_i_at	351	Renal organic anion transporter 1
972	972 Lymphoma	0.3943266	0.2787197	0.23193	0.13373856 t	/17236_s_	A HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(2) ALPHA CHAIN PRECURSOR
973	973 Lymphoma	0.3942747	0.2786675	0.231903	0.13370153 W38687	W38687_at	SH3 binding protein
974	974 Lymphoma	0.3942321	0.278616	0.231895	0.13362066	AA307896_a t	Nuclear localization signal deleted in velocardiofacial syndrome
975	Lymphoma	975 Lymphoma 0.3939648 0.2785364	0.2785364	0.231856	0.13360155	RC_AA4167 26 s at	EST: zu08a08.s1 Soares testis NHT Homo sapiens cDNA clone 731222 3', mRNA sequence. (from Genbank)
976	Lymphoma	976 Lymphoma 0.3938196	0.2785252	0.231786	RC_AA4 0.1335552 36_s_at	RC_AA4189 0.1335552 36 s_at	Homo sapiens mRNA for KIAA0795 protein partial cds
226	977 Lymphoma	0.393611	0.2783257	0.231736	0.13350788	U10493_s_a t	Mesenchyme homeo box 1
978	978 Lymphoma	0.3936067	0.2782948	0.231722	0.1334732	0.1334732 U70660_at	Copper transport protein HAH1 (HAH1) mRNA
979	Lymphoma	979 Lymphoma 0.3933139	0.2782579	0.231692	0.13340285 W28152 at	W28152 at	EST: 43f7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
086	980 Lymphoma	0.3932099	0.2782446	0.231635	0.13333799 t	\A278547_a	EST: zs76c04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703398 5', mRNA sequence. (from Genhank)
981	981 Lymphoma	0.3928986	0.2782059	0.231623	0.13331631	AA448946_r _at	EST: zx07a10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785754 5', mRNA sequence. (from Genbank)
982	Lymphoma	982 Lymphoma 0.3927018	0.2781959	0.231553	0.1332738	J03019 s at	0.1332738 J03019 s at Adrenergic, beta-1-, receptor
983	983 Lymphoma	0.3926567	0.2781689	0.231539	RC_A 0.13323556 47_at	A2591	EST: zs30f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686713 3', mRNA sequence. (from Genbank)
984	984 Lymphoma	0.3925375	0.2781552	0.231509	0.1332259t	1G2259- 1T2348_s_а	Tubulin, Alpha 1, Isoform 44
985 [985 Lymphoma	0.3924637	0.2781313	0.231384	0.13318346	J59286_at-2	0.13318346 U59286_at-2 precursor, mRNA, complete cds
1986	986 Lymphoma	0.3924637	0.2780981	0.231371	0.13314332 U59286_at	J59286_at	Beta-R1 mRNA, partial cds
1 286	987 Lymphoma	0.3922967	0.2779997	0.231358	. RC 0.13310249 91	_AA2521 at	Homo sapiens PAC clone DJ130H16 from 22q12.1-ater
1 886	988 Lymphoma	0.3920615	0.2779722	0.231339	0.13305867 X52222	at	Excision repair cross-complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D)
1 686	-ymphoma	989 Lymphoma 0.3916307 0.2779504	0.2779504	0.231328	0.13300815 H72630_at		EST: yu05a11.r1 Homo sapiens cDNA clone 232892 5'. (from Genbank)

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	1	T		 	T				T	Т	
RC_AA3982 EST: zt59b06.s1 Soares testis NHT Homo sapiens cDNA clone 05_at 726611 3', mRNA sequence, (from Genbank)	AA405937_a EST: zu66a10.r1 Soares testis NHT Homo sapiens cDNA clone t 742938 5', mRNA sequence. (from Genbank)	M57888_ma Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine	RC_AA4276 clone 770787 3' similar to contains MER17.b1 MER17 repetitive element;, mRNA sequence. (from Genbank)	EST: yo70h10.r1 Homo sapiens cDNA clone 183331 5'. (from Genbank)	EST: yi65a07.r1 Homo sapiens cDNA clone 144084 5'. (from Genbank)	AA083797_s POLYPEPTIDE VIIA-LIVER PRECURSOR (HUMAN): mRNA	sequence. (from Genbank)	RC_AA2819 IMAGE:712587 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)	AA057447_s 380905 5' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)	RC_AA2787 EST: zs77e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 17 at IMAGE:703518 3' mRNA sequence (from Ganhank)	Homo sapiens lysophospholipase (LPI 1) mRNA complete cds
RC_AA3982 05_at		M57888_ma 1_s_at	RC_AA4276 20_at	0.1327928 H43996_at	R77159_at	AA083797_s	at	RC_AA2819 34_at	AA057447_s _at	RC_AA2787 17 at	AA252436_a t
RC_A 0.13298032 05_at	0.13286473	M5788 0.1328373 1_s_at	RC_A 0.1327966 20_at	0.1327928	0.13273728 R77159 at		0.13271026 at	RC_A 0.13261746 34_at	AA(0.13258201_at	RC_A 0.13252158 17 at	0.1324749
0.231323	0.231295	0.231172	0.231137	0.231137	0.231116		0.231109	0.231053	0.230949	0.23094	0.230931
0.2779125	0.3909953 0.2778405	0.2778141	0.3905593 0.2777837	0.277604	0.2775927		0.2775575	0.2775382	0.2775143	0.2774331	0.2773911
		0.3907416		0.3904256	0.3901795		0.3901083	0.390039	0.3897223	0.3897168	0.3894596
990 Lymphoma 0.3913551	991 Lymphoma	992 Lymphoma 0.3907416	993 Lymphoma	994 Lymphoma	995 Lymphoma 0.3901795 0.2775927	•	996 Lymphoma	997 Lymphoma	998 Lymphoma 0.3897223	999 Lymphoma	1000 Lymphoma 0.3894596 0.2773911
066	991	992	993	994	995	C C	986	266	866	666	1000

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FIG. 7D3

						EST: zp32g12.s1 Stratagene neuroepithelium (#937231) Homo
						sapiens cDNA clone 611206 3' similar to contains Alu repetitive
					RC_AA1	RC_AA1768 element; contains element THR repetitive element;, mRNA sequence.
=	Melanoma	0.9608414	Melanoma 0.9608414 0.7808739 0.650197	0.650197	0.49018195 12_at	(from Genbank)
					AA406087_s	8_7
2	Melanoma	0.7282538	2 Melanoma 0.7282538 0.7080683 0.603304	0.603304	0.45713595 at	TAL1 (SCL) interrupting locus
	and the same of th					EST: ze35e10.s1 Soares retina N2b4HR Homo sapiens cDNA clone
					RC_AA0	RC_AA0131 361002 3' similar to contains Alu repetitive element;, mRNA
~	Melanoma	0 7215478	Melanoma 0.7215478 0.6774965 0.577166	0.577166	0.4393475 60 at	sequence. (from Genbank)
2 4	Melanoma	0.7208559	Melanoma 0,7208559 0.6629334 0.566053	0.566053	1	0.42809093 U06452_at MLANA Differentiation antigen melan-A
						EST: 30g3 Human retina cDNA randomly primed sublibrary Homo
rc.	Melanoma	0.7199685	5 Melanoma 0.7199685 0.6520526 0.554953	0.554953		0.4181803 W26392_at sapiens cDNA, mRNA sequence. (from Genbank)
5						

FIG 8A

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9	6 Melanoma	0.7067817	0.6412944	0.546567	0.41028038	373003_s_at	0.41028038 S73003 s at PMEL 17 PROTEIN PRECURSOR
2	7 Melanoma	0.6579034	0.6341255	0.538004	W 0.4043727 at	W39687_s_ at	EST: zc21e08.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 322982 5', mRNA sequence. (from Genbank)
8	8 Melanoma	0.655309	0.626457	0.534069	X 0.39945245	X84707_ma 1 at	MIA gene
6	9 Melanoma	0.6420086	10	0.5285	0.3947552 X96753 at	X96753 at	Melanoma-associated chondroitin sulfate proteoglycan (MCSP)
			i			RC_AA4314	
10	10 Melanoma	0.6314878	0.616363	0.523382	0.39050817 61 at	61_at	781581 3', mRNA sequence. (from Genbank)
7	11 Melanoma	0.6251587	0.6129066	0.517861	0.38645318 U58516	U58516_at	Breast epithelial antigen BA46 mRNA
12	12 Melanoma	0.5877349	0.610369	0.515463	0.3833637 Y07759	Y07759_at	Myosin heavy chain 12
13	13 Melanoma	0.5693535	0.6066617	0.513179	0.38003224 W26130_at	W26130 at	H.sapiens mRNA for ragB protein
4	14 Melanoma	0.5553511	0.6044484	0.510592	0.3769805 50 at	RC_AA4599 50 at	EST: zx66b03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796397 3', mRNA sequence. (from Genbank)
						X96381 ma	
5	15 Melanoma	0.5455789	0.6019571	0.506174	0.37361717	1 at	Erm gene, exon 2,3,4,5 (and joined CDS)
			1		RC_AA4175 E	RC_AA4175	EST: zv04f10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
16	16 Melanoma	0,5353896	0.6005628	0.504058	0.37151223	88 at	752683 3', mRNA sequence. (from Genbank)
						Annual An	EST: HUMGS0003774, Human Gene Signature, 3'-directed cDNA
17	17 Melanoma	0.5332507	0.5986225	0.500591	0.36880952	C01811_f_at	0.36880952 C01811_f_at sequence, mRNA sequence. (from Genbank)
							EST: zc55g02.r1 Soares senescent fibroblasts NbHSF Homo sapiens
							cDNA clone 326258 5' similar to SW:INI7_HUMAN P40305
							INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN;, mRNA
8	18 Melanoma	0.5239032	0.5962527	0.498758	0.366466	0.366466 W52706_at	sequence. (from Genbank)
						,	EST: zc03c04.s1 Soares parathyroid tumor NbHPA Homo sapiens
						RC_AA0373	
19	19 Melanoma	0.517573	0.5920323	0.497302	0.3646494 57_f at	57_f_at	
						RC_AA4790	
20	20 Melanoma		0.5169516 0.5900542	0.49433	0.3626759 44_s	44_s_at	clone 740081 3', mRNA sequence. (from Genbank)
21	21 Melanoma	-	0.5163391 0.5876654	0.491902	0.3609353 D45213	D45213_at	Homo sapiens mRNA for zinc finger protein, complete cds
22	22 Melanoma	+	0.5862659	0,490266	0.3591987 D81608	D81608 at	Polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)
							EST: zr65d04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668263 3' similar to WP-F59R2 3 CF00231 N-ACFTYL-
				,		RC AA2438	
23	23 Melanoma	0.5112641	0.5849024	0.488107	0.3570082 70 at	70 at	
						RC AA4247	EST: zw04a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
24	24 Melanoma	0.5029985	0.5806069	0.487111	0.35544914	0.35544914 89_at	
25	25 Melanoma			0.485787	0.35390604 U61374	U61374_at	
26		7 70007 0	110011	0,0,0	- COLCAL TOCKOOLO		

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EST: 22c2 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)	EST: zu70d02.s1 Soares testis NHT Homo sapiens cDNA clone 743331 3', mRNA sequence. (from Genbank)	Human renal cell carcinoma antigen RAGE-1 mRNA, complete putative cds	EST: H. sapiens putatively transcribed partial sequence; UK-HGMP sequence ID AAAEBCK; single read, mRNA sequence. (from Genhank)	EST: zs83a04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704046.31 mRNA sequence (from Conhant)	EST: zh83a05.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 427856 31 mRNA sequence (from Contract)	37 kDa LIM domain profein	EST: EST57664 Infant brain Homo sapiens cDNA 3' end, mRNA sequence. (from Genhank)	EST: yw37c07.r1 Homo sapiens cDNA clone 254412 5. (from Genbank)	EST: zn77a05.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 564176 3' mRNA segment (1997)	Daa-Rinding Dratoin As 2 Alt Callan	EST: zh97f02.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429243 3' similar to contains element MER22 repetitive	element;, mRNA sequence. (from Genbank)	Growth arrest-specific 7	Semaphorin V mRNA	Cholinergic receptor, neuronal nicotinic, alpha nofvnentirle 6	DCT Dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	APOD Apolipoprotein D	EST: zb14f12.r1 Soares fetal lung NbHL19W Homo sapiens cDNA	EST: 2119f07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502405.31 mRNA seguence. (from Cont.)	CYP27 Cytochrome P450, subfamily XXVII (steroid 27-hydroxylase, cerebrotendinous xanthomatosis)
W26204 at	RC_AA4005 08_at	U46192 at	Z21384 at	RC_AA2791 68_at	RC_AA0019 08_at	X93510 at	A3502	N75618 at	213	1		A3472		at	at			19089_s_	_AA1570 at	at
0.35051897 W26204	RC_A 0.34899518 08_at	0.3473155 U46192	0.34577134 Z21384 at	0.34444538 68 at	RC_A 0.34331143 08_at	0.34189883 X93510 at	RC_A 0.3404571 68_at	0.33946347 N75618	RC_AA1 0.3382586 60 s at	HG2465- 0.3370757 HT4871 at	RC_A	0.900910	0.33475953 88 at	0.33377916 U28369	0.33276048 U62435	0.3319937 D17547 at	0.3309769 J02611 at	w 0.32997867 at	0.32907262 01	0.32787684 X59812
0.482515	0.48009	0.478928	0.477293	0.476222		0.473651	0.47225	0.471325	0.470184	0.468796	0.468016	2000	0.467047	0.465969	0.464208	0.463146	0.462186	0.461228	0.46045	0.459692
0.5777413	0.5738001	0.5734929	0.5715763	0.5678329		0.5645617	0.5643998	0.5615582	0.5597639	0.5579929	0.5578898		0.5571774	0.5569509	0.5551281	0.5538403	0.5536631	0.5530116	0.5520168	0.551138
0.492696	0.4903655	0.4883161	0.4866879	0.4803894	0.4782808	0.4765272	0.4761572	0.4743735	0.4734101	0.4712272	0.4681326		0.4675642	0.46/0562 0.5569509	0.439244	0.4587679	0.4572299	0.4567213	0.4558684	0.4514387
27 Melanoma	28 Melanoma	29 Melanoma	30 Melanoma	Melanoma	32 Melanoma	33 Melanoma	34 Melanoma	35 Melanoma	36 Melanoma	37 Melanoma	38 Melanoma		39 Melanoma	40 Melanoma	Meiailolla	42 Melanoma	43 Melanoma	44 Melanoma	45 Melanoma	46 Melanoma
27	28	29	30	31	32	33	34	35	36	37	38	0	39	7 1	F	42	43	44	45	46 1

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) mRNA,	iens cDNA		sapiens cDNA	apiens cDNA		A clone	imo sapiens	v.	1	ens cDNA	;contains	inbank)	ST containing		clone			A clone	e element ;,				\ clone		VA clone	
0.32703128 S69231 s at tvrosine-related protein 2)	RC_AA4212 Homo sapiens putative tumor suppressor protein (101F6) mRNA, complete cds	EST: zw34b09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	CIVILE 11 101 3, INKINA Sequence. (from Genbank)	EST: 217200.ST Soares plinear grand N3HPG Homo sap clone 382451 3', mRNA sequence. (from Genbank)	EST: zl29d04.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA	clone 503335 5', mRNA sequence. (from Genbank)	EST: zu06b02.s1 Soares testis NHT Homo sapiens cDNA clone 731019 3', mRNA sequence, (from Genbank)	22a6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genbank)	Homo sapiens mRNA for zinc finger protein complete cds	Homo sapiens pescadillo mRNA, complete cds	EST: za05g06.r1 Soares melanocyte 2NbHM Homo sapiens cDNA	clone 291706 5' similar to contains Alu repetitive element; contains	LI.DI LI repetitive element;, mKNA sequence. (from Genbank)	EST: EST98661 Homo sapiens cDNA 5' end similar to EST containing s_at[Alu repeat. (from Genbank)	S100 alpha protein	EST: zt66e05.s1 Soares testis NHT Homo sapiens cDNA clone	727328 3', mRNA sequence. (from Genbank)	EDNRB Endothelin receptor type B	EST: zs55a11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone	INAGE:1013/2 3' Similar to contains element L1 repetitive element mRNA segrence. (from Genhank)	/	Glycophosphatidylinositol anchor attachment 1	RAN binding protein 3	EST: zx51d03.s1 Soares testis NHT Homo sapiens cDNA clone 795749 3' similar to contains Alu renetitive element mRNA	sequence. (from Genbank)	EST: zs37c01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687360 3', mRNA sequence. (from Genbank)	
S69231 s at tv	RC_AA4212 H 68_atc	44294	Angage	at	A130284_a		_AA4212 at	क्र	584	at		02818_s_		s_at	at	A4017				_AAZO19 at	12561	_at	_AA4428 _at	E: RC_AA4603 79		A2352	
0.32703128	RC_A 0.32626364 68_at	RC_A 0 32538444 72 at	0.0200444	0.32419178 27		0.32350677 t	0.32271257 64	0.32191643 W26187	RC_AA2 0.32120335 82 s at	0.3203532 U78310		W 0 34055900 24	760006100	0.31882584 T36219	0.31818065 X58079	1	0.31/303/5 45 at	U.31060905 D13168 at		0.3159954 08		0.31534612 31	RC 0.3148285 47		0.31423962 10_at	RC_A 0.31372064 95_at	
0.458696	0.457926	0 456482		0.456439		0.455106	0.454662	0.454417	0.45371	0.452255		0.451433	0.00	0.451146	0.450399	440000	0.448929	0.448344	 	0.44784		0.447596	0.447096		0.446662	0.445747	
0.5506679	0.549091	0.5477009	200	0.5468033		0.5455118	0.5452916	0.5449394	0.5436677	0.5432443		0.5425503			0.5402542	0.004000		0.0000100		0.5380696		0.5378286	0.5371596		0.535934	0.5356467	
0.4512526	0.4491101	0.4486821	10000	0.4465975	(0.4460179	0.4442079	0.4440554	0.4438705	0.439707		0.4386779		0.4341292	0.4324835	0.4394990	0.4320263	0.4020203		0.4308492		0.4290593	0.424973	1000	0.4194453	0.4170016	
47 Melanoma	48 Melanoma	49 Melanoma		50 Melanoma		51 Melanoma	52 Melanoma	53 Melanoma	54 Melanoma	55 Melanoma		56 Melanoma		57 Melanoma	58 Melanoma	50 Melanama	60 Melanoma	WCI III		61 Melanoma		62 Melanoma	63 Melanoma		64 Melanoma	65 Melanoma	

CELL SURFACE GLYCOPROTEIN MILC18 PRECLIRSOR	PMP22 Peripheral myelin protein 22		Transcription factor AP-2 alpha (activating enhancer-binding protein 2	EST: zx99g10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 811938 5' mRNA sequence (from Canhon)	AA455860_s 811966 5' similar to WP:C05C12.3 CE02966;, mRNA sequence.	(from Genbank)	AA421370_a 731074 5' similar to contains MER17.t2 MER17 repetitive element;,	Helicase-like protein (HI P) mRNA	AA426304_r EST: zw11g07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	EST: zv92e06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	orzog o, minas sequence. (nom Genbank)	Homo sapiens HRIHFB2017 mRNA, partial cds	Homo sapiens mRNA for KIAA0890 protein complete ade	Lunatic fringe (Drosophila) homolog	EST: zr24a12.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664318 31 mRNA socional (from Carbert)	EST: zx12e02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 786266.3" mRNA sequence. (from Gorback)	EST: 2029h12.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 588359.31 mRNA sequence (from Cenhank)	EST: zr53d12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	RPS13 RNA polymerase II polymentide D (440 PD)	GBA Glucosidase, beta: acid finclindes of inconferamidace)	Homo sapiens mRNA for putative seven transmembrane domain protein	Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c
RC_D51069 f at	D11428 at	A2353	AA458761_f at	AA455001_s	AA455860_s	ច្ច	AA421370_a	\top	AA426304_r	A4183	1987_a	٦,	_AAU/01	at	_AA2325 s at	AA4518 at	_AA1523 at	A2531	to	at	94 s	A2848
0.31324902	0.31253928 D11428	0.31203723 03 at	0.3112076	0.31057757	0.000	0.01010402	0.309572221	0.30920815 U09877 at	0.3083087		0.307400E6		0.30699998 84	0.30664283 U94354	RC 0.30591923 35	0.30538633 36	0.3050198 35	0.3045229 75 at	0.3040379 X04297	0.3035176 J03060	0.3031395	RC_A 0.30270478 79_at
0.445407	0.44503	0.443933				2101410	0.440882		0.439779		0.438637	0.430037	0.438043	0.437495	0.437197	0.436371	0.435826	0.435029	0.434706	0.434226	0.433638	0.433017
0.5353056	0.5339204	0.5326095	0.5320333		0.5342002	i	0.5305765		0.5289932	1	0.5283733	- 1		0.5276282	0.5273011	0.5264503	0.5243206	0.5232914	0.523262	0.5231977	0.5231722	0.5220988
0.4167444	0.4152276	0.4130476	0.4115631	0.410688	0.400856	0000	0.4038689	0.4036421	0.4031294	0.4026932	0.401972	1	0.4010919	0.4009986	0.4001854	0.3999188	0.3971598	0.3968127	0.3963689	0.3962359	0.3955722	0.3953007
66 Melanoma	67 Melanoma	68 Melanoma	69 Melanoma	70 Melanoma	71 Melanoma		72 Melanoma	73 Melanoma	Melanoma	75 Melanoma	76 Melanoma		77 Melanoma	78 Melanoma	79 Melanoma	80 Melanoma	81 Melanoma	82 Melanoma		84 Melanoma	85 Melanoma	86 Melanoma
99	29	68	69	70	7.1		72	73	74	22	9/		11	78	79	80	81	82	83	28	85	98

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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State Control Contro								
0.392553 0.5212368 0.432374 0.301946 57_at 0.392646 0.5210271 0.431914 0.30144435 87_at 0.3925528 0.5210271 0.431914 0.30144435 87_at 0.3905529 0.5205634 0.431019 0.30089706 1 0.3908699 0.5205634 0.431019 0.30041012 65_iat 0.3908791 0.5197888 0.430382 0.29985288 707868_s at 0.3906791 0.5197097 0.429493 0.29986414 20_at 0.38062614 0.5191097 0.429493 0.2986414 20_at 0.3862614 0.5191097 0.429493 0.2986414 20_at 0.3863054 0.5191097 0.429493 0.29864418 86_at 0.3863054 0.5151219 0.428515 0.2976946 D38293 at 0.3863054 0.5151219 0.428413 0.2976946 D38294 at 0.3862614 0.513658 0.426617 0.2976946 D38294 at 0.3808508	87	7 Melanoma		1	0.432391	0.30229777	X81832_s_a l	GIPR Gastric inhibitory polypeptide receptor
0.392646 0.5210271 0.431914 0.30144435 RC_AA1797 0.3925528 0.5210066 0.431179 0.30089706 HAA488122_a 0.3912602 0.5205634 0.431019 0.30084101 65 i at 0.3908869 0.5201041 0.430854 0.29985258 Y07868_s_at 0.3906791 0.519777 0.429868 0.29984284 t CAA4238 0.3862048 0.5191097 0.429868 0.2998428 t CAA4243 0.3862049 0.5191097 0.429868 0.2998428 t CAA4243 0.3862041 0.518314 0.428891 0.2984418 Sat 0.3862044 0.518314 0.428891 0.2997299 t RC_AA4256 0.3862044 0.5144354 0.428413 0.297299 t RC_AA4266 0.3802050 0.5143108 0.42706 0.29645768 t AA036900a 0.3802500 0.5136277 0.426617 0.29645768 t AA036900a 0.3780731 0.5136277 0.426033 0.29548684 21.s at 0.3776017 0.511921	88	3 Melanoma			0.432374	0.301946	RC_AA1212 57_at	EST: zn30f10.s1 Stratagene neuroepithelium NTZRAMI 937234 Homo sapiens cDNA clone 548971 3', mRNA sequence. (from Genbank)
0.3925528 0.5210066 0.431179 0.30089706 t 0.3912602 0.5205634 0.431019 0.30041012 65 i at 0.3902869 0.5201041 0.430854 0.2998528 Y07868 s at 0.3902303 0.5197888 0.430382 0.29986288 Y07867 at 0.3900459 0.5191097 0.429868 0.2986418 Y07867 at 0.3862048 0.5191097 0.429493 0.2989236 Y07867 at 0.3862048 0.5191097 0.429453 0.2984418 PAA4243 0.3862040 0.5193771 0.429415 0.2976946 D38293 at 0.3858051 0.5151219 0.428515 0.2976946 D38293 at 0.3858051 0.5151219 0.428413 0.2976946 D38293 at 0.3858051 0.5151219 0.428413 0.2976946 D38293 at 0.3858050 0.5139538 0.426749 0.29645768 t AA036900 a 0.38008003 0.5136665 0.426617 0.29645768 t AA03690 a 0.3780731 0.5139	38	Melanoma			0.431914	0.30144435	RC_AA1797 87_at	Homo sapiens mRNA for JM26 protein, complete CDS (clone LLOXNC01U138D3 (Baylor College))
0.3912602 0.5205634 0.431019 0.30041012 RC_AA1349 0.3908869 0.5201041 0.430854 0.29985258 Y07868 s_at 0.3905791 0.5197888 0.430382 0.29985258 Y07868 s_at 0.3902303 0.5193771 0.429493 0.2996414 20_at 0.3882048 0.5190097 0.429453 0.2989236 Y07867_at 0.3862614 0.519003 0.429453 0.2984418 98_at 0.3862614 0.519003 0.429453 0.2984418 98_at 0.3862614 0.5151219 0.4286515 0.2976946 D38293_at 0.3822756 0.5151219 0.428413 0.2976946 D38293_at 0.3822756 0.5144354 0.428413 0.2976947 RC_AA2556 0.3808508 0.5139538 0.426749 0.29645768 t 0.3808508 0.5136665 0.426617 0.29645768 t 0.38065362 0.5136277 0.4266378 0.29548684 t t 0.3776017 0.511921	36) Melanoma			0.431179	0.30089706	A488122	Pyruvate dehydrogenase kinase, isoenzyme 2
0.3908869 0.5201041 0.430854 0.29985258 Y07868 s at 0.3905791 0.5197888 0.430382 0.29966414 20_at 0.3902303 0.5193771 0.429868 0.29934284 t AA004231_a 0.3802459 0.5191097 0.429453 0.2989236 Y07867_at 0.3862614 0.5191097 0.429453 0.2989236 Y07867_at 0.3858051 0.5151219 0.428515 0.2984418 98_at 0.3858051 0.5151219 0.428515 0.2976946 D138293 at 0.3858051 0.5143108 0.428413 0.2972991 37_at 0.3822756 0.5143108 0.426749 0.29684716 L43964 at 0.3822756 0.5143108 0.426749 0.29684716 L43964 at 0.3822756 0.5136655 0.426749 0.29684716 L43964 at 0.3808508 0.5136655 0.426749 0.29684716 L43964 at 0.3808508 0.5136665 0.426617 0.29684768 RC_AA4266 0.38085362 0.51	9	Melanoma	0 1		0.431019	0.30041012	1349	EST: zo23g05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587768 3', mRNA sequence. (from Genbank)
0.3905791 0.5197888 0.430382 0.29966414 RC_AA4238 0.3902303 0.5193771 0.429868 0.29934284 t 0.3800459 0.5191097 0.429493 0.29934284 t 0.3862048 0.5191097 0.429493 0.2989236 Y07867_at 0.3862049 0.5191097 0.429453 0.2989236 Y07867_at 0.3852041 0.5151219 0.428418 98_at RC_AA4243 0.3858051 0.5151219 0.428515 0.2976946 D38293_at 0.3858051 0.5144354 0.428413 0.2976946 D38293_at 0.3822756 0.5144354 0.426749 0.29645768 t AA036900_a 0.3808508 0.5136535 0.426617 0.29645768 t RC_AA4266 0.3805362 0.5136277 0.426378 0.29548684 21 s at RC_AA4266 0.3780731 0.513986 0.426033 0.29548684 21 s at RC_AA4266 0.3776017 0.511921 0.4241956 t RC_AA4266 0.375896 0.511921	92	Melanoma	0.3908869		0.430854	0.29985258	Y07868 s at	Pirin
0.3902303 0.5193771 0.429868 0.29934284 t 0.39002303 0.5193771 0.429493 0.29934284 t 0.3800459 0.5191097 0.429493 0.2989236 Y07867 at 0.3862614 0.519003 0.429153 0.2984418 98 at 0.3858051 0.5151219 0.428891 0.2980733 86 at 0.3858051 0.5151219 0.428515 0.2976946 D38293 at 0.3852056 0.5144354 0.428413 0.2976946 D38293 at 0.3822756 0.5143108 0.42706 0.29684716 L43964 at 0.3808508 0.5139538 0.426749 0.29645768 t CAA42370 0.3808508 0.5136277 0.426617 0.29645768 t CAA4266 0.3805362 0.5136277 0.426378 0.29548684 21 s at 0.3780731 0.513928 0.426033 0.29548684 21 s at 0.375896 0.5117921 0.424411 0.29441956 t	93	Melanoma	0.3905791	0.5197888	0.430382	0.29966414	A4238	EST: zv33f03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755453 3', mRNA sequence. (from Genbank)
0.38020459 0.5191097 0.429493 0.2989236 Y07867_at 0.3882048 0.519003 0.429153 0.2984418 98_at 0.3862614 0.5188314 0.428891 0.2980733 86_at 0.3858051 0.5151219 0.428515 0.2976946 D38293_at 0.38580541 0.5144354 0.428413 0.2976946 D38293_at 0.3822756 0.51443108 0.42706 0.29684716 L43964_at 0.3808508 0.5139538 0.426749 0.29645768 t 0.3808500 0.5136565 0.426617 0.29645768 t 0.38085362 0.5136277 0.426378 0.29548684 21_s_at 0.3780731 0.5136277 0.426033 0.29512414 53_at 0.3775896 0.511921 0.424411 0.29473567 MA004333_a 0.3769374 0.511928 0.29441956 t AA004333_a	94	Melanoma	0.3902303		0.429868		AA004231_a	
0.3862048 0.519003 0.429153 0.2984418 PRC_AA4243 0.3862614 0.5188314 0.428891 0.2980733 RC_AA2837 0.3858051 0.5151219 0.428515 0.2976946 D38293 at 0.3852054 0.5144354 0.428413 0.2976946 D38293 at 0.3822756 0.5144364 0.42706 0.2972991 37 at 0.3808508 0.5139538 0.426749 0.29645768 t 0.3808508 0.5136585 0.426617 0.29645768 t 0.3808508 0.5136277 0.426378 0.29548684 t 0.3780731 0.5136277 0.426033 0.29548684 21.5 at 0.3776017 0.511921 0.425021 0.29473567 MA004333_a 0.3769374 0.511921 0.424289 0.29441956 t	95	Melanoma	0.3900459		0.429493	0.2989236	Y07867 at	Pirin, isolate 1
0.3862614 0.5188314 0.428891 0.2980733 0.3858051 0.5151219 0.428515 0.2976946 0.3832441 0.5144354 0.428413 0.2972991 0.3822756 0.5143108 0.42706 0.29684716 0.3808508 0.5136585 0.426617 0.29645768 0.3805362 0.5136277 0.426617 0.29548684 0.3776017 0.513928 0.426033 0.295473567 0.3775896 0.514921 0.425021 0.29473567 0.3775836 0.5117986 0.424289 0.29400867	96	Melanoma	0.3882048	0.519003	0.429153	0.2984418	RC_AA4243 38_at	EST: zv82e01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 760152 3', mRNA sequence. (from Genbank)
0.3858051 0.5151219 0.428515 0.2976946 0.3832441 0.5144354 0.428413 0.2972991 0.3808508 0.5139538 0.426749 0.29645768 0.3808003 0.5136665 0.426617 0.29645768 0.3805362 0.5136277 0.426617 0.29548684 0.3776017 0.513921 0.426033 0.29547367 0.3775896 0.511921 0.424411 0.29441956 0.3769374 0.5117986 0.424289 0.29400867	16	Melanoma	0.3862614		0.428891	0.2980733	A2837	EST: zt18f01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713497.3' mRNA sequence (from Genhank)
0.3832441 0.5144354 0.428413 0.2972991 0.3822756 0.5143108 0.42706 0.29684716 0.3808508 0.5139538 0.426749 0.29645768 0.3808003 0.5136665 0.426617 0.29601356 0.3805362 0.5136277 0.426378 0.29548684 0.3780731 0.513986 0.426033 0.29512414 0.3775896 0.511921 0.425021 0.29473567 0.3769374 0.5117986 0.424289 0.29400867	86	Melanoma	0.3858051	0.5151219	0.428515	0.2976946		Clathrin-like protein
0.3822756 0.5143108 0.42706 0.29684716 0.3808508 0.5139538 0.426749 0.29645768 0.3808003 0.5136665 0.426617 0.29601356 0.3805362 0.5136277 0.426378 0.29548684 0.3780731 0.513986 0.426033 0.29512414 0.3775896 0.511921 0.425021 0.29473567 0.3769374 0.511986 0.424289 0.29400867	66	Melanoma	0.3832441	0.5144354	0.428413	0.2972991	A4256	Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6
0.3808508 0.5139538 0.426749 0.29645768 0.3808003 0.5136665 0.426617 0.29601356 0.3805362 0.5136277 0.426378 0.29548684 0.3776017 0.513986 0.426033 0.29512414 0.3775896 0.511921 0.425021 0.29473567 0.3769374 0.5117986 0.424289 0.29400867	100	Melanoma	0.3822756	1	0.42706	0.29684716	.43964 at	PSEN2 Presenilin 2 (Alzheimer disease 4)
0.3808003 0.5136665 0.426617 0.29601356 0.3805362 0.5136277 0.426378 0.29548684 0.3780731 0.5133986 0.426033 0.29512414 0.3775896 0.511921 0.424411 0.29473567 0.3769374 0.5117986 0.424289 0.29400867	101	Melanoma	0.3808508	0.5139538	0.426749	0.29645768	\A036900_a	EST: zk29e11.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471980 5', mRNA sequence. (from Genbank)
0.3805362 0.5136277 0.426378 0.29548684 0.3780731 0.513986 0.426033 0.29512414 0.3775017 0.511921 0.425021 0.29473567 0.3775896 0.511921 0.424411 0.29441956 0.3769374 0.5117986 0.424289 0.29400867	102	Melanoma	0.3808003		0.426617	0.29601356	RC_AA2370 37_at	Transmembrane 7 superfamily member 1 (upregulated in kidney)
0.3780731 0.5133986 0.426033 0.29512414 0.3776017 0.511921 0.425021 0.29473567 0.3775896 0.511921 0.424411 0.29441956 0.3769374 0.5117986 0.424289 0.29400867	103	Melanoma	0.3805362		0.426378	0.29548684	A4017 at	EST: zt66c01.s1 Soares testis NHT Homo sapiens cDNA clone 727296 3', mRNA sequence. (from Genbank)
0.3776017 0.511921 0.425021 0.29473567 0.3775896 0.511921 0.424411 0.29441956 0.3769374 0.5117986 0.424289 0.29400867	104	Melanoma	0.3780731	0.5133986	0.426033	0.29512414	A4266	EST: zv47h02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756819 3', mRNA sequence. (from Genbank)
0.3775896 0.511921 0.424411 0.29441956 0.3769374 0.5117986 0.424289 0.29400867	105	Melanoma	0.3776017	0.511921	0.425021	0.29473567	ä	CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR
0.3769374 0.5117986 0.424289 0.29400867 L76687 at-2	106	Melanoma	0.3775896	0.511921	0.424411	0.29441956	\A004333_a	EST: zh91a01.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 428616 5', mRNA sequence (from Genhank)
	107	Melanoma	0.3769374	0.5117986	0.424289	0.29400867	.76687_at-2	Growth factor receptor-bound protein 14

The state of the s

108 Melanoma	0.3769374	0.5117167	0.424075	0.29359615 L76687	at IGrh14 mRNA
	0.3753549	0.5109736	0.423988	0.2933038 GMCSF at	
	0.3750506	0.5108213	0.42332	RC_AA0105 0.29296982 30_at	Human BAC clone GS025M02 fro
	0.3748601	0.5107618	0.422989	RC_AA4814	-
	0.3745289		0.422672	RC_AA2838	
	0101		0.424.0	0.23222321 46_at	Clone (1362/ 3', mRNA sequence. (from Genbank) SMPD1 Sphingomyelin phosphodiesterase 1. acid lysosomal (acid
	0.374063	0.5100325	0.42237	0.2918496 M59916_at	
	0.3723273	0.5100312	0 421678	RC_AA5997 0 29150435 64 at	
	0.3722669	ŧ	0.424400	RC_AA4300	
		ļ	2	RC AA4032	32 EST: zt44c06.s1 Soares ovary fumor NbHOT Home canions child
	0.3718415	0.5097877	0.42089	0.29059976 96_at	
	71,000			AA002245	a.
- 1	0.37/16345	7	0.420311		KIAA0663 gene product
	0.3/13444	,	0.420057	0.28997773 D88667	
1	0.3/0407	0.5074483	0.419427	0.28977737 R74226 at	
	0.3677971	0.507306	0.419076	RC_AA2274 0.28926557 48 at	
				RC_AA0858	-
	0.36/0363		0.418741	0.2889833 51_at	Homo sapiens clone 24658 mRNA sequence
	0.3650442	0.5068746	0.418516	0.2885621 X99920	at S100 calcium-binding protein A13
	0.3642675	0.505545	0.418327	0.28820908 U87593_f_at	at Endogenous retrovirus clone P1.8 polymerase mRNA, partial cds
					EST: zr75d02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
	-			CC / < CD	
	0.3638577	0.5047969	0.417886	0.28795332 81 at	54 group glycoprotein (HUMAN);contains Alu repetitive element;, mRNA
	0.3634589	I	0.417541		
	0.3617002	0.5039112	0.417234	RC_AA4185 0.287278145 at	10
1	0.3602343 0.5038836	0.5038836	0.417061	2529	at APOE Apolipoprofein E
-	0.3602291	0.5033534	0.416498	0.28666443 Z48804 at	
_	0.3588951	0.5017493	0.416196	0.28645402 t	
	0 2 5 7 7 4 40	0.00		RC_AA4775	
	0.35/7/49	0.501243	0.415909	0.2860714 61_at	clone 740589 3', mRNA sequence. (from Genbank)

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Dual specific protein phosphatase mRNA	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genbank)	EST: zl76c05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510536 31, mRNA sequence (from Genbank)	EST: zr56c12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667414 3', mRNA sequence, (from Genhank)	AA248169_a EST: csg1676.seq.F Human fetal heart, Lambda ZAP Express Homo	sapiens cDNA 5', mRNA sequence. (from Genbank)	S-100 PROTEIN, BETA CHAIN	0.2837967 M59488_at-2 S-100 PROTEIN, BETA CHAIN	Neuropilin 2	EST: zt79c09.s1 Soares testis NHT Homo sapiens cDNA clone	EST: zu44c08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740846 3, mRNA sequence (from Genhank)	. KIAA0475 gene product	EST: zo36a01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 588936 3' similar to SW:YBF7 YEAST P34222	HYPOTHETICAL 23.1 KD PROTEIN IN SHP1-SEC17 INTERGENIC REGION.: mRNA seguence (from Genhank)	EST: zw04b04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	Leukemia virus receptor 1 (GLVR1) mRNA	EST: zl29g04.s1 Soares pregnant uterus NbHPU Homo sapiens	CDNA clone 503382 3' similar to TR:G971709 G971709 LEUCINE AMINOPEPTIDASE : mRNA secilence (from Genhank)	NMB Neuromedin B	EST: zt44f05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	EST: zu05e01.s1 Soares testis NHT Homo sapiens cDNA clone	730968 3', mRNA sequence. (from Genbank)	EST: zs41g07,s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687804 3', mRNA sequence. (from Genbank)
1	0.28546867 D31417_at	A0558	279	AA248169_a	to		M59488_at-2	RC_AA4183 98_at	A4211	A4774	A4192			A4248	9 at		-AAI341 at	T	033	165	at_	A2359
0.28580204 U48807 at	0.28546867	RC_A 0.28526393 09 at	RC_AA2 0.2849233 41_s at	0.0045005	0.26436851	0.28407452 M59488 at	0.2837967	RC_A 0.28338763 98_at	RC_A 0.28307116 39 at	0.28286344 59 at	RC_A 0.28236294 00_at		0.2820291	RC A 0.28174967 13 at	0.2815182 1.20859		0.28123853 38	0.28104937 X76534 at	0 28088385 12 s at		0.28067264 51	RC_A 0.2803573 85_at
0.415416	0.415047	0.414921		70444307	0.414116	0.413774	0.413299	0.412741	0.412448	0.411969	0.411221	~	0.41108	0.410814	0.410676		0.410484	0.410433	0.41037		0.410142	0.409975
0.35631 0.5008451	0.5005862	0.5003932	0.5000116	0.499754	10	1 1	0.4980723	0.4979875	0.4978204	0.4976554	0.4966058		0.49639	0.4961314	1 !		0.4952997	0.4938434	0.4937563	00007	0.4932703	0.333278 0.4931972
0.35631	0.355712	0.3543488	0.3535736	0.3522672	0.3519219	0.3471006	0.3471006	0.3456042	0.3434531	0.3433566	0.3413		0.3411124	0.3408222	0.3405738			0.3355292	0.3353969		0.3341294	0.333278
131 Melanoma	132 Melanoma	133 Melanoma	134 Melanoma	135 Melanoma	136 Melanoma	137 Melanoma	138 Melanoma	139 Melanoma	140 Melanoma	141 Melanoma	142 Melanoma		143 Melanoma	144 Melanoma	145 Melanoma		-	147 Melanoma	148 Melanoma	140 Majoriogas	-	150 Melanoma
131	132	133	134	135	136	137	138	139	140	141	142		143	144	145	-	146	14/1	148	770	243	150

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

	The state of the s	No. of Concession, Name of Street, or other Persons and Street, or other P					
							EST: ym61b06.r1 Homo sapiens cDNA clone 52750 5' similar to
151	151 Melanoma	0.3317794	0.4931915	0 4097	0.28017464 H29683 at	429683 at	contains Alu repetitive element;contains KER repetitive element ;. (from Genhank)
						AA303745 s	
152	Melanoma	0.3313957	0.4927765	0.409468	0.27992666	_at	TAP binding protein (tapasin)
153	153 Melanoma	0.3313865	0.4919635	0.408626	RC_A 0.2795612 29_at	A1603	EST: zo56d04.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 590887 3', mRNA sequence, (from Genbank)
72	154 Melanoma	0.3308183	0.49153	0.408344	X: 0.27936518	X94628_ma 1 s at	MeCP-2 gene
155	Melanoma	155 Melanoma 0.3296454	0.4911068	0.40788	RC_A 0.2790183 40_at	A4187	EST: zv98e10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 767850 3', mRNA sequence. (from Genbank)
56	156 Melanoma	0.3287473	0.490314	0.40767	RC_AA4 0.2788566 83_s_at	RC_AA4565 83_s_at	Human PL6 protein (PL6) mRNA, complete cds
57	157 Melanoma	0.3276548	0,4897965	0.407292	0.27859926	RC_AA2365 16 at	33 kDa transcrintional co-activator
28	158 Melanoma		0.4895437	0.406972	1	x97230 f at	f at NK receptor, clone library 4M1#6
29	159 Melanoma	0.3266627	0.4894057	0.406562	0.2779128 U65092	at	Melanocyte-specific gene 1 (msq1) mRNA
99	160 Melanoma	0.3243132	0.4892736	0.406346	0.27751556 H21601 at		EST: yl33e08.r1 Homo sapiens cDNA clone 160070 5'. (from Genbank)
61	161 Melanoma	0.3239197	0.4891115	0.405955	. RC_A 0.27727428 75 at	A5989	EST: ae40c09.s1 Gessler Wilms tumor Homo sapiens cDNA clone 898288 3', mRNA sequence, (from Genbank)
62	162 Melanoma	0.3231382	0.48899	0.405499	0.2771026 M58297	at	ZNF42 Zinc finger protein 42 (myeloid-specific retinoic acid-responsive)
63	163 Melanoma	0.3230813	0.4888969	0.405458	RC_A 0.27676967 43_at	A2788	EST: zs80h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703831 3', mRNA sequence. (from Genbank)
64	164 Melanoma	0.3228191	0.4886015	0.405084	0.27630618	N89563_s_a t	EST: HFBEST-40 Human fetal brain QBoqin2 Homo sapiens cDNA, mRNA sequence. (from Genbank)
65	165 Melanoma	0.3225167	0.4875982	0.404974	0.2760943 X13589 at		CYP19 Cytochrome P450, subfamily XIX (aromatization of androgens)
166	Melanoma	0.3222618	0.487021	0.404547	0.27590296 00 at	A4783	CD39-like 2
27	167 Melanoma	0.3220997	0.4865582	0.404442	0.27572575 t	U19147_s_a t	GAGE4 G antigen 6 (GAGE-6)
88	168 Melanoma	0.3219174	0.4859242	0.404396	0.2753855 L03411	1	s_at RD Radin blood group
69	169 Melanoma	0.3211143	0.4854832	0.403627	0.27515632	4A477018_s at	AA477018_s EST: zu38a10.r1 Soares ovary tumor NbHOT Homo sapiens cDNA_at clone 740250 5', mRNA sequence. (from Genbank)
2	170 Melanoma	0.3204015	0.4851222	0.403513	0.27489066 1	177348_ma s_at	Pmel 17 mRNA

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Docket No.: 2	825.2020-002
Title: Genetic I	Markers for Tumors
Inventors: Sridha	ar Ramaswamy, et al.

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171 Melanoma	noma	0.3162881	0.4847945	0.403227	RC_A 0.27461043 03 at	RC_AA1521 03_at	Human Chromosome 16 BAC clone CIT987SK-A-735G6
172 Melanoma	noma	0.3161022		0.402744	0.27437636 X51420	X51420 at	TYRP1 Tyrosinase-related protein 1
						RC_AA6204	
173 Melanoma	noma				0.27414286 46_at	46_at	RecQ protein-like 4
174 Melanoma	noma	0.3158313	0.4843504	0.402373	0.27379596 M68520 at	M68520 at	CDK2 Cyclin-dependent kinase 2
175 Melanoma	noma	0.3154054	0.4843456	0.40202	0.27357447 U65011	U65011_at	Preferentially expressed antigen of melanoma (PRAME) mRNA
176 Melanoma	Canon	0.2427070			000000000000000000000000000000000000000		EST: yi04d08.r1 Homo sapiens cDNA clone 138255 5' similar to
I O Meia	Ollia	0.0101818	0.4042212	0.401845	0.2/320093 R566/8 at	H566/8 at	contains Alu repetitive element; (from Genbank)
177 Melanoma	noma	0.3136749	0.48422	0.401509	0.27283943 60 r at	30 r at	clone 377595.3" mRNA segrence (from Genhank)
178 Melanoma	noma	0.3130738	0.4840654	0.404045	N 22000000	M17446_s_a	
		0,00		0.40104.0	1 16020212.0	7000	protein 1, Kaposi sarcoma oncogene)
179 Melanoma	noma	0.3125835	0.4836405	0.400938	0.27246743 56	7C_AA4020 56_at	EST: Zu49e05.ST Soares ovary tumor NbHOT Homo sapiens cDNA clone 741346 3', mRNA sequence, (from Genbank)
						RC_AA4014	EST: zu56e12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
180 Melanoma	noma	0.3121697	0.4835044	0.4007	0.2721903 52_at	52_at	
181 Melanoma	пота	0.3119107	0.4832527	0.4007	RC 0.2720382 57	RC_AA4610 57_at	Nuclear localization signal deleted in velocardiofacial syndrome
182 Melanoma		0.3114898	0.4824477	0.400583	RC_AA 0.27179894 41 f at	RC_AA4238 41 f at	Homo saniens clone 23856 unknown mRNA nartial cds
183 Melanoma		0.3114713	0.4821109	0.400356	0.27151352 N36588 at	V36588 at	Ubiquitin-conjugating enzyme E2I (homologous to veast 1,18C9)
184 Melanoma	пота	0.3112968	0.4813416	0.400297	0.271249651	∿A293400_a	AA293400_a EST: zt53e06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
						RC_AA2531	EST: zr53e08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
185 Melanoma	-	0.3109159		0.399981	0.27097747 79	79 at	667142 3', mRNA sequence. (from Genbank)
186 Melanoma	-	0.3106763	0.4807326	0.399862	0.27065808 D31120	031120_at	Clathrin adaptor complex 1, sigma 1B subunit
187 Melanoma		0.3088199	0.4806334	0.39943	0.27043283 R13638	313638 at	FST: vf60d01 r1 Home canians cDNA clone 28852 5' (from Genhaut)
188 Melanoma	-	0.3087396	0.4803071	0.399364	0.27012375 Y12065		Homo sapiens mRNA for nucleolar profein hNon58
189 Melanoma		0.308367	0.4802392	0.398812	0.26989028 U18009	J18009 at	Chromosome 17a21 mRNA clone I F113
190 Melanoma		0.3083558	0.4802286	0.398628	0.2695829 U40380 at	J40380 at	PSEN1 Presenilin 1 (Alzheimer disease 3)
191 Melanoma	-	0.3079231	0.4800832	0.398436	RC_A 0.26937652 18_at	A2794	EST: zs85d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704269 3', mRNA sequence. (from Genbank)
192 Melanoma	-	0.3076862	0.4788971	0.398112	0.26913765 X04143	(04143 at	BGLAP Bone gamma-carboxyglutamate (qla) protein (osteocalcin)
193 Melanoma	-	0.3076298	0.4788971	0.397967	0.26890305 X72304	<72304_at	CORTICOTROPIN RELEASING FACTOR RECEPTOR 1 PRECURSOR
194 Melanoma	-	0.3063073	0.4778435	0.397748	HG3991- 0.26872072 HT4261_at		Cpg-Enriched Dna, Clone E18

196 Me					0.500.00		יייייייייייייייייייייייייייייייייייייי
	Melanoma	0.3059957	0.4773791	0.397181	0.26794228 M84349	at	CD59 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, EL32 and G344)
							Human DNA sequence from clone 149A16 on chromosome 22q12-13. Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene, the RFPL3 and RFPL3S genes for Ret finger protein-like 3 and sepectively, a gene for a novel Immunoblobulin Lambda Chain V family protein, a novel gene for a protein similar to mouse RGDS (RALGDS, RALGEF, Guanine Nucleotide Dissociation Stimulator A) and rabbit oncogene RSC, a novel gene for the human ortholog of worm F16A11.2 and bacterial and archea-bacterial predicted proteins, a novel gene for a protein
197 Me	197 Melanoma	0.30579	0.4772935	0.396782	RC	_AA1518	similar to BPI (Bacterial Permeability-Increasing Protein) and rabbit LBP (Liposaccharide-Binding Protein), and a the 5' part of a novel gene. Contains ESTs, STSs, GSSs, genomic marker D22S1175, a ca
198 Mei	198 Melanoma	0.303889	1	0.396745	0.26755148 25 s at	AA4279 s at	EST: zw50e01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773496 3' mRNA sequence (from Genhank)
199 Mel	199 Melanoma	0.3037446	0.4769441	0.396347	0.26733598 t	\A449637_a	AA449637_a EST: zx08f09.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA tolone 785897 5', mRNA sequence. (from Genbank)
200 Mei	200 Melanoma	0.3023086	0.4766648	0.396134	0.2670427 N98660_at		EST: yy66c03.r1 Homo sapiens cDNA clone 278500 5'. (from Genbank)
201 Me.	201 Melanoma	0.3021154	0.3021154 0.4764675	0.396087	0.26681006 U18934_at RC_AA431		TYRO3 Receptor protein-tyrosine kinase sky EST: zw70g08.s1 Soares testis NHT Homo sapiens cDNA clone
203 Mel	203 Melanoma	0.3017628	1 1	0.395466	0.2662759 31 at		/81598 3', mRNA sequence. (from Genbank) EST: ae32h12.s1 Gessler Wilms tumor Homo sapiens cDNA clone 897575 3', mRNA sequence. (from Genbank)
204 Mel	204 Melanoma	0.3012943	0.4754742	0.395235	0.2659247 t	!	Dopamine D2 receptor, mRNA
205 Mel	205 Melanoma	0.3006956	0.4754098	0.394916	U.26565087 t	U19145_s_a t	Gantigen 4
206 Melanoma	lanoma	0.3002045	0.4754098	0.394844	RC 0.2654657 57	AA0354 at	EST: zk27h06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471803 3', mRNA sequence. (from Genhank)
207 Melanoma	anoma	0.2998828	0.4746822	0.394738	0.26525465 t	A009913_a	AA009913_a Diptheria toxin resistance protein required for diphthamide to biosynthesis (Saccharomyces)-like 2
208 Melanoma 209 Melanoma		0.2998321	0.2998321 0.4742857 0.2996786 0.4739449	0.394552	RC_AA1 0.26504958 95_at 0.26484486 U33822	350 at	Homo sapiens Sox-like transcriptional factor mRNA, complete cds Tax1-binding protein TXBP181 mRNA

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PLOD Lysyl hydroxylase	MGP Matrix protein gla	EST: zu38d11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740277 3', mRNA segience (from Genhank)	EST: zs30h07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone		sequence. (from Genbank)	EST: ab15c03.r1 Stratagene lung (#937210) Homo sapiens cDNA clone 840868 51 mRNA seguence (from Genhank)	EST: af15d11.s1 Soares testis NHT Homo sapiens cDNA clone	CARS Cysteinyl-tRNA synthetase	Zinc finger protein 42 (myeloid-specific refinalic acid- responsive)	EST: zv62f11.s1 Soares testis NHT Homo sapiens cDNA clone	CATHEPSIN K PRECURSOR	Zm85a05.r1 Stratagene ovarian cancer (#937219) Homo sapiens	AA074897 a ANDROGEN-REGILI ATED PROTEIN DRECTIDSOD: "DNA	sequence. (from Genbank)	EST: zs48e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	Doc2 beta	Homo sapiens mRNA expressed in placenta	Fertilin befa mRNA	RC_AA4965 EST: zv38h01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	EST: ze74d01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	EST: zr54e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	LAMA4 Laminin alpha 4	EST: zs36c07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687276 3', mRNA sequence. (from Genhank)	Serine Protease Met1
L06419_at	0.2644364 X53331 at	RC_AA4769 37 s at	RC_AA2590 0.2639375 62 at	AA295819_s	at	AA482319_f at	RC_AA6095	L06845 at	W31698 at	RC_AA4373 23 at	X82153 at		AA074897 a		_AA2851 at	D70830 at	D81308_s_a t	X99374_s_a t	RC_AA4965	RC_AA0252	A2362		ω	
0.26459083 L06419_at	0.2644364	0.2641502	0.2639375 62	or oct coo	0.263/29/8	0.26352856	RC_A	0.26305094 L06845 at	0.26281342 W31698 at	RC 0.26260287 23	0.26240373 X82153 at			0.26232177 t	RC 0.26217356 62	0.2619341 D70830	0.26165384 t	0.26133451	0.26118717 69	RC A	0.26085648 75 at	0.26062638 S78569 at	RC_A 0.26041773 99_at	HG3104- 0.26013744 HT3280_at
0	0.39329	0.393024	0.392945		0.392807	0.392563	0.39223	0.39188	0.391524	0.391505	0.391455			0.391322	0.391205	0.391133	0.390977	0.39075	0.390451	0.390328	0.389878	0.389578	0.389368	0.389188
0.4736541	0.4731139	0.4728627	0.4726846	AAAACTA ()	- 1	0.472102	0.4720918	1	0.4717935	0.4717935	0.471613			0.471531	0,4715292	0.4713063	0.4704381	0.4703044	0.4702158	0.4697903	0.4693813	0.4693238	0.4693238	0.4683735
-	0.2973461	0.2971224	0.296005	0.2957572		0.2953342	0.2944885	0.2933273	0.2927195	0.2920193	0.2915961	_		0.2912415	0.2911212	0.2901944	0.2896082	0.2889461	0.2887219	0.2885264	0.2877094	0.2874858	0.2872049	0.2871278
210 Melanoma	211 Melanoma	212 Melanoma	213 Melanoma	214 Melanoma	מווסווומ	215 Melanoma	216 Melanoma	217 Melanoma	218 Melanoma	219 Melanoma	220 Melanoma			221 Melanoma	222 Melanoma	223 Melanoma	224 Melanoma	225 Melanoma	226 Melanoma	227 Melanoma	228 Melanoma	229 Melanoma	230 Melanoma	231 Melanoma
210	211	212	213	214	1	215	216	217	218	219	220			221	222	223	224	225	226	227	228	229	230	231

Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

-						AA459542 s	
32	232 Melanoma		- 1			_at	Regulatory factor X-associated ankyrin-containing protein
<u></u>	233 Melanoma	0.2866696	0.4683651	0.388669	0.25963005 D50550_at	D50550_at	LLGL mRNA
2	234 Melanoma	0.2853845	0.4681579	0.388501	0.25937495 _t	AA147543_a t	Immunoglobulin superfamily, member 3
							Human DNA sequence from clone 149A16 on chromosome 22q12-13. Contains an IGLC (Immunoglobulin Lambda Chain C) pseudogene, the RFPL3 and RFPL3S genes for Ret finger protein-like 3 and sepectively, a gene for a novel Immunoblobulin Lambda Chain V family protein, a novel gene for a protein similar to mouse RGDS (RALGDS, RALGEF, Guanine Nucleotide Dissociation Stimulator A) and rabbit oncogene RSC, a novel gene for the human ortholog of worm F16A112 and hardarial
≥	235 Melanoma	0.285368	0.4680657	0.388011	W 0.25924543 at	W26116_s_ at	and archea-bacterial predicted proteins, a novel gene for a protein similar to BPI (Bacterial Permeability-Increasing Protein) and rabbit LBP (Liposaccharide-Binding Protein), and a the 5' part of a novel gene. Contains ESTs, STSs, GSSs, genomic marker D22S1175, a carebeat polymorphism and putative CoG is lander.
≥ 9	236 Melanoma	0.2853295	0.467448	0.387737	0.25899255 02 at	A4478	EST: aa20h07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 813853.3' mRNA sequence (from Genhank)
237 M	Melanoma	0.2845084	0.4671087	0.387638	0.25880787	A0318	EST: 2k17g04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470838 3', mRNA sequence, (from Genhank)
<u>≥</u>	238 Melanoma	0.2840831	0.4669968	0.387605	0.2586726 t	AA306479_a t	AA306479_a EST: EST177452 Jurkat T-cells VI Homo sapiens cDNA 5' end, t mRNA sequence. (from Genbank)
- 6	239 Melanoma	0.2838782	0.4667283	0.3876	0.25841814	U80987_s_a t	Transcription factor TBX5 mRNA
- ≤	240 Melanoma	0.2821052	0.4665916	0.387166	0.25813666	AA455318_a t	AA455318_a EST: aa30b07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t [MAGE:814741 5', mRNA sequence, (from Genbank)
<u>\S</u>	241 Melanoma	0.281963	0.4660838	0.387008	RC_AA4 0.2579898 13_i_at	1005	H.sapiens mRNA for GAR22 protein
_∑	242 Melanoma	0.28163	0.466047	0.38668	0.25776437	AA442274_a	AA442274_a EST: zv54a06.r1 Soares testis NHT Homo sapiens cDNA clone t 757426 5', mRNA sequence. (from Genhank)
<u>Z</u>	243 Melanoma	0.2813524	0.4659845	0.386425	HG4518- 0.25757813 HT4921_at		Transcription Factor Btf3 Homolog (Gb:Mg0355)
_ ≥ ;	244 Melanoma	0.2810766		0.386154	0.25744718 M21388_at		Unproductively rearranged lg mu-chain mRNA V-region (VD), 5' end, clone mu-3A1A
≥	245 Melanoma	0.2805463	0.4653033	0.385898	0.25730935 M60502 at	100	Filaggrin
Ξ	246 Melanoma	0.2797754	0.4651707	0.385693	0.25711423 83_at	200	1069961 3', mRNA sequence. (from Genbank)

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247	247 Melanoma	0.2797386	0.4651313	0.385388	0.25697386 76 at	A4178	EST: zv05f04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 752767 3', mRNA sequence. (from Genbank)
248	Melanoma	0.2792157	0.4649149	0.385264	A 0.0567836+	A027760_a	
2	Melanon	+-		0.00004	0.2301020	DO AAARR	Intrivia sequence, (non centralia)
249	Melanoma	0.2789914	0.4647157	0.385119	0.25657552 88	88 at	Homo sapiens BC-2 protein mRNA complete cds
			1				
250	250 Melanoma	0.2788058	0.4643362	0.385085	0.25627553 t		TYRP1 Tyrosinase-related protein 1
251	051 Melanoma	9090826.0	79677967	7007000	2001.00	AA071223_a	
27.0	Melanona		۱-	0.304021	76010070		clone 383179 5, mKNA sequence. (from Genbank)
727	252 Melanoma	0.2779724	0.464198	0.38462	0.25578913 X69090	at Jat	Skeletal muscle 190kD protein
, F	1			9		158761_i	Transcription factor AP-2 alpha (activating enhancer-binding protein 2
253	253 Melanoma	0.277904	0	0.384506	0.2555034		alpha)
254	254 Melanoma	0.277324	0.464048	0.384222	0.25534534 U24153_at	U24153_at	P21-activated protein kinase (Pak2) gene
255	255 Melanoma	0.9768664	0.4836004	0 384082	RC_A	RC_AA4344	Trained (Date and the Control of the
2		1000017	- 1	7001000	0.2020200	ווייין מו	LITZIEU (DIOSOPIIIIA) HOHIOUG /
ŗ		01010		0	1		
220	Zoo Melanoma	0.2767919		0.383869	0.25498685 HT415	HT415_at	Lectin, Galactoside-Binding, Soluble, 2
25/	25/ Melanoma	0.2767766	0.4628518	0.383559	0.25480798 X78712	at	GKP2 Glycerol kinase 2 (testis specific)
5	-					A0293	EST: zk12d10.s1 Soares pregnant uterus NbHPU Homo sapiens
228	258 Melanoma	0.2766601	0.4626747	0.383334	0.2546019 56_at	56_at	cDNA clone 470323 3', mRNA sequence. (from Genbank)
i i	-	1				RC_AA1310	
259	259 Melanoma	0.276047	- 1	0.383275	0.25424954 84_at	84_at	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3
760	260 Melanoma	0.2750642	0.4625938	0.383256	0.25412503 X57206_at		ITPKB Inositol 1,4,5-trisphosphate 3-kinase B
0						A4647	EST: zx86b07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
261	261 Melanoma	0.2745334	- 1	0.383076	0.2539976 41_at	41_at	clone 810613 3', mRNA sequence. (from Genbank)
262	262 Melanoma	0.2743796	0.4622538	0.382908	0.25381115 D10704	D10704_at	CHK Choline kinase
						B002303_a	
263	263 Melanoma	0.2741447	0.4618519	0.382901	0.25366384 t		KIAA0305 gene product
							NRAMP1 Natural resistance-associated macrophage protein 1 (might
264	264 Melanoma	0.2741037	0.4617618	0.382635	0.25348043 D50402_at		include Leishmaniasis)
265	265 Melanoma	0.2733528	0.4617061	0.382284	RC	RC_AA4355	Lomo gonione observation 10 goomid E000E0
			- 1	0.005201	0.5000000	מר מון	TOTION SAPIETS CHICHIOSOUTHE 13, COSHIIC F23030
266	Melanoma	0.273051	0.4612471	0.382142	NC_A 0.25315657 37_at	AZ360	EST: zs05g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684350 3', mRNA sequence. (from Genbank)
				***************************************		AA036794 a	EST: zk29a01.r1 Soares pregnant uterus NbHPU Homo sapiens
267	267 Melanoma	0.2724566	0.4606605	0.382086	0.25293934 t	1	sequence. (from Genbank)
268	268 Melanoma	0.2721901	0.4605867	0.38208	X 0.2527135311	62654_ma at	ME491 gene extracted from H sanions gone for Mo4047CD63 antigen
							מיום פסיום כאוומים אינו וויפתאומיום אפוופ וסו אופלפ וויסוסים מוויאפנון

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269	Melanoma	0.2721322	269 Melanoma 0.2721322 0.4601359	0.381833		0.2526074 U14550 at	Siahltransfarasa SThM (ethm) mDNA
270	270 Melanoma	0.2720224	4 0 460121E		0 05044000	RC_AA2937	
					0.23244333 19 at	ıy aı	Gone 726293 3, mRNA sequence. (from Genbank)
			Warman .				control solutes senescent fibroblasts NbHSF Homo sapiens cDNA clone 325211 5' similar to PIR:A55093 A55093 fatty acid
271	271 Melanoma	0.2713678	3 0.4600159	0.381668	0.25221696	W48808_s_ at	transport protein precursor - mouse ;, mRNA sequence. (from Genbank)
272	272 Melanoma	0.270191	0.4599043	0.381624	RC_A 0.2520347 85 at	RC_AA4888 85_at	EST: aa55f10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
273	273 Melanoma	├	0.2698903 0.4598771		0.25180337 U44105	U44105 at	Rab9 expressed neer dogen menu.
274	274 Melanoma	0.2604044		0		62293	LIMK1 gene (LIM-kinase1) extracted from Human LIM-kinase1 and
1	Nicial Of Fa		0.45983	0.381324	0.25166315	s at	alternatively spliced LIM-kinase1 (LIMK1) gene
					•		Human DNA sequence from clone 1409 on chromosome Xp11.1-
							11.4. Contains a inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Author MAACH 1775
							gene and a 6-Phosphofructo-2-kinase (Fructose-2 6-hisphosphatase)
275	275 Melanoma	0.2687703	0.45971	0.381164	RC_A 0.25139314 80_at	RC_AA4516	LIKE pseudogene. Contains ESTs, STSs and genomic marker
						RC AA4243	700007
276	276 Melanoma	0.2669215	0.4596454	0.380814	0.25123549 31 at	31 at	Homo sapiens ST15 mRNA, complete cds
277	277 Melanoma	0.2667739	0.459614	0.380814	RC 0.25109968 97	_AA1560 s_at	EST: zo45d03.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 589829.31 mRNA seguance (from Combant)
0.70		(402	EST: EST45737 Fetal kidney III Homo saniens chNA 31 and mbNA
278	278 Melanoma	0.2664683		0.380406	0.2508476 93_at		sequence. (from Genbank)
617	crs melanoma	0.2661312	0.4594032	0.380341	0.25071457 W26928 at		Homo sapiens mRNA for ARPP-19 profein
280	280 Melanoma	0.2660767	0.4590868	0.380248	RC_A 0.2504662 49 at	A1428	EST: zl40h02.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 504435.31 mRNA seguance (from Contract)
281	281 Melanoma	0.2654603	0.4588867	0.380017	0.25038958	93867 at.2	0.25038958 [193867 at.2 Himan DNA notimenant III at. 11 (1938)
282	282 Melanoma	0.2654603	0.4587846	0.379651	0.2501965 U93867	193867 at	RNA polymerase III subunit (RPC62) mRNA, complete cds
283	283 Melanoma	0.264911	0.4586162	0.379577	RC AA4366 I	RC_AA4366 56 at	EST: zv57c04.s1 Soares testis NHT Homo sapiens cDNA clone 757734 3', mRNA sequence (from Genhank)
284 N	284 Melanoma	0.2644135	0.4582253	0.379454	R 0.24979512 5	RC_AA4249 52 s at	EST: zw03g12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 768262 31 mRNA sequence (from Conbody)
285 N	285 Melanoma	0.2642682	0.4581252	0.379378	RC_A 0.24970591 29_at	A5996	EST: ag10a01.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1069896 3', mRNA seguence (from Genhank)
286 N	286 Melanoma	0.2634239 0.4580195	0.4580195	0.379125	0.24948074 06 s at	7771	19489066E mand made = 1
287 N	287 Melanoma	0.2633251	0.4578561	0.379039	0.24925558 M33374	te	Cell adhesion protein (SOM4) mena
						5	den autresion protein (OQIVI) MRINA

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<u>A</u>	4	T			A			nce.	unit		A				-		1					
RC_AA4589 EST: zx88e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 52_at clone 810844 3', mRNA sequence, (from Genbank)	EST: ab12a04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone 840558 3', mRNA sequence. (from Genbank)	Galactokinase (GALK1) gene	EST: zk69h02.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 488115 3', mRNA sequence. (from Genbank)	EST: Homo sapiens thymus mRNA (randomly primed, normalized),	RC_AA2996 EST: EST12479 Uterus tumor I Homo sapiens cDNA 3' end, mRNA sequence.	Nucleolar autoantiden No55 mPNA	INHBB Inhibin, beta B (activin AB beta polypeptide)	EST: Human fetal brain cDNA 5'-end GEN-405D05, mRNA sequence. (from Genbank)	AA313977_s Homo sapiens RNA polymerase II transcription factor SIII p18 subunit	GJA4 Gap junction protein alpha 4 37kD (connexin 37)	EST: zx80a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	cione 8 (00zb 3, mRNA sequence. (from Genbank)	ID31: 2823601.81 NOT_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686232 3' similar to WP:R05G6.4 CE07417: mRNA	sequence. (from Genbank)	KRT9 Keratin 9	EST: zx47c07.r1 Soares testis NHT Homo sapiens cDNA clone 795372 5', mRNA sequence, (from Genhank)	Transforming growth factor-beta-2 mRNA	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	ATP5D ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	EST: zr51e07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666948 3. mRNA sequence (from Ganhank)	EST: yh81g01.r1 Homo sapiens cDNA clone 136176 5' similar to contains MSR1 repetitive element: (from Genhank)	KIAA0356 gene product
RC_AA4589 52_at	RC_AA4878 79_at	L76927_ma1 at	RC_AA0547 04_at	0.2483921.44367.91	RC_AA2996	U47621 at	M31682 at	0.2476867 D61469 at	AA313977_s		A4552	מו	_AA2622			√A453369_a		0.24632998 X63422 at-2	(63422 at	AA2362 at		\B002354_a
RC 0.24910279 52	RC_A 0.24896085 79_at	0.24870886	RC_A 0.24848868 04_at	0.248392	RC A 0.248202 55 at	0.24803293 U47621 at	0.24792519 M31682	0.2476867	0.2475044	0.24731573 M96789 at	RC_A	0.441 19341		0.24706388 61	0.24697755 Z29074_at	0.24676791	0.2466273 M19154 at	0.24632998	0.24619456 X63422 at	RC 0.24601288 41	0.24586938 R33301 at	0.24574246 t
0.378884	0.378808	0.378552	0.378338	0.37823	0.377888	0.377747	0.377521	0.377435	0.377335	0.3777172	0.377066			0.376831	0.376589	0.376429	0.376283	0.376064	0.375672	0.37549	0.375048	0.375033
0.4577746	0.4576396	0.4576065	0.4574878	0.4574501	0.4574042	0.457235	0.4571506	0.4570983	0.4569655	1 1	0,4565921		1	0.456431	0.4559673	0.4559435	0.4559423	0.4558926	0.4558028	0.4557305	0.4555065	0.4554679
0.2618309	0.260758	0.260383	0.2601063	0.2592943	0.2592537	0.2579902	0.2570428	0.2569929	0.2558652	0.255715	0.2544765		T	0.2542394	0.254125	0.2537687	0.253736	0.2536844	0.2536844	0.2532991	0.2524737	0.2523058 0.4554679
288 Melanoma	Melanoma	290 Melanoma	291 Melanoma	292 Melanoma	293 Melanoma	294 Melanoma	295 Melanoma	296 Melanoma	297 Melanoma	298 Melanoma	299 Melanoma				SO I MEIATIONIA	302 Melanoma	303 Melanoma	304 Melanoma	305 Melanoma	306 Melanoma	307 Melanoma	308 Melanoma
288	289	290	291	292	293	294	295	296	297	298	299		000	201	3	302	303	304	305	306	307 1	308

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14 000		The state of the s				3C_AA2435	RC AA2435 EST: zs15h06.s1 NCI CGAP GCB1 Homo sapiens cDNA clone
SUBJIME	309 Melanoma	0.2522372	0.455388	0.374894	0.24551013 62_at	72_at	IMAGE:685307 3', mRNA sequence. (from Genbank)
310 Melanoma	anoma	0.2520279	0.455204	0.374624	0.24539483 t	AA028171_a	EST: ze75h09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364865 5' similar to contains element MER35 repetitive element mRNA sequence (from Genbank)
311 Melanoma	anoma	0.2516953		0 374443	0.24514343 14595	to	SLC1A4 Solute carrier family 1 (glutamate/neutral amino acid
312 Melanoma	anoma	0.2513504		0.374322	0.24501704 U28249 at		MAT8 protein
313 Melanoma	anoma	0.25055	0.4543239	0.374022	0 24484888 04 at	A0467	EST: zk62b07.s1 Soares pregnant uterus NbHPU Homo saptens
314 Melanoma	anoma	0.2505134	1	0.373988	RC_A 0.24477321 30 at	A2581	EST: 2s35f03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:687197 3' mRNA sequence (from Genbank)
315 Melanoma	anoma	0.2503504	1	0.373885	0.24452819	77_s_a	P/Q-type calcium channel albha1 subunit
316 Melanoma	anoma	0.2494522	0.4535285	0.373709	RC_A 0.24425334 24_at	A4636	EST: zx98g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 811826 3', mRNA sequence. (from Genbank)
317 Melanoma	anoma	0.2486976	0.4535079	0.373641	0.244134	4A374109_a	AA374109_a EST: EST86231 HSC172 cells I Homo sapiens cDNA 5' end, mRNA tequence, (from Genbank)
318 Melanoma	anoma	0.2485793	0.4533404	0.373337	0.2438887	AA043157_a	Zk48f06.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486083 5', mRNA sequence, (from Genbank)
319 Melanoma	anoma	0.2481357	0.4530735	0.373307	0.24387982	RC_D58185	EST: Human aorta cDNA 3'-end GEN-354C01, mRNA sequence. (from Genbank)
320 Melanoma	anoma	0.2477354	0.4528528	0.373236	RC 0.24370642 96	AA5209 at	EST: aa70c08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826286 3', mRNA sequence. (from Genbank)
321 Melanoma	anoma	0.247037	0.4527831	0.37315	0.24351954 68 s at	509	Ran GTPase activating protein 1
323 Melanoma	anoma	0.2461558	0.4526792	0.372944	0.24334027 U91316 HG2171- 0.24320692 HT2241	r at	at Acyl-CoA thioester hydrolase mKNA r af 12-I inoxvaenase
324 Melanoma 325 Melanoma		0.2459892	0.4522368	0.372876	RC_AA2 0.24298309 05_at 0.24282981 X71125	4	EST: zs90e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704770 3', mRNA sequence. (from Genbank) Glutamine cyclotransferase
326 Melanoma 327 Melanoma		0.2455135	0.4513044	0.372842	0.24271628 U84720_at		mRNA export protein Rae1 (RAE1) mRNA Ve24q11 r1 Homo saniens cDNA clone 118724 5' (from Genhank)
328 Melanoma	anoma	0.2452174	1	0.372748	0.2423966 t	ω,	Cp0694.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', mRNA sequence. (from Genbank)
329 Melanoma	anoma	0.2441149	0.4510652	0.372436	0.2421939 t	\A005190_a	Zh95d06.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429035 51, mRNA sequence. (from Genbank)

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HG544- 0.24208695 HT544 at
0.24192439 47 at
0.24184497 T95377
0.2416644 24 f at
0.24158628 M93311
AA482319_ _at
HG270- 0.24111953 HT270_at
AA314096_a EST185947 Colon carcinoma (HCC) cell line II Homo sapiens cDNA to sequence, (from Genbank)
RC_AA4214 87_at
AA096094_s
N75215_s_a EST: yw33h05.r1 Homo sapiens cDNA clone 254073 5'. (from t
N24990_s_a t
0.24018386 L14927 at
AF001900_a t
0.23994544 U30998 at
RC_AA4439 0.23971084 13 at
AA5214 at
0.23944761 L18920 f
0.23933634 87_at
RC_AA4359 41_at
RC_AA4061 63_at

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0.2389092 U84569_at-2 Chromosome 21 open reading frame 2	YF5 mRNA	AA263056_a EST: PMY0404 KG1-a Lambda Zap Express cDNA library Homo	sapiens cDNA 5', mRNA sequence. (from Genbank)	EST: zv26h12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 754823 5' similar to contains Alu repetitive element: mRNA	sequence. (from Genbank)	EST: zr44g03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	666292 3', mRNA sequence. (from Genbank)		Homo sapiens snurportin1 mRNA, complete cds	Clones 23920 and 23921 mRNA sequence	EST: yi36b03.r1 Homo sapiens cDNA clone 141293 5'. (from	Genbank)	T847E0 21 COUNTY Sources testis NH1 Homo sapiens cDNA clone	70170U.S. IIIKINA sequence. (Irom Genbank)	EST: 2081603.81 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 760036 3", mRNA sequence (from Genhank)			cDNA clone 504414 3', mRNA sequence. (from Genbank)	EST: ag34c05.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1091432 31 mRNA seguence (from Genhank)			LOR Loricrin	Uridine phosphorylase	EST: zd50g02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 344114 5', mRNA sequence. (from Genbank)	EST: zx10a05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 786032 3' similar to contains Alu repetitive element; mRNA	sequence. (from Genbank)	EST: zr78g10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	sequence. (from Genbank)	Smooth muscle myosin heavy chain isoform SMemb [human, at umbilical cord. fetal aorta mRNA Partial 971 ntl	Rab 13
U84569_at-2	0.23878157 U84569 at	AA263056_a	1	AA422123 f		RC_AA2623	51_f_at	RC_AA4044	26 <u>_a</u> t	U79271_at	07770	K04412 at		01 at	RC_A44241 48 at	0.23735528 J00117 f at	RC_AA1428	58_at	RC_AA5992 14 at	Property Company of the Company of t	0.23701487 T85532 f at	0.23695934 M94077 at	X90858_at	10000	W / 3805_at	RC_AA4486	27_f_at	BC 440340	25 at	ဟ	m
0.2389092	0.23878157		0.23862992 t		0.238443		0.23833175 51 f at	1	0.23825628 26_at	0.23811057 U79271	0.0000000000000000000000000000000000000	U.237 09830 R04412	0.03770474 E4	0.431.0414	0.23755601 48 at	0.23735528		0.23729226 58	RC 0.23714967 14		0.23701487	0.23695934	0.23683812 X90858 at	2000	U.23653269 W / 3805		0.23641627 27_f_at		0.23630421 25 at	0.23615283 S67247	0.2359986
0.369091	0.368958		0.368883		0.368485	- (0.368443	6	0.368284	0.368236	0 26 0000	0.300201	0 367066	0.301.900	0.367887	0.367669		0.367622	0.367503		0.36746	0.367369	0.367187	7236 0	0.3071		0.366932		0.366899	0.366758	0.366714
	0.447635		0.4474765		0.4473677		0.4473242		l.	0.4468163	0 4465264	- !	0.4463403		0.4463089	0.4462811		0.4462335	0.4457164		0.4455922	0.4453097	0.4452436	3070440	0.4449700		0.4448954		0.4446248	0.4444301	0.4444104
0.2351726	0.2351726		0.2350654		0.2345394		0.2341184		0.2336422	0.2331909	0 2328422	0.6.020 122	0.2312847	102102:0	0.2312143	0.2307322		0.2306058	0.2305651		0.229695	0.2293435	0.2287281	0 2285694	0.2203001	1	0.228322		0.2281575	0.2275346	0.2274068
351 Melanoma	352 Melanoma		353 Melanoma		354 Melanoma		355 Melanoma		356 Melanoma	Melanoma	358 Melanoma	Weldi John	359 Melanoma	5	360 Melanoma	361 Melanoma		362 Melanoma	363 Melanoma		364 Melanoma	365 Melanoma	366 Melanoma	367 Majapama	Melallolla		368 Melanoma		369 Melanoma	370 Melanoma	371 Melanoma
351	352		353		354	į	355		300	35/	358	3	350	3	360	361		362	363		364	365	366	367	3		368		369	370	371

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372	372 Melanoma	0.226995	0.226995 0.4443952	0.366297	0.23577452 03 i at	AA2358 i at	RC_AA2358 EST: zs42g06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 03 i at 687898 3', mRNA sequence. (from Genbank)
5					RC	2435	
373	373 Melanoma	0.226912	0.4443952	0.366274	0.23561932 82_at		Hemoglobin, gamma A
374	374 Melanoma	0.2265553	0.4440478	0.36607	0.23547302 M99564	ä	P PROTEIN
375	375 Melanoma	0 2258148	0.443518	0.365952	HG4322- 0.23536366 HT4592 at		Tubulin, Befa
376	376 Melanoma	diam	0	0.365733	0.23516381 X51801		BMP7 Bone morphogenetic protein 7 (osteogenic protein 1)
2		1.0			AA	71_s	EST: zx74g11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
377	377 Melanoma	0.225499	0.4430509	0.365599	0.23498346 at		clone 809540 5', mRNA sequence. (from Genbank)
1		0.0040690	0.4420570	0.365/87	Y08682	- ma	Carnitine nalmitoultransferase type
0.0	o foreigning	_		20100.0	RC	4771	EST: zu37f03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
379	379 Melanoma	0.2229818	0.4424886	0.365287	0.23471211 32 at		clone 740189 3', mRNA sequence. (from Genbank)
380	380 Melanoma	0 2227774	0.4423669	0.365188	0.23463127 t	N42272_s_a	EST: yw85f08.r1 Homo sapiens cDNA clone 259047 5' similar to WP:T15H9.1 CE01664 DNAJ ; (from Genbank)
3					HC		L
381	381 Melanoma	0.222104	0.44207	0.365105	0.23448561 H14255 at		Cpg-Enriched Dha, Cione EU4
382	382 Melanoma	0.2212297	0.4416662	0.364828	RC_AA4 0.23428619 01 f at	1014	PET112 (yeast homolog)-like
					- R	3203	EST: af07d11.s1 Soares testis NHT Homo sapiens cDNA clone
383	383 Melanoma	0.2210947	0.4413311	0.364819	0.23421432 61 at		1030965 3', mRNA sequence. (from Genbank)
					R	A6099	EST: af18a06.s1 Soares testis NHT Homo sapiens cDNA clone
384	384 Melanoma	0.2210868	0.4412695	0.364578	0.23402794 88_at		1031986 3', mRNA sequence. (from Genbank)
100	0.00	0 2208468	0 4440347	0.364449	RC_A 0.23386137195_at	A2523	EST: zs12g10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGF-685026 3. mRNA sequence. (from Genbank)
3	SOS INICIALIONIA	0.2200100	- 1	21.100.0	AA	AA234651 a	EST: zr75f06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
386	386 Melanoma	0.2207078	0.4410715	0.364382	0.23376092 t		669251 5', mRNA sequence. (from Genbank)
3						RC_AA6207	EST: af95b02.s1 Soares testis NHT Homo sapiens cDNA clone
387	387 Melanoma	0.2205552	0.4409433	0.364255		at at	1055499 3', mRNA sequence. (from Genbank)
388	388 Melanoma	0.2201491	0.4408959	0.364213	0.23348783 Y07909 at	7909 at	B4B
				7777	RC	_AA1141	EST: zn76d01.s1 Stratagene NT2 neuronal precursor 937230 Homo
385	389 Melanoma	0.2201347	0.4406/31	0.304174	0.23342110 30	1 at	
390	390 Melanoma	0.2198687	0.4406556	0.363888	0.23327684 t	AA432420_d t	
301	301 Melanoma	-	0 4406005	0.363871	0.23317158 46	RC_AA0183 46 at	EST; ze41d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone 361559 3', mRNA sequence. (from Genbank)
3		0.2406257			0.23303775 N42022	42022 at	EST: yw69g06.r1 Homo sapiens cDNA clone 257530 5'. (from Genhank)
25	Melalionia	392 Melaliulia U.Z.130201			0.20000		V(1) V(1)

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plantaris)	EST: ab05f07.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 839941 3', mRNA sequence. (from Genbank)	MitF mRNA	 	IMAGE:814097 3', mRNA sequence. (from Genbank)	Zinc Finger Protein (Gb:M88357)	1				742685 3', mRNA sequence. (from Genbank)		-	Ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease)		EST: zn85b02.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 564939 3', mRNA sequence. (from Genbank)	Calcium/calmodulin-dependent protein kinase II delta E mRNA, partial cds		INTERLEUKIN ENHANCER-BINDING FACTOR		PROTEIN [1]; mRNA sequence. (from Genbank)	Homo sapiens PAC clone DJ130H16 from 22a12.1-ater	Chromosome 1q subtelomeric sequence D1S553		sapiens cDNA done 664383 3', mRNA sequence. (from Genbank)	EST: zu52e12.s1 Soares ovary fumor NbHOT Homo sapiens cDNA clone 741646 3', mRNA sequence, (from Genbank)		
1 s at	RC_AA4901 42_at	Z29678_at	RC_AA4653	67_at	HG3565- 0.2321932 HT3768 at	RC AA4594	12_at	X63522_s_a t	RC_AA4002	92_at	RC_AA1329	69_s_at	RC_AA1299 23_at	TTT 100	RC_AA1293 90_at	U73738 at	X60787 s a		RC_AA4859	45 at	RC_AA2521 91_at	U06155 at	RC_AA2430	58_at	RC_AA4011 99_at	RC_AA0539 17 at	
0.23290403	RC_A 0.232771 42_at	0.23249954 Z29678		0.2324291 67	0.2321932		0.23211613 12_at	0.23198104 t		0.23189938 92		0.23172878 69_s_at	RC_A 0.23165119 23 at	The state of the s	RC_A 0.23145026 90_at	0.23135072 U73738		0.23122585 t	o o o o o o o o o o o o o o o o o o o	0.23109692 45 at	RC 0.23099001 91	0.23087378 U06155		0.23069708 58 at	RC_A 0.23053299 99_at	RC 0.23036164 17	
0.363716	0.363615	0.363578		0.363407	0.362978		0.362769	0.362695		0.36264		0.362486	0.362423		0.362363	0.362304		0.362258		0.302177	0.361997	0.361931	-	0.361885	0,361795	0,361721	
0.4405788	0.4405689	0.4405542		0.4405357	0.4405352		0.4404236	0.4403733		0.4403655		0.4403376	0.4402937		0.4402593	0.4401411		0.4400079	700007	0.4399087	0.439644	0.4396075		0.4395179	0.4394898	0.4389108	
0.2192921	0.2191667	0.2190425	10000	0.21819/1	0.217784		0.2171904	0.217164		0.21713	0,000	0.216/618	0.2165646		0.2159537	0.2159416		0.2157674	70074600	177/617.0	0.215441	0.2149619	1	0.2148667	0.2147125	0.2143141	,
393 Melanoma	394 Melanoma	395 Melanoma		396 Melanoma	397 Melanoma		398 Melanoma	399 Melanoma		400 Melanoma	- N A	401 Melanoma	402 Melanoma		403 Melanoma	404 Melanoma		405 Melanoma	406 Mologogy	Melalioilla	407 Melanoma	408 Melanoma		Melanoma	410 Melanoma	411 Melanoma	
393	394	395	0	350	397		398	399	9	400	Ç	401	402		403	404		405	406	400	407	408	Ç	804	410	411	

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. AA316686_s EST: EST188361 HCC cell line (matastasis to liver in mouse) II Homo RC_AA4521 | Transcription factor AP-2 alpha (activating enhancer-binding protein 2 RC_AA4282 EST: zw51d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA Human fetal brain cDNA 5'-end GEN-421F03, mRNA sequence. (from RC_AA3986 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION.;; mRNA AA424897_s EST: zv47b09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA RC_AA4599 EST: zx73f07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA AA012885_a EST: ze27f07.r1 Soares retina N2b4HR Homo sapiens cDNA clone RC_AA4560 EST; aa03d01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: HUMGS0005644, Human Gene Signature, 3'-directed cDNA EST: zr52b12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667007 3', mRNA sequence. (from Genbank) EST: yu73c07.r1 Homo sapiens cDNA clone 239436 5' similar to EST: zw71g02.s1 Soares testis NHT Homo sapiens cDNA clone 727689 3' similar to SW:YKU7_YEAST P36039 HYPOTHETICAL EST: zt70d05.s1 Soares testis NHT Homo sapiens cDNA clone AA043223_a Homo sapiens clone 486790 diphosphoinositol polyphosphate SP:S35643 S35643 BTEB2 PROTEIN - ;. (from Genbank) sapiens cDNA 5' end, mRNA sequence. (from Genbank) clone 756761 5', mRNA sequence. (from Genbank) clone 809413 3', mRNA sequence. (from Genbank) clone 773575 3', mRNA sequence. (from Genbank) Protein-tyrosine-phosphatase (tissue type: testis) Homo sapiens chromosome 19, cosmid F23149 812161 3', mRNA sequence. (from Genbank) 781682 3', mRNA sequence. (from Genbank) sequence, mRNA sequence. (from Genbank) 360229 5', mRNA sequence. (from Genbank) Gastric H,K-ATPase catalytic subunit gene phosphohydrolase mRNA, complete cds 0.22921386 X93921_at-2 Dual specificity phosphatase 7 sequence. (from Genbank) ADP-ribosylation factor 1 Genbank) AA082668_a RC_AA2530 H49499_s_a M63962_ma RC AA4321 0.22985701 C02053_at 0.22902337 X93921 at 0.22885567 H81241 at क् 0.22785403|D61596 0.22877741 78_at 0.23000693 08 at 0.22860296 43 at 0.22992824 39, at 0.2295157 05 at 0.22853592 74_at 0.22809754 40 at 0.22815207 1 at 0.2296199 at 0.22935697|t0.22976142 0.23033188 0.22797056t 0.22837286 0.361385 0.360426 0.361638 0.361135 0.360984 0.360918 0.360725 0.360203 0.360155 0.360867 0.360649 0.360465 0.360013 0.359458 0.359368 0.361271 0.360062 0.359867 0.359746 417 | Melanoma | 0.2120888 | 0.4380468 | 419 | Melanoma | 0.2115293 | 0.4379143 0.4387619 415 Melanoma | 0.2129301 | 0.4384987 418|Melanoma | 0.2116727| 0.4380354| 421 Melanoma | 0.2113843 | 0.4377695 0.4388792 420 Melanoma | 0.2113843 | 0.4378288 424 | Melanoma | 0.2110319 | 0.4373793 | 425|Melanoma | 0.2110153| 0.4373013 430 | Melanoma | 0.2095192 | 0.4367441 | 416 Melanoma | 0.2122679 | 0.4381451 422 | Melanoma | 0.2112357 | 0.4377505 423 | Melanoma | 0.2112098 | 0.4374024 | 426 Melanoma | 0.2107318 | 0.4369316 0.2133391 0.4387061 427|Melanoma | 0.2105456| 0.4369161| 428|Melanoma | 0.2102353| 0.4368807| 0.436777 0.2143084 0.214153 429 | Melanoma | 0.2095892 | 412 Melanoma 414 Melanoma 413|Melanoma

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EST: zx51b08.s1 Soares testis NHT Homo sapiens cDNA clone 795735 3' similar to TR:G1196644 G1196644 BAT-4.;, mRNA	sequence. (from Genbank)	Homo sapiens clone 638 unknown mRNA, complete sequence	Myelin associated glycoprotein	Autoantigen mRNA		Glone 77241b 3', mKNA sequence, (from Genbank)	RAD23A gene (human RAD23A homolog) extracted from Horno sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272	and R28549 containing the EKLF, GCDH, CRTC, and RAD23A genes, genomic sequence	Mitochondrial RNA polymerase mRNA, nuclear gene encoding mitochondrial protein	Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial profein	EX-1	EST: zx32g10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788226 3', mRNA sequence. (from Genbank)	EST: zw35h03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 771317 3', mRNA sequence. (from Genbank)	Cellular retinoic acid-binding protein 1			EST: zv20b06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754163 3', mRNA sequence, (from Genbank)	Human sialvltransferase SThM (sthm) mRNA complete cdc	EST: zt45g06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	Homo sanjens mRNA for laukemia associated gone 4	EEF1G Translation elongation factor 1 gamma	IL6 Interleukin 6 (B cell stimulatory factor 2)	Interleukin 6 (interferon, beta 2)
RC_AA4602	93_at	D31389_at	0.2274584 X98405_at	L26339 at	RC_AA4055	45 at		AD000092_c ds7_s at	U75370 at	N98666 at	S81914 at	RC_AA4534 31 at	RC_AA4762	35_at	RC_AA4030 41_at	J04444_at	AA328993_s at	A4787	RC_AA4243 46 at	RC_AA2917	RC_AA4785 87_at	X05855 at	X04602_s_a t	X04602_s_a t-2
	0.22770998 93	0.22760746 D31389_at	0.2274584	0.22736652 L26339 at	0 2272240E 42	0.62122.0		AD0 0.22712642 ds7	0.22699864 U75370 at	0.22679035 N98666 at	0.22663519 S81914	0.22660254 31	1000000	0.226380/ 35_at	RC_A 0.2262669 41_at	0.22616643 J04444	0.22610559	RC_A 0.22600846 78 at	0.22585885 46 at	RC 0 22578618 71	0.22568338 87	0.22551976 X05855 at	0.225324291	X0 0.2251814 t-2
		0.359133	0.359099	0.358958	0 358000	0.50050		0.358909	0.358782	0.358729	0.358713	0.358576	0.0000	0.358478	0.3584	0.358092	0.358052	0.357899	0.357772	0.357759	0.357607	0.357516	0.357417	0.357413
1	0.4367388		0.4367304	0.436706	0.4366873	- 1		0.4364752	0.436435	0.4364017	0.4363637	0.4361584	705050	0.4359535	0.4358276	0.4357776	0.4357337	0.4356204	0.4354142	0.4354035	0.4353237	0.4351651	0.4350275	0.4344044
	0.209282	0.2092453	0.2092362	0.2083055	0.2081056	2001007:0		0.208016	0.2078692	0.2074884	0.207364	0.2073615	0.0064077	U.2U012/1		0.2057747	0.2050022	0.2047467	0.2042919	0.2034747	0.2027902	0.2023935	0.2023352	0.2023352
	431 Melanoma	432 Melanoma	433 Melanoma	434 Melanoma	435 Melanoma	5		436 Melanoma	437 Melanoma	438 Melanoma	439 Melanoma	440 Melanoma	AA41 Molopoopo	Melanoma		443 Melanoma	444 Melanoma	445 Melanoma	446 Melanoma	447 Melanoma	448 Melanoma	449 Melanoma	450 Melanoma	451 Melanoma
	431	432	433	434	435	2		436	437	438	439	440	777	+	442	443	444	445	446	447	448	449	450	451

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0.2	0.2022497	0.4343902	0.357402	0.22503994 t	
0.2014993	993	0.4342621	0.357231	0.22486462 80_at	EST: ze91d10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366355 3', mRNA sequence. (from Genbank)
0.2011292	292	0.4342141	0.356987	0.22477579 R22673_at	EST: yg08a04.r1 Homo sapiens cDNA clone 31308 5'. (from Genbank)
		- party and			EST: zl73e05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510272 3' similar to TR:E243948 E243948 CHROMOSOME VII
0.2009812	812	0.4342006	0.356903	RC_AA0531 0.22459036 39 at	READING FRAME ORF YGL054C.;, mRNA sequence. (from Genbank)
		1		RC_AA3987	
0.2003417	3417	0.4341824	0.356819	0.22449128 08 at	Cell division cycle 10 (homologous to CDC10 of S. cerevisiae)
0.2000301	3301	0.4333594	0.356711	RC_AA2534 0.22437325 32_at	EST: zr77f04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669439 3', mRNA sequence. (from Genbank)
				The state of the s	EST: ag03a06.s1 Soares testis NHT Homo sapiens cDNA clone
0.1996321	6321	0.4333543	0.356661	RC_AA6209 0 22418156 98 at	1056178 3' similar to WP:C16A3.1 CE04002 HELICASES OF SNIE2/PADE4 EAMILY: BONA SECURIOR (FOR COLUMN)
0.199	5644		0.356562	0.22412516 12350 at	THRS2 Thrombospondin 3
0.1993956	3956	0.4326458	0.356424	0.22388084 U76421 at	DSRNA adenosine deaminase DRADA2h (DRADA2h) mPNA
0.1992854	2854	0.4324863	0.356307	0.22371888 36 at	EST: zt2za05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713840 3', mRNA sequence, (from Genhank)
0.1992078	2078	0.432301	0.356221	HG3570- 0.22368261 HT3773_at	Protein Phosphatase Inhibitor Homolog
0.1990525	0525	0.4322276	0.356193	RC_AA2919 0.22351474 27 at	EST: zr58g09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667648 3. mRNA sequence (from Genhank)
0.1989889	9889	0.4322276	0.355945	RC_AA4320	EST: zw89c10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
				RC AA4492	EST: zx04b11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
0.198	9587		0.355893	0.22320239 38 s at	clone 785469 3', mRNA sequence. (from Genbank)
0.19	0.198394	0.4314396	0.355751	0.22313479 U10685_at	MAGE-10 antigen (MAGE10) gene
0.19	0.198394	0.4313746	0.355653		0.22304982 U10685 at-2 Melanoma antiden family A. 10
0.1982618	2618	0.4311813	0.355544		XPA Xeroderma pigmentosum, complementation group A
0.1979379	9379	0.4308189	0.355437	RC_AA1943 0.22287999 09_s_at	Reticulon 2
0.1977596	7596	0.4306039	0.35542	AA428025_a	Transforming growth factor heta-stimulated protein TSC.22
0.1976767	3767	0.430593	0.355384	0.22268313 M55621 at	MGAT1 N-acetyglucosaminyltransferase I
0.19	0.197651	0.4305851	0.355319	M29277_s_a 0.22255063 t	CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR
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Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. All the state of t

0.22243537 16
D31833 0.22231315 t
0.22217534 D87942
0.22216122 1_f_at
AA313990_a cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid C30A5.3 mRNA seminare from Carbark
RC_AA0558 0.22186141 at
RC_AA0259 0.22176902 30_at
RC_AA4010 0.22152926 98_f_at
AA074407_a 0.22140273 t
0.22128811 M80563 at
0.22113751 U90546 at
0.2210264 U90546 at-2 Human butyrophilin (BTE4) mRNA complete add
RC_AA4055 0.22097507 01_at
RC_AA2566 0.22087514 64 at
AA197134_a EST: zq11b11.r1 Stratagene muscle 937209 Homo sapiens cDNA clone 629373 5', mRNA sequence. (from Genbank)
HG3731- 0.22060122 HT4001 r
X52611_s_a Transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

107	404 Malanoma	0 1916102	0.4274349	0,353042	X52 0.220248 t		TRANSCRIPTION FACTOR AP-2
100	402 Melanoma	0.1913768	0,4274195	0.353041	0.22017564 06	AA4646 at	EST: aa11g01.s1 Soares NnHMPu S1 Hollio sapiens Corra cons 812976 31, mRNA sequence. (from Genbank)
493	493 Melanoma	0.1908572	1 1	0.352942	HG67- 0.22003287 HT67_f	at	Zinc Finger Protein (Gb:X61870)
494	494 Melanoma	0.1904382	0.4271973	0.35278	0.21988222 R29077	ja,	EST: F1-110D 22 week old human fetal liver cDNA library Homo sapiens cDNA clone F1-110D 5', mRNA sequence. (from Genbank)
F 0				0.352757	M3 0.21982396 t	M32304_s_a	TIMP2 Tissue inhibitor of metalloproteinase 2
498	495 Melanoma		- 1	0.352574	0.21970604 J00	0231_f_at	0.21970604 J00231 f at Immunoglobulin gamma 3 (Gm marker)
497	497 Melanoma			0.35253	RC_A 0.21955216 72_at	2 AA4497 at	RC_AA4497 EST: zx07n06.s1 Soares total retus Nozrin o 3w 1 choice supported 72 at clone 785819 3', mRNA sequence. (from Genbank)
498	498 Melanoma		0.1879698 0.4267349	0.352435	0,21938972 R14545_at		EST: yf84f08.r1 Homo sapiens cDNA clone 29219 5'. (from Genbank)
2		<u> </u>	0.4267203	0.352368	0.21936227 at	55916_s	Homo sapiens mRNA from chromosome 5q31-33 region
500	500 Melanoma			0.352143			Mac-2 binding protein mRNA
3			0.4263006	0.352138	RC_A 0.21904933 46 at	A4210	EST: zu09f09.s1 Soares testis NHT riom Saprens contraction 731369 3', mRNA sequence. (from Genbank)
201	201 Metanolina				A	AA081209_a	and the second s
502	502 Melanoma	0.1871408	0.4262551	0.351984	0.2188/6991	A027766 a	AA027766 a EST: HPI A CCLEE 69a10u HPLA CCLee Homo sapiens cDNA,
503	503 Melanoma	0.1869301	0.4262493	0.351956	0.21876281	20011200	mRNA sequence. (from Genbank) in The sequence of the sequence
207	FOA Melanoma	0 1869133	0 4261301	0.351948	RC_A 0.21868828 69_at	C_AA1239 9_at	clone 511398 3', mRNA sequence. (from Genbank)
50	Melalio		1	١_	Α.	AA027765_a	EST: HPLA_CCLEE_65h7r HPLA CCLee Homo sapiens count,
505	505 Melanoma		- 1		0.218634591	25340 at	InklyA sequence, (non concern) CRYBR1 Crystallin beta-B1
506	506 Melanoma		٦) C	0.21040999 050540	72514 at	Column Co
507	507 Melanoma	0.1859926	0.425513	0.331121	0.61.2001.20	5	EST; yi02e03.r1 Homo sapiens cDNA clone 138076 5'. (from
508	508 Melanoma	0.1857141	0.4247508	0.351632	0.2182833 R53717	53717_at	Genbank) Construction To Desization Chines RS-[34, 6])
506	509 Melanoma		6 0.424706	0.351439	0.21822624 J00277	00277_at	(genomic clones lambda-lonz-1z, 100101), control clones lambda-lonzer complete coding sequence
			0 40457E4	0.054123	0.21800635	A007583_a	AA007583_a 22q11.2-qter. Contains two possibly alternatively spliced unknown the nenes, one with homology to a worm protein. Contains ESTs
집	510 Melanoma		0.184/509 0.4246/54		1		S C C C C C C C C C C C C C C C C C C C

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Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds	H.sapiens hGDS mRNA for smg GDS	Homo sapiens mRNA for KIAA0859 protein, complete cds	EST: zt69h05.s1 Soares testis NHT Homo sapiens cDNA clone 727641 3' similar to gb:X14850_cds1 HISTONE H2A.X (HUMAN);, mRNA sequence. (from Genhank)	Nuclear orphan receptor LXR-alpha mRNA	EST: zl47e06.s1 Soares pregnant uterus NbHPU Homo sapiens	cDNA clone 505090 3', mRNA sequence. (from Genbank)	, alpha-2 (VI) collagen		BOX RNA HELICASES: ;, mRNA sequence, (from Genbank)	Mannaca D dalichal utilitization defeat 1	Midali Noset Edulution deliction delection	IEST: 2W300103.ST Society total retus NDZHF8 9W Homo sapiens cunny clone 774101 3', mRNA sequence. (from Genbank)	-	(45kD)	BMP1 Bone morphogenetic protein 1	EST: EST23600 Frontal lobe Homo sapiens cDNA 3' end similar to EST containing Alu repeat, mRNA sequence. (from Genbank)		+		EST: zw26d12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770423 31, mRNA sequence, (from Genbank)	Transforming growth factor beta 1 induced transcript 1	EST: zx36d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788551 3' similar to TR:G595950 G595950 PROTEIN N-	TERMINAL ASPARAGINE AMIDOHYDROLASE.;; mRNA sequence.	(from Genbank)	EST: zk40g10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485346 3', mRNA sequence. (from Genbank)
RC_AA4780 17_at	RC_AA1608 76_at	RC_AA2274 63_at	RC_AA4169 63_at	U22662 at	A1	28_at	0.21722925 M20777_at	RC_AA4614	76_at	RC_AA2817	90 at	44_at	RC_AA2825	21_at	0.21680659 U50330_at	RC_AA3211 46 at	D31628_s_a t	M23234_s_a		RC_AA4306 74 at	RC_AA2332 57_at		RC_AA4528	0.21618266 30_at	RC_AA0397 58_at
0.21800408 17	RC 0.21781966 76	RC 0.21763417 63	RC_A 0.21762049 63_at	0.2174755 U22662		0.21726757 28_at	0.21722925		0.2171997	RC_A	0.4170410	0.21699817 44_at		0.21688838 21	0.21680659	RC_A 0.21673584 46 at	0.21660347		0.21647744	RC_A 0.21638247 74 at	RC_A 0.21635504 57_at			0.21618266	RC 0.21613759 58
0.351433	0.351369	0.351264	0.35112	0.351081		0.351061	0.350885		0.350783	0.350783	0.000	0.350589	-	0.350588	0.350534	0.350458	0.350324		0.350138	0.350031	0.349852		-	0.349725	0.349615
0.4244558	0.4242718	0.4242469	0.4241274			_	0.4238995		0.4238286	0.4237262		0.4237137		- 1	0.4230932	0.4227979	0.4227945		0.4227658	0.4227137	0.422467			0.4223196	0.4221661
0.1846325	0.1845188	0.1839874	0.1837206	0.1835473		0.1834348	0.1830188		0.1825981	0.182339	0.104000	0.1822734		0.1822424	0.1821363	0.1818144	0.1810391		0.1809776	0.1808598	0.1806435			0.1806164	0.1799611
511 Melanoma	512 Melanoma	513 Melanoma	514 Melanoma	515 Melanoma	- A	516 Melanoma	517 Melanoma		518 Melanoma	519 Melanoma		520 Melanoma		521 Melanoma	522 Melanoma	523 Melanoma	524 Melanoma		525 Melanoma	526 Melanoma	527 Melanoma			528 Melanoma	529 Melanoma

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors And the state of t

Docket No.:	2825.2020-002
Title: Geneti	c Markers for Tumors
Inventors: Srie	dhar Ramaswamy, et al.

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530	530 Melanoma	0.1799459	0.4221318	0.349279	RC_A 0.21604268 72_at	RC_AA4022 72 at	EST: zu48b11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741213 3, mRNA sequence from Canhank
531	531 Melanoma		0.1798918 0.4219402	0.349164	0.21593903 049928	U49928 at	TAK1 binding protein 1 (TAB1) mRNA
		-					EST: EST24395 Cerebellum II Homo sapiens cDNA 3' end. mRNA
532	532 Melanoma	0.1795847	0.4217333	0.349121	0.21579422 33_at	33_at	sequence. (from Genbank)
533	533 Melanoma	0.1795117	0.4216305	0.349116	0.21560128 D30954	D30954 at	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. (from Genhank)
534	534 Melanoma	0.1791461	0.4216085	0.349113	RC_A 0.21553794.16.at	A6	EST: af15g02.s1 Soares testis NHT Homo sapiens cDNA clone
			1		100011	N75611 s a	EST: yw37b04.r1 Homo sapiens cDNA clone 254383 5' (from
535	535 Melanoma	0.1789497	9	0.349103	0.21540767		Genbank)
000	oco ivielanoma	0.1788928	0.421485	0.348997	0.21533713 S78187	S78187_at	M-PHASE INDUCER PHOSPHATASE 2
537	537 Melanoma	0.1785964	0.4214769	0.348988	0.21529533		AA174173_a EST: PTH156 HTCDL1 Homo sapiens cDNA 5/3', mRNA sequence. (from Genbank)
538	538 Melanoma	0.1783743	0.421444	0.348814	0.21517867 D31286 at	D31286 at	Homo sapiens mRNA for smallest subunit of ubiquinol-cytochrome c
539	539 Melanoma	0.1776384	0.4213603	0.348732	0.2149825	0.2149825 D13640 at	HLA-C Major histocompatibility complex, class 1 C
				-		AA292745 a	EST: zt55h02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726291 5' similar to TR:G984317 G984317 TEVDSIN
540	Melanoma	540 Melanoma 0.1771608 0.4212545	0.4212545	0.34867	0.2148057		RELATED PROTEIN; mRNA sequence (from Genbank)
							EST: af85c04.s1 Soares testis NHT Homo sapiens cDNA clone
							1048806 3' similar to SW:YK61_YEAST P36160 HYPOTHETICAL
541	541 Melanoma	0 1767132	0.4212402	0 340464	0.04475050	RC_AA6213	39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC REGION.;
-		0.1101102		0.340404	0.21475953 40	40_at	mKNA sequence. (from Genbank)
542	542 Melanoma	0.1764979	0.421196	0.348367	0.21470709	AA382383_f	EST: EST95583 Testis I Homo sapiens cDNA 5' end, mRNA
				1000		- di	sequence. (Irom Genbank)
543	543 Melanoma	0.1763369	0.421051	0.348321	0.21461616		A2M Alpha-2-macroglobulin
544	544 Melanoma		0.1761146 0.4210094	0.348195	0 24454747 40	_AA4500	EST: zx33f04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
				2	47.101.7.0	, e	Golle / 8628/ 3, mRNA sequence. (from Genbank) Hypothetical human protein R31240 2 nene extracted from Homo
							Sabiens DNA from chromosome 19n13 2 cosmids R31240 R30222
i						00092_c	cland R28549 containing the EKLF, GCDH, CRTC, and RAD23A
545	545 Melanoma	0.1757035	0.4208742	0.348036	0.21441372 ds2	at	genes, genomic sequence
546	546 Melanoma	0.1755118	0.42087	0.34789	0.21432891 1149785 at		DCT Dopachrome tautomerase (dopachrome delta-isomerase, turosina-related protein 2)
547	547 Melanoma	0.1752885	0.4208263	0.347805	0.21419992 1.04751		CYP4A11 Cytochrome P450 Suhfamily IVA nolymentide 11
						2335	EST: zr30h12.s1 Stratagene NT2 neuronal procursor 037220 Homo
548	548 Melanoma	0.1749978 0.4207246	0.4207246	0.347629	0.21413423 45 at		sapiens cDNA clone 664967 3', mRNA sequence. (from Genbank)

549 Melanoma	ma 0.1746173	173 0 4203002	0 34760		RC_AA3994	RC_AA3994 EST: zt50e07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
550 Melanoma	-	1 1	0.3		0.21409173114 at	clone 725796 3', mRNA sequence. (from Genbank)
551 Molonomo					YEL019c/M	Cione 20132 InKNA, partial cds
ואומושווס	11a 0.1742542	042 0.4200515	5 0.347502	2 0.21393442 MS21 at	2 MS21_at	
552 Melanoma	na 0.1740017	0.4198775	5 0.347477	RC_A 7 0.21381629 67_at	RC_AA4285)67_at	EST: zw74b07.s1 Soares testis NHT Homo sapiens cDNA clone 781909 3', mRNA sequence. (from Ganhank)
553 Melanoma	na 0.1739702	702 0.4197269	9 0.347206	5 0.21370651		AA315930_a EST: EST187807 Colon carcinoma (HCC) cell line II Homo sapiens to CDNA 5' end, mRNA seguence (from Gashark)
554 Melanoma	na 0.1736185	85 0.4195799	9 0.347203		R29548 f at	0.21359609 R29548 f at Proteasomo (monages 1.1.)
555 Melanoma	na 0.1730741	741 0.4195797	7 0.347187		RC_AA4432 12_at	EST: aa14d01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 813217 3', mRNA sequence (from Genhank)
556 Melanoma	па 0.1730713	13 0.4194993	3 0.347141		0.2134245 X54936 at	PGF Placental growth factor, vascular endothelial growth factor-
557 Melanoma	na 0.1730232	32 0.4193354	4 0.347092		RC_AA2356 04_at	EST: zt36b07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 724405.31 mRNA sequence of the contract of th
558 Melanoma	na 0.1728407	07 0.4192781	0.347068		RC_AA4256 36_at	
559 Melanoma	ia 0.1728082	82 0.4192761	0.346734	0.21298885 R12538 at	R12538 at	FST: v#R@b40 v4 11.
560 Melanoma	a 0.1726556	56 0.4192098	0.346644		RC_AA4364 71_at	EST: zv08e05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753056 3', mRNA sequence (from Gorbon)
561 Melanoma	a 0.1726251	51 0.4191891	0.346516	0.21277319 X76040_at	X76040_at	HLON ATP-dependent protease mRNA, nuclear gene encoding mitochondrial protein
562 Melanoma	a 0.1723469	39 0.4191715	0.346282	0.2126996 t	AA422029_a t	AA422029_a EST: zv26g08.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
563 Melanoma	a 0.1722348	18 0.4191453	0.346185	RC_A 0.21264328 62_at	A4323	Homo sapiens mRNA for KIAA0678 gratain
564 Melanoma 565 Melanoma	a 0.1720402			RC_A 0.21259494 99_at	60	Homo sapiens mRNA for JM4 protein, complete CDS (clone IMAGE 546750 and LLNI c110E185707 (pages pages)
566 Melanomo		- 1	_	0.21249521 R54918 at D26561 cd	318 at 561 cds	Vj78h06.r1 Homo sapiens cDNA clone 154907 5'. (from Genbank) ORF for F7 protein control of the c
EGT Melanolla			0.345902	0.21228649 3 at	.66 s a	3 at genome integrated into human carcinoma DNA C01766 s a EST-HIMASON0274 U.
568 Melanoma	0.1700993	6 0.4188809 3 0.4185803	0.345889	0.21228442 t		Sequence, mRNA sequence. (from Genbank)
569 Melanoma		0.1700562 0.4184842	0.345638	0.21206182 53 at	A4471	EST: zw93h05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
o/U Melanoma		0.1700185 0.4183255	0.345604	0.21201916 IL2 at		No info for gene

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Figure Comparison Compari					11 12 13 14 15 15 16 17 17 17 17 17 17 17 17 17 17 17 17 17		And Then and acid for bed to the second acid for the second acid f
0.1698767 0.417914 0.345577 0.21189353 M98528_at 0.1698465 0.4176918 0.345471 0.21189353 M98528_at 0.1697034 0.4175581 0.345457 0.21156103_at 0.1697034 0.417581 0.345437 0.21156103_at 0.1697034 0.4174145 0.345403 0.21151495 55_at 0.168758 0.4174167 0.34536 0.21121506 7_at 0.1687387 0.4168473 0.345115 0.21037471 2_at 0.1687387 0.4168473 0.345115 0.21097471 2_at 0.1678978 0.4166479 0.34507 0.21091444 12_at 0.167787 0.4166479 0.344823 0.21083665 95_at 0.1677897 0.4165682 0.344823 0.21077015 M63959_at 0.167699 0.4165682 0.344871 0.21046741 X054861 0.167699 0.4165882 0.344871 0.21046741 X05345_at 0.167699 0.416584 0.344871 0.21046841	571 Melanoma		0.4183255	0.345583			Small GTP-binding protein mRNA
0.1698465 0.4176918 0.345471 0.21173748 RC_AA4264 0.1697034 0.4175581 0.345457 0.2115561 0.3 at 0.1697034 0.4174145 0.345434 0.21151495 55 at 0.1691612 0.4174145 0.345403 0.21151495 55 at 0.1688578 0.417167 0.34536 0.21130994 AA043111_s 0.1688678 0.417167 0.34537 0.21130994 AA043111_s 0.1688678 0.417167 0.34536 0.21121006 7 at 0.1687387 0.4168473 0.34507 0.21037471 2 at 0.1676978 0.4166603 0.34507 0.21097471 2 at 0.1676998 0.416603 0.344823 0.21037471 2 at 0.1676999 0.4161204 0.344871 0.2104808 52 at 0.1676991 0.4161204 0.344371 0.2104808 52 at 0.1663601 0.4158745 0.344316 0.2104608 52 at 0.1658524 0.4156921 0.344064	572 Melanoma			0.345577	0.211893531	1	BRAIN NEURON CYTOPLASMIC PROTEIN 1
0.1697034 0.4175581 0.345457 0.2115561 03 at RC_AA4264 0.1692975 0.4174145 0.345434 0.21151495 55 at AA043111_s 0.1688578 0.4174145 0.345434 0.21151495 55_at AA043111_s 0.1688578 0.417167 0.34536 0.21121506 7 at D62377_ma 0.1687387 0.4168473 0.345115 0.21097471 2_at D87002_cds 0.1677827 0.4166479 0.344923 0.2101701464 12_at RC_AA4603 0.1677827 0.4166479 0.344823 0.21077015 M63959_at 0.167699 0.4161298 0.344823 0.21077015 M63959_at 0.1676976 0.4161298 0.344824 0.2104808 52_at RC_AA4861 0.1676976 0.4161298 0.344877 0.2108464 12_at RC_AA4861 0.166581 0.4161298 0.344371 0.21048081 83_at 0.166373 0.4158725 0.344371 0.21048081 83_at 0.1658624 0.4158923 0.344316 0.21018654 23_at 0.1658624 0.415892 0.344043 0.20998488 W02342_at 0.1658042 0.4156921 0.344043 0.20998488 W02333_at 0.1651086 0.4156921 0.344043 0.20998488 W02333_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.164975 0.4156928 0.2095725 M36205_at 0.164975 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.16650042 0.4156925 0.343897 0.20974827_at 0.1650042 0.4156925 0.343897 0.20974827_at 0.164975 0.4156925 0.343897 0.20974827_at 0.164975 0.4156925 0.343897 0.20974827_at 0.164975 0.4156925 0.343897 0.20974827_at 0.164975 0.4156925 0.343897 0.20974827_at 0.164975 0.4156925 0.343897 0.20974827_at 0.164975 0.4156925 0.343897 0.20974827_21 1.11000000000000000000000000000000000	573 Melanoma			0.345471	0.21173748	774	EST: zu42f03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740669 3', mRNA sequence, (from Genbank)
0.1692975 0.4174145 0.345434 0.21151495 55_at 0.1691612 0.4173892 0.345403 0.21130994 at 0.1688578 0.417167 0.345358 0.21121506 7_at 0.1687387 0.4169852 0.345307 0.21111076 t 0.1687387 0.4169852 0.345307 0.21111076 t 0.1687409 0.4168473 0.345115 0.21097471 at 0.1677827 0.4166603 0.34507 0.21091464 12_at 0.1677827 0.4165682 0.344823 0.21097471 2_at 0.1677829 0.4161298 0.344816 0.21066098 5_at 0.1676976 0.4161204 0.344871 0.21045741 XG5A456 at 0.1666581 0.41610848 0.344371 0.2104541 XG5A4861 0.1663773 0.4158745 0.344386 0.21045741 XG5345 at 0.1663605 0.4158723 0.344386 0.21045741 XG5A423 0.1657034 0.4156921 0.344041 <t< td=""><td>574 Melanoma</td><td>1-1-2</td><td></td><td>0.345457</td><td>0.2115561</td><td>264</td><td>EST: zv05g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 752790 3. mRNA sequence. (from Genbank)</td></t<>	574 Melanoma	1-1-2		0.345457	0.2115561	264	EST: zv05g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 752790 3. mRNA sequence. (from Genbank)
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0.1688578 0.417167 0.345358 0.21121506 7 at 10.0345358 0.21121506 7 at 10.034538 0.1688578 0.417167 0.345358 0.21121506 7 at 10.0345387 0.21111076 1t 10.00125 s.a 0.1687387 0.4168473 0.345115 0.21097471 2 at 10.01665409 0.4166479 0.34507 0.21097471 2 at 10.0167782 0.1677827 0.4166479 0.344923 0.21097471 2 at 10.0167782 0.4166479 0.344816 0.21083865 95 at 10.0167782 0.167699 0.4166479 0.344871 0.21083865 95 at 10.0166581 0.4161204 0.344571 0.21048081 83 at 10.0166581 0.166581 0.4161204 0.344571 0.21048081 83 at 10.0166581 0.4158745 0.21045741 X05345 at 10.0166581 0.1663773 0.4158745 0.344386 0.21045741 X05345 at 10.01658524 0.4156921 0.344043 0.20998488 W02342 at 10.0165708 0.1657034 0.4156921 0.3440641 0.20998488 W02342 at 10.0165042 0.1650042 0.20974827 at 10.0164978 0.1657034 0.4156925 0.343897 0.20998488 W02342 at 10.0164975 0.343897 0.209974827 0.41530	Molopological States			0.045400			EST: zk48b08.r1 Soares pregnant uterus NbHPU Homo sapiens
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0.1651086 0.4156921 0.344043 0.20988046 M23533 at AA033766_s 0.1650042 0.4155925 0.343897 0.20974827 at 0.164975 0.4153034 0.343593 0.20967725 M36205_at	89 Melanoma		- 1	0.344051	0.20998488	਼ੁਕ	complete cds
0.1650042 0.4155925 0.343897 0.20974827 at 0.164975 0.4153034 0.343593 0.20967725 M36205 at	390 Melanoma	1		0.344043	0.20988046		Alpha 2 adrenergic receptor gene
0.164975 0.4153034 0.343593 0.20967725 M36205 at	91 Melanoma	-		0.343897			EST: zk19b12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470975 5', mRNA sequence. (from Genbank)
	92 Melanoma	-	1	0.343593	0.20967725		SYNAPTOBREVIN 2

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					H. Leaft Carry D. Craft Lack	South Tares und The	The state of the s
59	593 Melanoma	0.1647443	0.4153034	0.343503	0.20956992	U08198_rna 1 at	Complement C8 namma subunit presureor (C8C) sons
59	594 Melanoma	0.1646106	0.4151892	0.343479	0.20952077	RC_AA4818 62_at	
59	595 Melanoma		0.1644774 0.4150965			132976 at-2	
59	596 Melanoma	0.1644774	0.4150607			L32976_at	
							EST: af88f01.s1 Soares testis NHT Homo sapiens cDNA clone 1049113 3' similar to SW:PUA1 MOUSE P28650
59.	597 Melanoma	0.1643526	0.4148867	0.34326	0.20933764	RC_AA6209	ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME
23	598 Melanoma	0.1641523	0.4147874	0.343244	0.20926857 U96922 at	U96922 at	Inositol polyphosphate 4-phosphatase two II alaba and II
59(599 Melanoma	0.1640507	0.4147636	0.343143	0.20895597	RC_AA4243 43 at	EST: zv82c10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 760146.31 mRNA sequence (from Contact)
09	600 Melanoma	0.1638886	0.4146904	0.343084	RC_AA2522	RC_AA2522	EST: zr63g05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
90	601 Melanoma	0.1633869	1 1	1	0.2088934 D79985 at	D79985 at	A cell surface protein
205	602 Melanoma	0.1632321	0.4143687	0.34296	0.20884775	RC_AA3995 92_s_at	Homo sapiens Dim1n homolog (hdim14) mDNA
99	603 Melanoma	0.1632116	0.4143323	0.342917	0.2087036 70 at	402	EST: zf05e04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 376062 31 mRNA sociations (from Control of the Control of t
90	604 Melanoma	0.163021	0.4143316	0.342914	0.20857981	AF008442_a	RNA nolymerase I cubinal
305	605 Melanoma	0.1629673	0.4139958	0.342763		AA4170 at	
90	606 Melanoma	0.1627408	0.1627408 0.4137412	0.342582	0.208364951	AA009826_a	EST: ze82b02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
202	607 Melanoma	0.1624795 0.4132887	0.4132887	0.342514	0.20828451 L39060 at		Transcription factor St 1 mRNA
3	608 Melanoma	0.1624795	0.4128082	0.342383	0.20816506 L39060 at-2	.39060 at-2	Homo sapiens transcription factor SL1 mRNA complete cds
60	609 Melanoma	0.1623464	0.4126639	0.342291	0.20805807 t	AF000545_a t	Putative purineraic receptor P2Y10 gene
9	610 Melanoma	0.1623273	0.4125285	0.342262	0.20793438 X04325 at		GJB1 Gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-Tooth neuropathy X-linked)
611	Melanoma	0.1622748	0.4125083	0.341841	RC_A 0.2077572 85_at	-	EST: af12c06.s1 Soares testis NHT Homo sapiens cDNA clone 1031434 3' similar to SW:INO1_SPIPO P42803 MYO-INOSITOL-1-PHOSPHATE SYNTHASE: mRNA sequence (from Genhank)
12	612 Melanoma	0.1620027	0.4124818	0.341782	H H 0.20772921	119570_s_a	EST: yn59b03.r1 Homo sapiens cDNA clone 172685 5' similar to contains Alu repetitive element; contains PTR5 repetitive element; (from Genhank)
13	613 Melanoma	0.1617696	0.4124554	0.341514	0.20765826 M73077 at		Glucocorticoid receptor repression factor 1 (GRE-1) mRNA

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614 Melanoma 0.1617623 615 Melanoma 0.1617525 616 Melanoma 0.16108 617 Melanoma 0.1609976 618 Melanoma 0.1609453 619 Melanoma 0.1609452	623 0.4124381 525 0.4123822		RC_AA4777	7 EST; zu34a07.s1 Soares ovary fumor NhHOT Home
0 0.0		1		ANGS SIGNO TOLION TOLION SINCE STATE TO THE SINCE STAT
0.0		22 0.341248		Clone 739860 3, mRNA sequence. (from Genbank)
0.0				
0.0	0.16108 0.4121076	76 0.341213		
-	0.1609976 0.4120706		0.2072262 X84746 at	mRNA sequence. (from Genbank)
-				FEF10 Entrangle 480 gene, exon 1
	453 0.4118742 122 0.4118303	}		nucleotide exchange profein)
-		0.040959	0.20709316	TAR RNA binding protein (TRBP) mRNA
620 Melanoma 0.1606792	792 0.4118208	8 0.340871	RC_AA0629 0.20705383 15_at	Endothalia come di
621 Melanoma 0.1592472	172 0.4116835	5 0.340782	0.20697534 106070	endourem Converting enzyme 1
622 Melanoma 0.1591439	39 0.4115713		HG862-	MIMIPZ Matrix metalloproteinase 2 (gelatinase A; collagenase type IV)
623 Melanoma 0.1589046	1			Transition Protein 2 EST: w38f12.r1 Soares fetal liver spleen 1NFI & Homo conjudents
624 Melanoma 0.1587690	3		0.200702921 AB000584_a	
-	- 1	0.340523	0.20651266 t	Prostate differentiation factor mRNA
626 Melanoma 0.1587646			0.20646665 HT2241 at	12-Linoviganasa
-	04 0.4113576	0.340412		H4 histone gene
627 Melanoma 0.1576769	39 0.4111387	0.340374	0.20623243 41 at	EST: aa65e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825822 3', mRNA sequence, (from Genhank)
628 Melanoma 0.1576515	15 0.4111219	0.340267	RC_AA0741	EST: zm76b01.s1 Stratagene neuroepithelium (#937231) Homo
		44		sapiens cDNA clone 531529 3', mRNA sequence. (from Genbank)
629 Melanoma 0.1573105	5 0.4111149	0.34025	0.20612557 09 at	RC_AA2232 EST: zr06c11.s1 Stratagene NT2 neuronal precursor 937230 Homo
630 Melanoma 0.157262	0.1572623 0.4109894	0.340224	X68733_ma 0.206067771_at	The section of the court of the section of the sect
631 Melanoma 0.1569663	3 0.4109894	700760	896	Alpha1-antichymotrypsin, exon 1
632 Melanoma 0.155695		0.340111	0.20581071 M68864 at	Eukaryotic translation initiation factor 3, subunit 4 (delta, 44kD)
633 Melanoma 0.155559	9 0.4109672	0.34008	479	EST: zw82g03.s1 Soares testis NHT Homo sapiens cDNA clone
634 Melanoma 0.1553542	0.4109068	0.34006	44534	EST: 2x45b04.s1 Soares testis NHT Homo sapiens cDNA clone

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63_at IMAGE:814083 3', mRNA sequence. (from Genbank)	KIAA0367 gene, partial cds	EST: zd52b01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344233 5', mRNA sequence. (from Genbank)	EST: zv35h07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755677 3' similar to contains element MSR1 repetitive element mRNA sequence. (from Genbank)	EST: EST95571 Testis I Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)	AA129547_a EST: zn83f01.r1 Stratagene lung carcinoma 937218 Homo sapiens t	EST: zk85c01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489600 3', mRNA sequence. (from Genbank)	EST: zi06h12.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 430055 3', mRNA sequence. (from Genbank)	PLP Proteolipid protein (Pelizaeus-Merzbacher disease, spastic paraplegia 2, uncomplicated)	Homo sapiens clone 638 unknown mRNA, complete sequence	I kappa B epsilon (IkBe) mRNA	GARS Glycyl-tRNA synthetase	EST: zn94d01.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 565825 3', mRNA sequence. (from Genbank)	EST: zm58d10.s1 Stratagene fibroblast (#937212) Homo sapiens cDNA clone 529843 3', mRNA sequence. (from Genbank)	EST: aa55a10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824826 3', mRNA sequence. (from Genbank)	EST: zm95f07.s1 Stratagene colon HT29 (#937221) Homo sapiens cDNA clone 545701 3', mRNA sequence. (from Genbank)	Clone N9 Rep-8 mRNA	Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA
63_at	AB002365_a t	W70167 at	RC_AA4107	RC_AA3823 72_s_at	AA129547_a t	A0993	RC_AA0341 89_at	M54927_at	RC_AA4530 22_at	U91616_at	U09587_at	RC_AA1372 69_s_at	RC_AA0710 75_at	RC_AA4888 43_at	RC_AA0789 32_at	D83767_at	AF006084_a t
0.20553188 63_at	0.20548458 t	0.20540215 W70167	0.2053735114	0.20514625 72_s	0.205143361	RC_A 0.2049741 57_at	RC_A 0.2049223 89_at	0.20484224 M54927	RC_A 0.20469436 22_at	0.20461649 U91616	0.2045588 U09587	RC_AA1 0.20444237 69_s_at	RC_A 0.2044160275_at	RC_A 0.2043104 43_at	RC_A 0.20423162 32_at	0.204171 D83767	0.20403653
0.340005	0.33995	0.339807	0.339741	0.339573	0.339345	0.33934	0.339228	0.33915	0.339068	0.338861	0.338812	0.338722	0.338556	0.338542	0.338509	0.338479	0.338396
0.4108117	0.4105207	0.4103411	0.410048	0.4099736	0.4099084	0.4097418	0.4096412	0.4095921	0.4095879	0.4094783	0.4093291	0.4092308	0.4090834	0.4089777	0.4088474	0.408763	0.4086798
0.1552873	0.1547989	0.1543463	0.154187	0.1540165	0.1540105 0.4099084	0.1539971	0.1539887	0.1537932	0.1535034	0.1534117	0.1533542	0.1526722	0.1525199	0.152433	0.1524173	0.1523878	0.152278
635 Melanoma	636 Melanoma	637 Melanoma	638 Melanoma	639 Melanoma	640 Melanoma	641 Melanoma	642 Melanoma	643 Melanoma	644 Melanoma	645 Melanoma	646 Melanoma	647 Melanoma	648 Melanoma	649 Melanoma	650 Melanoma	651 Melanoma	652 Melanoma

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Docke	t No.:	2825.2	2020	-002		
Title:	Genet	ic Mark	ers f	or Tur	nors	
Invent	ors: Sri	dhar Ra	mas	wamy	, et al	•
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					HG2260-	
į.	-			1	HT2349_s_a	
65	653 Melanoma	-	9	0.338295	0.20395334 t	Duchenne Muscular Dystrophy Protein (Dmd)
654	654 Melanoma	0.1514909	0.408477	0.338285	0.20381165 U43368_at	Vascular endothelial growth factor B
i C		-		1	AA490685_a	
ဂ္ဂိ	655 Melanoma	0.1511821	0.4084748	0.338251	0.203758t	823853 5', mRNA sequence. (from Genbank)
929	656 Melanoma	0.1510878	0.4083822	0.338197	0.20361517 91 at	EST: ag28h10.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1090915 3', mRNA sequence. (from Genbank)
		-			RC_AA1328	.1
657	657 Melanoma	0.1510479	0.4083098	0.338146	0.20346221 74_at	clone 587356 3', mRNA sequence. (from Genbank)
1		-			Y08374 rna	GP-39 cartilage protein gene extracted from H.sapiens gene encoding
929	658 Melanoma	0.1508188	0.4082077	0.337873	0.20339692 1_at	
1		-			AA094752_a	
309	659 Melanoma	-	- 1	0.337746	0.203314 t	(calcineurin A beta)
099	660 Melanoma	-	0.4080437	0.337705	0.20326771 U32907 at	P37NB mRNA
661	661 Melanoma	0.1502544	0.4080264	0.337628	0.20314482 X02956 f at	Interferon, alpha 5
						EST: yi53g09.r1 Homo sapiens cDNA clone 143008 5' similar to ob: M15182 BETA-GI IICI IRONIDASE PRECIIESOR (HI IMAN):
662	662 Melanoma	0.1497564	0.4080111	0.337543	0.20310876 R71205 at	(from Genbank)
663	663 Melanoma	0.1496204	0.4079685	0.337524	0.20306845 M27826 at	Endogenous retroviral professe mRNA
					The state of the s	
664	664 Melanoma	0.1495073	0.4079287	0.337434	0.20297052 37 at	EST: zh92b04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 428719 3'. mRNA sequence. (from Genbank)
					U51003_s_a	
665	665 Melanoma	0.1492769	0.4079234	0.337403	0.2028724 t	DLX-2 (DLX-2) gene
999	666 Melanoma	0.1488662	0.4079145	0.33738	X83301_s_a 0.202829881t	SMA5 mRNA
687	687 Molandan	0 440744		000200	RC_AA4259	
5	Micial IOI Ia	0.1407 14	0.4070024	0.33/323	0.202/35/4 21 at	Homo sapiens I-1 receptor candidate protein mRNA, complete cds
668	668 Melanoma	0.1486256	0.4078138	0.337294	0.20268215 1 at	Pigment enitheli m-derived factor gene
699	669 Melanoma	0.1485013	0.4077911	0.337225	0.20255241t	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(2) ALPHA CHAIN PRECLIRSOR
670	670 Melanoma	0.1484353	0.4077572	0.337045	HG491- 0.20247227 HT491 at	Fc Receptor lib3 For Iqa, Low Affinity
67.1	671 Melanoma	0 1484263	0.4076456	0.337014	RC_AA2232	-
672	672 Melanoma	-	0.1484085 0.4076387	0.336911		
		-	100010110	1100000	0.505.50	o, Illings acquerice. (noin cermann)

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Inventors: Sridhar Ramaswamy, et al.

674 Melanoma	0.1014.0	00101010	20000	くころで	D 70	
aligina	7000777	1	0 000000	0777770000		containing the Hrrivi gene
	0.1478334	0.4076123	0.336633	0.20211/49 U52682		IRF4 Interferon regulatory factor 4
					M91368_s_a	
675 Melanoma	0.1476832		0.33649	0.20209406 t		Na+/Ca+ exchanger (CNC) mRNA
676 Melanoma	0.1473922	- 1	0.336459	0.20196345 D79998	D79998_at	KIAA0176 gene, partial cds
677 Melanoma	0.1473374	0.4074722	0.336459	0.20180266 D50914	D50914_at	KIAA0124 gene, partial cds
678 Melanoma	0.1472847	0.1472847 0.4074695	0.336384	0.2017409 U48263	U48263 at-2	Prepronociceptin
679 Melanoma	0.1472847	0.4074688	0.33634	0.2016399 U48263	U48263 at	Pre-pro-orphanin FQ (OFQ) mRNA
680 Melanoma	0.1469678	0.4073905	0.336294	0.20150504	W26785 i a t	EST: 15d6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA mRNA sequence (from Genhank)
681 Melanoma	0.1468993	0.4073892	0.336226	0.20146188	W26649 at	Zinc finger protein 140 (clone pHZ-39)
amoue	0.1464878		0 336340	0.004.004.00	M26657_s_a	M26657_s_a DCP1 Dipeptidyl carboxypeptidase 1 (angiotensin I converting
	0 4 4 5 0 4 2 5		1000000	0.50103498	X87871_s_a	enzynie)
andia	0.1409100	- 1	0.336085	0.20130838		HEPATOCYTE NUCLEAR FACTOR 4
684 Melanoma	0.145714	0.4070824	0.335956	0.20123917	RC_AA4856 97 at	EST: ab10e09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone 840424 3', mRNA sequence. (from Genbank)
Melanoma	0.145382	0.4069882	0.335821	0.20112543	D21163 at	KIAA0031 gene
686 Melanoma	0.1452742	0.4069247	0.335812	0.20097478	AA282300_a t	SET binding factor 1
687 Melanoma	0.1451272	0.4069037	0.33571	0.20092842	RC_AA1672 73 at	KJAA0468 gene product
688 Melanoma	0.1438857	0.4067208	0.335663	0.20086873	A1222	EST: zn83a11.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 564764 3', mRNA sequence. (from Genbank)
689 Melanoma	0.1438632	0.4066826	0.335424	0.20080958	RC_AA2830 74_at	Homo sapiens mRNA for KIAA0819 protein, partial cds
anoma	0.1437447		0.335398	7007006 0	222260 at	EST: yh26c06.r1 Homo sapiens cDNA clone 130858 5'. (from
691 Melanoma	0.1434109		0.335242	0.20068964	X87838 at	CTNNB1 Catenin (cadherin-associated profein) heta 1 (88kD)
692 Melanoma	0.1428416	0.406521	0.335207	0.20061766		EST: Human fetal brain cDNA 3'-end GEN-020E05, mRNA sequence. (from Genbank)
693 Melanoma	0.1427493	0.4064244	0.334989	0.2005153		EST: aa52g12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824614 3' similar to TR:G1293732 G1293732 O3625P.;, mRNA sequence. (from Genbank)
694 Melanoma	0.1425003	0.4064232	0.334703	0.20040062	_AA2823 at	EST: zt12g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712964 3, mRNA sequence, (from Genhank)
	680 Melanoma 682 Melanoma 683 Melanoma 684 Melanoma 685 Melanoma 686 Melanoma 689 Melanoma 690 Melanoma 691 Melanoma 691 Melanoma 693 Melanoma		0.1469678 0.1468993 0.1464878 0.1459135 0.145382 0.1451272 0.1438857 0.1437447 0.1437447 0.1437493 0.1427493	0.1469678 0.4073905 0.1468993 0.4073892 0.1464878 0.4073837 0.145714 0.4070824 0.145714 0.4069247 0.1452742 0.4069247 0.1451272 0.4069237 0.1438857 0.4066226 0.1438417 0.4066334 0.1428416 0.406521 0.1427493 0.4064244 0.1427493 0.4064232	0.1469678 0.4073905 0.336294 0.20150504 0.1468993 0.4073892 0.336226 0.20146188 0.1464878 0.4073837 0.336218 0.20139492 0.145714 0.4070824 0.335956 0.20123917 0.145742 0.4069882 0.335821 0.200112543 0.145742 0.4069247 0.335812 0.20097478 0.1451272 0.4069037 0.335812 0.20092842 0.1438857 0.4066826 0.335663 0.20069058 0.1437447 0.4066334 0.335342 0.20060968 0.14374109 0.406521 0.335242 0.200609664 0.1428416 0.406521 0.335207 0.20061766 0.1427493 0.4064232 0.334703 0.20040062	0.1469678 0.4073905 0.336294 0.20150504 to 0.14688 W26649 at 0.1468893 0.4073892 0.336226 0.20146188 W26649 at 0.1464878 W26657_s_a 0.1464878 0.4073837 0.336218 0.20139492 to 0.146657_s_a X87871_s_a 0.1459135 0.4070824 0.336956 0.2013947 RC_AA4856 0.145382 0.4069882 0.335821 0.20123917 97_at 0.1452742 0.4069824 0.335821 0.20123917 97_at 0.1451272 0.4069037 0.335812 0.20123917 RC_AA4856 0.1451272 0.4069037 0.33571 0.20092842 73_at 0.1438632 0.4066826 0.335424 0.20086873 74_at 0.1437447 0.4066334 0.335242 0.20069864 X87838 at 0.1428416 0.406521 0.335242 0.20069864 X87838 at 0.1428416 0.4064244 0.335207 0.20061766 i at 0.1428003 0.4064244 0.334703 0.20040062 47_at

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90_at clone 810826 3', mRNA sequence. (from Genbank)	EST: 56a9 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)	DNA polymerase delta small subunit mRNA	AND THE RESIDENCE OF THE PROPERTY OF THE PROPE	SCO1 (yeast homolog) cytochrome oxidase deficient 1	EST: zw54g08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 773918 3', mRNA sequence. (from Genbank)	GLUTAMATE RECEPTOR 3 PRECURSOR	Glutamate receptor, ionotrophic, AMPA 3	AA249119_a Ec0276.seq.F Human fetal heart, Lambda ZAP Express Homo	sapiens cDNA 5', mRNA sequence. (from Genbank)	EST: zu36b12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	cione 740065 3, INKNA sequence. (Irom Genbank)		GFBP3 Insulin-like growth factor binding protein 5	ACTH-R gene for adrenocorticotropic hormone receptor	0.19927162 D25216_at-2 KIAA0014 gene product	KIAA0014 gene	Human Bcl-2 binding component 3 (bbc3) mRNA, partial cds	Bcl-2 binding component 3 (bbc3) mRNA, partial cds	FUSE binding protein 2 (FBP2) mRNA, partial cds	DAX-1		GLUT1 C-terminal binding protein	EST: EST93352 Supt cells Homo sapiens cDNA 5' end, mRNA	sequence, (from Genbank)	EST: zv34e11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755564 3' similar to SW:PTN2 RAT P35233 PROTEIN-	TYROSINE PHOSPHATASE PTP-S;, mRNA sequence. (from	Genbank)	a EST: zl39g07.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA	Homo sapiens mRNA for H-2K binding factor-2 complete cds	H2K binding factor 2 (KBF2) mRNA	JTV-1 (JTV-1) mRNA
90_at	W29077_at	U21090_at	RC_AA0530		280		X82068_at	at-2	AA249119_a		44790	9	M62/82_s_a			D25216_at-2	D25216_at	at-2	at	U69126_s_a t		RC_AA1499	40_at	A380393_a			RC_AA4190		A151565_	08904 at-2		
0.20033479 90_at	0.20028089 W29077	0.20019725 U21090		0.20009515 21_at		0.19998549 28 s_at	0.19985531 X82068_at	0.19978759 X82068		0.19970787	RC_A 0.10062082 40_24	0.13902903	0.40065547	0.19352247	0.19936337 X65633_at	0.19927162	0.19921839 D25216_at	0.19914496 U82987	0.19906245 U82987	0.19902317tt	0.19881782 S74720_at		0.1988162 40_at	000000000000000000000000000000000000000	0.130049001			0.19858003 26_at	0.108/7052	0.19839214	0.19835356 108904	0.19828278 U24169 at
0.334687	0.334643	0.334624		0.334575		0.334357	0.334299	0.334247		0.334091	0.224043	0.554045	0007660	0.334009	0.333869	0.333742	0.333664	0.333527	0.333491	0.333482	0.333367		0.333314	000000	0.333239			0.333196	0 333469	0.332925	0.332891	0.332886
0.4064048	0.4063966	0.4062741	the same of the sa	0.4062607		0.4062389	0.4061989	0.4060484		0.4058664	0.4056443	0.4000140	0 4050040	0.4030043	0.4055601	0.4054221	0.4051966	0.4049565	0.4049431	0.4048721	0.4045708		0.4044474	000000000000000000000000000000000000000	0.4040588			0.4041789	0.4041316	0.404078	0.4040715	0.4039998
0.1420614	0.1418886	0.1418705		0.141763		0.1415603	0.1415497	0.1415497		0.1415045	0 4/12/78	0.1413470	0 444047	0.14124/	0.1412253	0.1409109	0.1409109	0.140788	0.140788	0.1407813	0.1407781		0.1397577	0 4306766	0.1330100			0.1395071	0 1394334	0.1393092	0.1393092	0.1389471
695 Melanoma	696 Melanoma	697 Melanoma		698 Melanoma		-	-	701 Melanoma		702 Melanoma	703 Moleness	No Meial Olica	704 Malonomo	O4 INICIALIDITIA	705 Melanoma	706 Melanoma	707 Melanoma	708 Melanoma	709 Melanoma	710 Melanoma	711 Melanoma		712 Melanoma	Molopopus	7 13 INIGIALIOLEIA			714 Melanoma	715 Melanoma	716 Melanoma	1	1

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Mela	719 Melanoma	0.1389367	0.4039849	0.332814	0.19818299 S79281_at	S79281_at	Pancreatic ribonuclease [human, mRNA Recombinant Partial, 491 nt]
Mela	720 Melanoma	0.1388918	0.4039556	0.332785	RC_A 0.19809368 89_at	A2165	EST: zq94e07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 649668 3', mRNA sequence. (from Genbank)
						AB002319_a	
Mela	+	0.1385533		0.332781	0.19797772 t	ţ	Human mRNA for KIAA0321 gene, partial cds. (from Genbank)
Mela	722 Melanoma	0.1385215	0.4034226	0.332677	0.19790241 D61391	D61391_at	Phosphoribosypyrophosphate synthetase-associated protein 39
Mela	723 Melanoma	0.1383693	0.4033905	0.332582	0.1977957 HT273_at		Lymphocyte Antigen Hla-G3
						M91490_s_a	
Mela	724 Melanoma	0.1383447	0.4033891	0.332252	0.19775091		EST: HUMRTPGEAI Homo sapiens cDNA. (from Genbank)
Mela	725 Melanoma	0.1383432	0.4032182	0.332065	RC_AA2 0.19764198 55 s at	364	EST: zr75g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669266 31, mRNA sequence. (from Genbank)
00	000	120004E	1	COOCCO O		AA156838_a	Li mora timora timora timora (TECADA) m DNA
Mela	/ Zo Melanoma	0.1382843	0.4031147	0.332032	0.19/302/4	1	Human tumor susceptionty protein (136101) mixiva, complete cas
Mela	727 Melanoma	0.1381723	0.4029766	0.331914	RC 0.19750789169	RC_AA2817 69 s at	Human Hoast (HPAST) mRNA. complete cds
						AA4221	EST: zv28g12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
Mela	728 Melanoma	0.1377631	0.4029068	0.33181	0.19745281 46_at		clone 755014 3', mRNA sequence. (from Genbank)
Mela	729 Melanoma	0.1370225	0.4028711	0.331769	0.19739631 X51985	X51985_at	LAG3 Lymphocyte-activation gene 3
							Mitochondrial intermediate peptidase precursor (MIPEP) mRNA,
Mela	730 Melanoma	0.1368334	0.4026319	0.331713	0.19722208 U80034	U80034_at	mitochondrial gene encoding mitochondrial protein
							PAX3 Paired box homeotic gene 3 (Waardenburg syndrome
Mela	731 Melanoma	0.1367962	0.4022857	0.331674	0.19718078 S69369	S69369_at	1){alternative products}]
		1		700	0		EST: yh91b09.r1 Homo sapiens cDNA clone 137081 5'. (from
Mela	/ 32 Melanoma	0.1305472	0.4022035	0.33/1506	0.19/10423 R36221	K36221_at	Genbank)
		1		1		RC_AA1612	
Mela		0.1303534	0.4022202	0.331477	0.19/0121992	92 s at	Interieron, alpha-inducible protein 27
Mela	734 Melanoma	0.1361048	0.1361048 0.4021548	0.331383	0.19690977 L11931 at	L11931_at	SHMT1 Serine hydroxymethyltransferase 1 (soluble)
-		100001		0000	1	RC_AA4 107	
Mela	/35 Melanoma	0.1359024	0.4021312	0.331206	0.196/9315 23 at	23 at	KIAAU446 gene product
						RC AA4217	Homo sapiens NADH:ubiquinone dehydrogenase 51 kDa subunit (NDUFV1) mRNA, nuclear gene encoding mitochondrial protein.
Mela	736 Melanoma	0.1357039	0.4020033	0.331204	0.1967593 81_at	81_at	complete cds
Mela	737 Melanoma	0.1352835	0.4019288	0.331166	0.19663438 X66358 at	X66358 at	mRNA KKIALRE for serine/threonine protein kinase
						RC AA4551	EST: aa15g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
Mela	738 Melanoma	0.135255	0.4019068	0.330972	0.19660686 81	at	813366 3', mRNA sequence. (from Genbank)
(C)		0.425002		0000000	0.40846664	A4900	EST: ab05d09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
Mela	/ 39 Meianoma	0.135093	0.4017475	0.330933	U.19040004 09 at	oy at	Gione 839921 3, mikiva sequence. (Ironi Genbank)

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RC_AA1286 EST: 2l15d10.s1 Soares pregnant uterus NbHPU Homo sapiens 17_at cDNA clone 502003 3', mRNA sequence. (from Genbank)	PTPRM Protein tyrosine phosphatase, receptor type, mu polypeptide	EST: HUMGS0008169, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)	EST: ae49b03.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950189 3", mRNA sequence, (from Genbank)	Homo sapiens mRNA for putative Sqv-7-like protein, partial	ATP-binding cassette protein (ABC2) mRNA HFBCD04 clone, partial cds	Oncodene Tis/Chop Flision Activated	HUMMLC2At; Homo sapiens; ; 593 base-pairs	Murine leukemia viral (bmi-1) oncogene homolog	EST: zx79c12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809974.5' mRNA sequence (from Genhank)	EST: zx44g07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 789372 3', mRNA sequence. (from Genbank)	Homo sapiens casein kinase I gamma 2 mRNA, complete cds	EST: zu63c08.r1 Soares testis NHT Homo sapiens cDNA clone 742670 5' mRNA segrence (from Genhank)	TAL1 (SCL) interrupting locus	EST: zs91h04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:704887 3', mRNA sequence. (from Genbank)	EST: aa68h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826151 3', mRNA sequence. (from Genbank)	EST: zr30c03.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664900 3', mRNA sequence. (from Genbank)	OPRD1 Opioid receptor, delta 1	EST: zw52e11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773708 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)
RC_AA1286 17_at	X58288_at	C00627_at	RC_AA5986 95 at		U18235 at	HG2724- HT2820 at	M94547 at	AA478194_a t	AA454908_s	1	47_at	RC_AA2808 40_at	AA401510_s	RC_AA1948 81_at	RC_AA2830	66_at	RC_AA5213 54_at	RC_AA2334 59 at	U07882 at	RC_AA4339 30_at
RC 0.19458172 17	0.19442078 X58288	0.1943254 C00627	RC 0.19422564 95	0.19409238	0.19403484 U18235	HG2724 0.19392638 HT2820	0.19384022 M94547	0.19378556	0.19373389		0.19370347 47	RC_A 0.1935958 40_at	0 19354512	0.19347076 81	The state of the s	0.1933746 66	RC 0.19328494 54_	RC 0.19322516 59	0.19316153 U07882	RC 0.19307594 30
0.328998	0.32898	0.328919	0.328745	0.328637	0.328586	0.328516	0.328442	0.328427	0.328336		0.328332	0.328254	0.328226	0.32818		0.328031	0.328001	0.32782	0.327724	0.327698
0.3997881	0.3997402	0.3996834	0.3995092		0.399214	0.3991802	0.3990843	0.3988671	0.398865		0.3988339	0.3987913	0.3987612	1	1	0.3986388	0.3985798	0.3985745	0.3985241	0.3984626
0.1296622	0.1295995	0.1293769	0.1290219	0.128814	0.1286864	0.1285017	0.1281797	0.1280772	0.1279452		0.1279317	0.1278742	0.1277539	0.1275922		0.127352	0.1270126	0.1268752	0.1268664	0.1262611 0.3984626
762 Melanoma	763 Melanoma	764 Melanoma	765 Melanoma	766 Melanoma	767 Melanoma	768 Melanoma	769 Melanoma	770 Melanoma	Melanoma		772 Melanoma	773 Melanoma	774 Melanoma	775 Melanoma		776 Melanoma	777 Melanoma	778 Mefanoma	779 Melanoma	780 Melanoma
762	763	764	765	99/	767	768	769	770	777		772	773	774	775		776	777	778	779	780

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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Colored Broad Br		1.1257661		0		R57419_s_6	EST: F3059 Fetal heart Homo sapiens cDNA clone F3059 5' end, mRNA sequence. (from Genbank)
0.3982446	-	.1257356	Î	0		RC_AA4656 3 94_r_at	
B		1255551				RC_AA2434	
8 0.3981143 0.327393 0.19271116 Total 4 0.3980862 0.327347 0.19260463 at 1 0.3979709 0.327339 0.1925554 M77810 at 1 0.3979473 0.327233 0.19243136 M20030 f at at 1 0.3979473 0.326952 0.19225538 K03430 at RC_AA2813 1 0.3978472 0.326522 0.19215532 RC_AA2813 RC_AA4114 2 0.3977305 0.326534 0.1920443 0.44114 at 2 0.3976594 0.326343 0.1920443 RC_AA4114 at 0.3976594 0.326341 0.19201964 at at 0.3977445 0.326321 0.19201964 at at 0.39774658 0.326321 0.19192186 ll.12 p40 at 0.397364 0.326192 0.19174205 X92762 at 0.3972339 0.326192 0.1915767 M34516 at	-	1254365	ſ			RC_AA1761 64 i at	
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3 0.3979473 0.327233 0.19243136 M20030 f at at at at at at at at at at at at at	0		0.3980862	0.327347		L19686_rna1 at	Macrophage migration inhibitory factor (MIF) gene
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1 0.3978472 0.326801 0.19225538 KO3430 at 2 0.3977416 0.326696 0.19215532 37 at 2 0.3977305 0.326522 0.19209646 HT1067 r at 3 0.3976594 0.326434 0.1920443 00 at 0.3976594 0.326375 0.1920443 00 at 0.3974744 0.326375 0.19201964 04 at 0.3974658 0.326321 0.19192186 IL12 P40 at 0.3973614 0.326193 0.19174205 X92762 at 0 0.3972339 0.326192 0.19157267 M34516 r at 0		1244471	0.3979473	0.327233	0.19243136	M20030 f at X99268 at	0.19243136 M20030 f at Small proline rich protein (sprII) mRNA, clone 930 0.19236399 X99268 at B-HLH DNA hinding protein
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0.3976594 0.326434 0.3975432 0.326375 0.3974744 0.326321 0.3974658 0.326321 0.3973614 0.326192	92 Melanoma 0.1.		3.3977305	0.326522	0.19209646	HG1067- HT1067 r at	Mucin (Gb:M22406)
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0 397244 0 226476		- 1		0.326192	0.19157267 N	/34516 r at C	Jmena light chain protein 44.4 (2.1)
0.320110 0.19155142	9 Melanoma 0.12		0.397211	0.326176	0.19155142 31 at	C AA6211 F	RC_AA6211 EST: af61a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 11 at 1046480 3', mRNA sequence, (from Genhank)

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RC_AA2370 EST: zs01c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 17 at IMAGE:683922 3', mRNA sequence. (from Genbank)	KIAA0469 gene product	DS-1 mRNA	EST: 18d8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)	EST: zh81d12.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	contact the 427703 similar to contains Alu repetitive element;, mRNA sequence, (from Genbank)	HSST Heparan sulfate-N-deacetylase/N-sulfotransferase	PLAT Plasminogen activator, tissue type (t-PA)	PTGIR Prostaglandin I2 (prostacyclin) receptor (IP)	Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	EST: zi08f07.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	cDNA clone 430213 3", mRNA sequence. (from Genbank)	EST: zw06a06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 768466 3' mRNA sequence (from Cenhank)		PRKAR1B Protein Kinase, cAMP-dependent, regulatory, type I, beta	Omega light chain protein 14.1 (lg lambda chain related) gene, exon	RC_AA4165 EST: zu05b09.s1 Soares testis NHT Homo sapiens cDNA clone	130937 3, INKINA Sequence. (Ifom Genbank) EST: 765641 11 Source roting NOb4 UD Home continue about along	231836 5', mRNA sequence. (from Genbank)	Guanine nucleotide exchange factor mss4 mRNA	PEBP2aC1 acute myeloid leukaemia mRNA	DbpB-like protein mRNA			Iranscription Factor Itt-1	EST: ZITTCOZ:ST Soares NNHMPU ST Homo sapiens cDNA clone 668834 3' similar to TR:G969170 G969170 PX19 MRNA sequence.	(from Genbank)	EST: yr36a04.r1 Homo sapiens cDNA clone 207342 5' similar to contains Alu repetitive element: (from Genbank)	NECDIN related protein mRNA
RC_AA2370 17_at	RC_AA1561 18_at	X81788_at	W26054_at	DC AA0018	86 at	U18932 at	K03021 at	D38128_at	RC_AA6096 72_at	RC AA0102	11_at	RC_AA4959 50_at		Mosupo at	M34516_at	RC_AA4165		_at	U74324 at	Z35278_at	U04810_at	HG2591-	HT2687_s_a		RC_AA2629	f_at	ä	at
RC 0.19150853 17	0.19125849 18	0.19119929 X81788	0.19109996 W26054		0.1910341886	0.19096377 U18932	0.19090624 K03021	0.19078447 D38128 at	RC_A 0.19074327 72_at		0.19061303 11_at	RC_A 0.19055262 50_at	0 40045744	0.190437 14 IM05000	0.19040914 M34516_at	0.10032752 38	0.13032133	0.19026989	0.19017744 U74324 at	0.19004424 Z35278	0.18987063 U04810		19001060	0.10901000		0.1896937 69	0.18957858 H58818	0.1895497 U35139
0.326107	0	0.32602	0.325959		0.325929	0.325604	0.325445	0.325411	0.325351		0.325331	0.325195	7 200 0	0.020109	0.325065	0 324964	1004.70.0	0.32494	0.324906	0.324834	0.324689		0 324684	0.324004		0.324663	0.324602	0.324567
0.3972036	0.3969826	0.3969459	0.3968384		0.3967301	0.3965745	0.3964731	0.3964352	0.3964336		0.3963173	0.3962691	0.3061207	0.3301307	0.3961369	0.3960993	0.000000	0.3960033	0.3958509	0.3958509	0.3956665		0 3955/102	0.0000402		0.3953739	0.3952682	0.3952252
0.1212943	0.1210167	0.1209745	0.1206663		0.1204253	0.1203127	0.1195421	0.1194001	0.1191858		0.1191147	0.1190739	0.4480652	0.1100002	0.1185296	0 1184965	0001	0.1184959	0.1179602	0.1177455	0.1172975		0 1160099	0.000	**************************************	0.1153999	0.1150892	0.1146236
800 Melanoma	801 Melanoma	802 Melanoma	803 Melanoma		804 Melanoma	805 Melanoma	806 Melanoma	807 Melanoma	808 Melanoma		809 Melanoma	810 Melanoma	Melonomo		812 Melanoma	813 Melanoma		814 Melanoma	815 Melanoma		Melanoma		818 Melanoma			819 Melanoma		821 Melanoma
800	801	802	803		804	805	806	807	808		608	810	24		812	813	2	814	815	816	817		818	2	******	819	820	821

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RC_AA2326 EST: zr75d05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 86_i_at 669225 3', mRNA sequence. (from Genbank)	Unknown gene extracted from Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene,	receptor for advanced glycosylation end products (RAGE) gene, and 6 unidentified cds. complete sequence	EST: aa59e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	RC A43985 EST: zt70a05.s1 Soares testis NHT Homo sapiens cDNA clone	727664 3', mRNA sequence. (from Genbank)	EST: yf24f04.r1 Homo sapiens cDNA clone 127807 5' (from	Genbank)	EST: zs85g09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704320 3', mRNA sequence. (from Genbank)	AA485038_a Aa41g01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:815856 5', mRNA sequence. (from Genbank)	RC_AA1005 EST: zn46g09.s1 Stratagene HeLa cell s3 937216 Homo sapiens	cDNA clone 550528 3', mRNA sequence. (from Genbank)	RC_AA4872 EST: ab19g10.s1 Stratagene lung (#937210) Homo sapiens cDNA 18 at clone 841314 3', mRNA sequence. (from Genbank)	EST: af62h11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	1046661 3', mRNA sequence. (from Genbank)	AA047045 a 380375 5' similar to contains Alu repetitive element: mRNA	sequence. (from Genbank)	RC_AA4440 EST: zv45f09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 756617 3', mRNA sequence. (from Genbank)	EST: yi71h07.r1 Homo sapiens cDNA clone 144733 5'. (from Genbank)		Homo sapiens mRNA for dTDP-D-glucose 4,6-dehydratase	SPRR1B Small proline-rich protein 1B (cornifin)	0.18845952 U77845 at-2 Human hTRIP (hTRIP) mRNA, complete cds	HTRIP (hTRIP) mRNA	0.18826305 K03183 f at Chorionic conadotronin hata subunit cana	RXRA Retinoid X recentor alpha	0.18806313 X52773_at-2 Retinoid X receptor, alpha
0.18949603 86_i_at		89336_cds at	AA5041	RC AA3985	78 96_at		0.18927787 R08723_at	_AA2794 at	AA485038_a	61 t	RC_AA1005	179 21_at	RC_AA4872 0.18906522 18_at	RC_AA6215	0.18899734 00_at	AA047045 a		RC_AA4440		R76185_s_a t		.72 42_at	0.1885513 M19888 at)52 U77845 at-2	0.18834326 U77845_at	105 K03183 f at	0.18815212 X52773 at	113 X52773 at-2
0.189496		0.18944205 7	0 18037255 46	0.100	0.1893278 96		0.189277	RC 0.18921457 67		0.18918161 t		0.1891167921	0.189065		0.188997		0.18892995		0.188826	0.18870665		0.18864472 42	0.18855	0,188459	0.188343	0.188263	0.188152	0.188063
0.32453		0.324448	0.32444	0.0	0.32436		0.3243	0.32426		0.324224		0.324123	0.324123		0.324104		0.324036		0.323892	0.323837	1 0	0.323805	0.323711	0.323658	0.323536	0 32347	0.323387	0.323368
0.395089		0.3950616	0.3050544		0.3949163		0.3949138	0.3949101	Į.	0,3948787		0.3948531	0.3948292		0.3948292		0.3948282		0.3946242	0.3944597			0.3942312	0.3941664	0.3937046	0.3937046	0.3936746	0.3935966
0.1141343		0.1140791	0.1130370	200	0.1134549		0.113358	0.1132343		0.1131499		0.1124555	0.1123063		0.1122078		0.1120003		0.11142	0.1111291		0.1110274	0.1106474	0.1106379	0.1106379	0.4404998	0.1104912	0.1104912
822 Melanoma		823 Melanoma	824 Melanoma	2	825 Melanoma		826 Melanoma	827 Melanoma		828 Melanoma		829 Melanoma	830 Melanoma		Melanoma	11.1	832 Melanoma		833 Melanoma	834 Melanoma		835 Melanoma	836 Melanoma	837 Melanoma	838 Melanoma	839 Melanoma	840 Melanoma	Melanoma
822		823	824	5	825		826	827		828		829	830		831		832		833	834	L	335	836	837	838	839	840	841

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors

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EST: zd30c02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342146.5' mRNA sequence (from Ganhank)	EST: zt86e06.s1 Soares testis NHT Homo sapiens cDNA clone 729250 3', mRNA sequence. (from Genbank)	EST: yw97f08.r1 Homo sapiens cDNA clone 260199 5'. (from Genbank)	EST: zw37h03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 772277.3' mRNA sequence (from Genhank)	EST: ze83a02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	Phospholipase A2, group X	0.18749177 L27671 s at Intercellular adhesion molecule 4. Landsteiner-Wiener blood groun	RC_AA0195 EST: ze55b02.s1 Soares retina N2b4HR Homo sapiens cDNA clone 362859 3', mRNA sequence. (from Genbank)	EST: ae49a02.s1 Stratagene lung carcinoma 937218 Homo sapiens	EST: zs42g06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	08/898 3, mKNA sequence, (from Genbank)	NGFB Nerve growth factor beta SKI V-ski avian carroma viral oncount homological	STAT induced STAT inhibitor 2	EST: zw30e10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	Profilegarin	AA136369_a EST: zk93d06.r1 Soares pregnant uterus NbHPU Homo sapiens	The section of the section (not deliberty)	Osteopontin gene	Z78285 Homo sapiens brain fetus Homo sapiens cDNA clone 1A7, mRNA sequence	CCND1 Cyclin D1 (PRAD1: parathyroid adenomatosis 1)	VAI VI TRNA SYNTHETASE	Unknown product	Protein phosphatase-1 inhibitor mRNA
0.18797132 W60965 at	RC_AA3989 37_at	N45402 at	RC_AA4045 43_at	RC_AA0095	U95301_at	L27671 s at	RC_AA0195 28_at	RC_AA5986 84 s at	2358	VEDENO ST	A52599 at U73377 at	RC_AA2922	AA4276	1	AA136369_a	20758_rna	at	0.18663722 Z78285 f at		X59303_s_a	1	
0.18797132	RC_A 0.18790708 37_at	0.18778257 N45402	0.18767127 43 at	RC_A 0 1876313.27 at	0.18754692 U95301	0.18749177	RC_A 0.1874309 28_at	0.1873654 84	RC AA	0.10722000 U3 at	0.18708922 U73377 at	0.18701448 28	0.18690999 38 at	HG2271- 0.18684049 HT2367 at	0.18675248		0.186703061	0.18663722	0.18658338 X59798	0.18652064	0.1864017 D28124 at	0.1863747 U48707 at
0.323281	0.32324	0.323217	0.323119	0.323081		0.322965	0.322935	0.322896	0 397888	0.322000	0.322806	0.322746	0.322718		0.322583		0.322425	0.322393	0.322365	0.322365	0.322244	0.322145
0.393548	0.3935442	0.3935015	0.3935015	0.3934807	1 !	0.3933455	0.3933285	0.3932181	0.393106	0.3929525	0.3929499	0.3928169	0.3925747	0.3925746	0.3925106	27.000	0.3924542	0.3923574	0.3923568	0.3921631	0.3920976	0.3920807
0.1100458	0.1099631	0.1095692	0.1095227	0.109249	0.1091305	0.1087535	0.1081799	0.1079254	0.1078999	0.1074504	0.1074084	0.1073041	0.1071516	0.1068336	0.1060727	700040	0.10001100		0.1057677	0.1052273		0.1046773
842 Melanoma	843 Melanoma	844 Melanoma	845 Melanoma	846 Melanoma	847 Melanoma	848 Melanoma	849 Melanoma	850 Melanoma	851 Melanoma	852 Melanoma	853 Melanoma	854 Melanoma	855 Melanoma	856 Melanoma	857 Melanoma	858 Molonomo	Meianoma	859 Melanoma	860 Melanoma			863 Melanoma
842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	252	000	859	860	861	862	863

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Docket No.: Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. EST: zw94h05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA AA095045_s EST: cp2563.seq.F Fetal heart, Lambda ZAP Express Homo sapiens RC A40225 EST: ze72c10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA KINASE C-BINDING PROTEIN BETA 15.;, mRNA sequence. (from EST: II6470.seq.F Fetal heart, Lambda ZAP Express Homo sapiens EST: zu52h04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA RC_AA4113 EST: zv28c04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zt28g07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zt32e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA RC_AA4870 | EST: ab18e01.s1 Stratagene lung (#937210) Homo sapiens cDNA clone 714492 3' similar to TR:E91187 E91187 NMDA RECEPTOR RC_AA6210 EST: ag03e04.s1 Soares testis NHT Homo sapiens cDNA clone EST: zu10a06.s1 Soares testis NHT Homo sapiens cDNA clone AA091231_a EST: cchn2158.seq.F Fetal heart, Lambda ZAP Express Homo clone 724060 3' similar to TR;G1199669 G1199669 PROTEIN GLUTAMATE-BINDING SUBUNIT.;; mRNA sequence. (from Homo sapiens mRNA for KIAA0462 protein, partial cds Putative endothelin receptor type B-like protein mRNA sapiens cDNA 5', mRNA sequence. (from Genbank) clone 741655 3', mRNA sequence. (from Genbank) clone 841176 3', mRNA sequence. (from Genbank) clone 364530 3', mRNA sequence. (from Genbank) clone 754950 3', mRNA sequence. (from Genbank) clone 784665 3', mRNA sequence. (from Genbank) က Eukaryotic translation initiation factor 4 gamma, 1056222 3', mRNA sequence. (from Genbank) 731410 3', mRNA sequence. (from Genbank) cDNA 5', mRNA sequence. (from Genbank) cDNA 5', mRNA sequence. (from Genbank) THROMBOXANE-A SYNTHASE MYOD1 Myogenic factor 3 PROS1 Plasma protein S 0.18618384 L48546 at-2 Tuberous sclerosis 2 Crystallin, beta B2 TSC2 Tuberin Genbank) Genbank) 0.18574013 99_at RC_AA4122 AA367473_a AA092290_f RC_AA2924 RC_AA6090 RC_AA4358 RC AA2357 0.1850564 42 s at 0.18497916 M14338 at 0.18546972 M80647 at ਲੱ 0.18522058 X56677 at 0.18605064 L48546 at 0.18488216 27_s_at 0.18530053 U87460 0.18625675 43 at 0.18601082|50 at 0.18581009 41 at 0.18574595|99 at 0.18524969 37 at 0.18537652|54 at 0.18483162 90 at 0.18628754|51 at aţ 0.18591599 0.18557717 0.18553251 0.18515226 0.321416 0.320704 0.322009 0.321866 0.321646 0.3214080.321295 0.321165 0.320926 0.321912 0.321847 0.321705 0.320864 0.32075 0.320623 0.322141 0.32121 0.321017 0.32077 0.320748 0.322061 878 | Melanoma | 0.1013224 | 0.3908899 | 883 | Melanoma | 0.1004886 | 0.3907372 | 0.3918513 0.1028432 0.3915756 0.39139350.1026259 0.3913217 876 Melanoma | 0.1015902 | 0.3912096 | 0.1013599 0.3910843 879 Melanoma | 0.1012426 | 0.3908723 884 Melanoma | 0.1004353 | 0.3906381 0.3917824 0.3917522 0.3916954 0.3916188 874 Melanoma | 0.1023213 | 0.391227 0.1019788 0.3912212 0.392052 881 | Melanoma | 0.1007301 | 0.3907448 | 0.3917522 0.1007926 0.3908723 0.1005677 0.3907435

0.1034102

870 Melanoma

871 Melanoma

0.1027382

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873 Melanoma

875 Melanoma

877 Melanoma

880 Melanoma

882 Melanoma

0.1041958

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0.1042421

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0.1041631

869 Melanoma

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885 N	885 Melanoma	0.1003836	0.3905987	0.320549	RC_A 0.18471456 72_at	RC_AA1523 72_at	EST: zo07c04.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 566982 3', mRNA sequence. (from Genbank)
886 N	886 Melanoma	0.1002404	0.3905306	0.320431	HG417. 0.18466358 HT417	. s.	Cathensin R
887 N	887 Melanoma	0.1002299	0.3903944	0.320332	0.18457657 M86752	at .	TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521
888	888 Melanoma	0.0998752	0.3903006	0.320327	HG1153 0.18453667 HT1153	HG1153- HT1153 at	Niclansida Dinhasahata Kinasa Nim23 H2s
№ 889	889 Melanoma	0.0997796		0.320312	0.1844451	0.1844451 D86961 at	KIAA0206 gene, partial cds
890 N	890 Melanoma	0.0997444	0.3901956	0.320252	0.18438782 M29335 at	M29335 at	MHC class II DO-alpha mRNA, partial cds
200	-					AF006609_a	
RA1 IV	Melanoma	0.0997242	0.3900967	0.320094	0.18427648 t	+-	RGS3 mRNA, 5' UTR
892 N	892 Melanoma	0.0992877	!	0.320054	0.18421733	U03735 f at	0.18421733 U03735 f at MAGE-3 antigen (MAGE-3) gene
893 M	893 Melanoma	0.0987119	- 1	0.320027	0.18412265 X79200 at	X79200_at	Homo spaiens mRNA for SYT-SSX protein
894 M	894 Melanoma	0.0986034	0.3900199	0.320019	0.18407716 X04011_at	X04011_at	CYBB Chronic granulomatous disease
895 M	895 Melanoma	0.0986034	0.3900199	0.319995	0.1840112	0.1840112 X04011 at-2	
896 M	896 Melanoma	0.0985939	0.3899832	0.319846	0.183946	0.183946 U43328 at	CRTL1 Cartilage linking protein 1
897 M	897 Melanoma	0.0982294	0.3899099	0.319821	RC_A 0.18387742 28 at	A2321	Sarcoglycan, epsilon
000	800	00004	700000			A3984	EST: zt62a05.s1 Soares testis NHT Homo sapiens cDNA clone
020	ola olla	0.0301440	0.3098084	0.319781	0.183/914/		726896 3', mRNA sequence. (from Genbank)
899 M	899 Melanoma	0.0981261	0.38986	0.319781	RC_A 0.18370776 06_at	A4244	EST: zv82g01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 760176 3', mRNA sequence. (from Genbank)
M 006	900 Melanoma	0.0980848	0.3898141	0.319658	RC_A 0.18361829 12 at	A6000	EST: ag29h10.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1091011 3', mRNA sequence, (from Genhank)
901 M	901 Melanoma	0.0979518	0.3897422	0.319547	RC_A 0.1835669 98 at	RC_AA1792 98_at	Homo sapiens chromosome 9. P1 clone 11659
902 M	902 Melanoma	0.0977802	0.3895993	0.319532	0.18351091	7_s_a	Homo sapiens mRNA for KIAA0851 protein complete cds
					A CANADA		Homo sapiens mitochondrial DNA polymerase accessory subunit
903 M	903 Melanoma	0.0977496	0.3895966	0.319361	0.18345913 U94703	te	precursor (MtPoIB) mRNA, nuclear gene encoding mitochondrial protein, complete cds
904 M	904 Melanoma		0.3895849	0.319346	0.1833842 X92896	at	TBA2 protein
905 Mi	905 Melanoma	0.0973293	0.3895712	0.319312	0.18335311 M20471	म्	CLTA Clathrin light chain A
906 Me	906 Melanoma	0.0971652	0.389535	0.319111	0.1832331 t	C00810_s_a t	Homo sapiens clone 24733 mRNA sequence
907 Mc	907 Melanoma	0.0965471	0.3895115	0.319029	0 18316567	AA464368_s	AA464368_s EST: zx81c11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
			21.0000	0.0000	0.10010001		GIOTIE O LU 104 3, MKINA Sequence. (from Genbank)

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8	3 Melanom	ia 0.096482	908 Melanoma 0.0964824 0.3892891	0.319029		0.18313889H 01406 at	
306	909 Melanoma	la 0.0964487	37 0.3891713	0		RC_AA2566	
910	910 Melanoma			0	_	06 at U66468 at	682227 3', mRNA sequence. (from Genbank) Cell growth regulator CGR11 mRNA
911	911 Melanoma	а 0.0960448	.8 0.389056	0.318794	RC_A 0.18287022 10_at	RC_AA1668 10_at	EST: zo87a05.s1 Stratagene ovarian cancer (#937219) Homo Sapiens cDNA clone 593840 3' mRNA common (#5000000000000000000000000000000000000
312	912 Melanoma	a 0.0960059	9 0.3889403	0.318793		AA479567_a t	EST: zu42b02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740619 5' mPNA company to the contract of the
13	913 Melanoma	a 0.09£9051	1 0.388918	0.318612	0.18273012	X95463_s_a t	EMR2 Fracile X montal retardation of
4	914 Melanoma	a 0.0958561	1 0.3888968	0.318588	RC_A 0.18263909 14 at	RC_AA5048 14 at	Ribosomal protain 114
15	915 Melanoma	a 0.0956575	5 0.3888289	0.318529		RC_AA2517 72 at	H.sapiens mRNA for HEC4 and to its
16	916 Melanoma	в 0.0956069	9 0.388728	0.318501	0.18237096 06 at	RC_AA4472 06_at	Homo canians mbn/A for MAAGEA
1	917 Melanoma	0.0954152	0.3886916	0.318382	0.1823179	AA210757_a t	Transcription factor 3 (E2A immunoglobulin enhancer binding factors
8	918 Melanoma	0.0949926	0.3886501	0.318344	0.18223679	C01803_s_a t	EST: HUMGS0003762, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)
6 6	919 Melanoma		- 1	0.318255	0.18217865 N57359	at	EST: yw86f09.r1 Homo sapiens cDNA clone 259145 5' similar to contains Alu repetitive element; contains element MSR1 repetitive element :. (from Genhank)
2	A COUNTY OF THE	0.0343553	0.3886012	0.318175	0.18210067 X74801	at	T-COMPLEX PROTEIN 1, GAMMA SUBUNIT
==	Melanoma	921 Melanoma 0.0946426	0.3885637	0.318154	RC_A 0.18202373 12_at	RC_AA5984	RC_AA5984 EST: ae48b08.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950103 31 mRNA sequence (from Cont. 12)
2	922 Melanoma	0.0942835	0.3883481	0.318112	RC_A 0.18197712 32 at	A5990	EST: ae41h03.s1 Gessler Wilms tumor Homo sapiens cDNA clone
8	923 Melanoma	0.0941602		0.318043	RC 0.18187974 04	_AA2566	EST: zr86g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
- -	az4 Melanoma	0.0941322	0.3881894	0.318031	0.18174182 X78342 at		(clone PK2J) CDC2-related profein kinase (PISS) DE)
2	925 Melanoma	0.0940312	0.3881287	0.317904	0.18169144 04	_AA2801 s_at	EST: 2105h09.s1 NCI_CGAP_GCB1 Homo saplens cDNA clone
≥ 0	926 Melanoma	0.0938226	0.3880296	0.317847	RC_AA(0.18159491 05 f at)259	domo canians TNE indicate.
<u> </u>	927 Melanoma	0.0933703 0.3880194		0.317702	0.18155839 17	3333	EST: zr69h02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
		1			- 1,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	מו	oogost 3, mKNA sequence. (from Genbank)

					13. 15. 15. 15. 15. 15. 15. 15. 15. 15. 15	Total that the tar	is the first first the fourth that the first world world first that the first
928	928 Melanoma	0.0933541	0.3879547	0.317565	RC 0.18151687 10	RC_AA4105 10_at	RC_AA4105 EST; zv16g03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 10_at 753844 3', mRNA sequence. (from Genbank)
929	929 Melanoma	0.0932733	0.3879547	0.317407	0.18137814	HG2566- HT4792 r at	HG2566- 0.18137814 HT4792 r at Microtubule-Associated Protein Tau, Alt. Splice 3, Exon 8
930	930 Melanoma	0.0929806	0.3879485	0.317344	0.18126793\W25933 at	W25933 at	EST: 15b2 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
931	Melanoma	0.0926989	1	0.317221	0.18121965 43 at		EST: zr71a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668824.3. mRNA sequence. (from Genbank)
932	Melanoma	0.0926205	1	0.317189	0.18113133 M63835	 M63835 at	HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A FORM" PRECURSOR
933	933 Melanoma	0.0926039	0.3878423	0.317161	RC_A 0.18109566 69 at	RC_AA2820 69_at	KIAA0603 gene product
934	934 Melanoma	0.0924361	0.3876936	0.317156	RC_A 0.18109117 69_at	A4280	EST: zw57b01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774121 3', mRNA sequence. (from Genbank)
935	935 Melanoma	0.092388	0.387603	0.317136	0.18100832	RC_AA2561 57_at	EST: zr79b01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681865 3', mRNA sequence. (from Genbank)
936	936 Melanoma	0.0920761	0.3873778	0.31707	0.18091042 C00358_at	C00358_at	EST: HUMGS0003384, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)
937	937 Melanoma	0.0915411	0.3873482	0.316937	0.18088587	AA017283_a t	EST: ze52b01.r1 Soares retina N2b4HR Homo sapiens cDNA clone 362569 5', mRNA sequence. (from Genbank)
938	938 Melanoma	0.0913049	0.0913049 0.3873269	0.316873	0.1807297	0.1807297 X95191_at	Delta-sarcoglycan
939	939 Melanoma	0.0911804	0.3872909	0.316873	RC_A 0.18070118 42_at	RC_AA4274 42_at	Guanine nucleotide regulatory factor
940	940 Melanoma	0.0905795	0.3872227	0.316858	0.18065019	AA082546_a t	EST: ze88h10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366115 5', mRNA sequence. (from Genbank)
941	941 Melanoma	0.0903393	0.3872016	0.316817	RC_A 0.18057401 38_at	A4525	EST: zx35e05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788480 3', mRNA sequence. (from Genbank)
942	942 Melanoma	0.0902495	0.3871875	0.316772	0.18051295 W23913	W23913_at	EST: zb47b02.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 306699 5', mRNA sequence. (from Genbank)
943	943 Melanoma	0.0897958	1	0.316734	0.1804641	D80002_at-2	0.1804641 D80002_at-2 Human mRNA for KIAA0180 gene, partial cds. (from Genbank)
944	944 Melanoma	0.0897958	0.3868024	0.316547	0.18038586 D80002	D80002_at	KIAA0180 gene, partial cds
945	945 Melanoma	0.0894883	0.3867989	0.316535	0.18030895 M97936	M97936_at	SIGNAL TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION 1- ALPHA/BETA
946	946 Melanoma	0.0893936	0.3867657	0.316531	0.18025132 X95876_at	X95876_at	G-protein coupled receptor
947	947 Melanoma	0.0891839	0.3866815	0.316466	0.18017781 U26591_at	U26591_at	ICA1 Islet cell autoantigen 1 (69kD)
948	948 Melanoma	0.0891555	0.3866746	0.31637	RC 0.18012705 69	RC_AA4592 69_at	EST: aa27d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814471 3', mRNA sequence. (from Genbank)

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

					RC A	RC AA1495	4.0.1 that her and and that her her than the the than the than the than the than the the than the the than the the the the the the the the the the
949	949 Melanoma	0.0888772	0.3866697	0.316333	0.18009418 30 at	30 at	Interferon regulatory factor 3
950	950 Melanoma	0.0888387	0.3865062	0.31616	0.18001218 L77701	L777701_at	COX17 mRNA
						RC_AA2368	EST: zs43a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
951	951 Melanoma	0.0887662	0.3864703	0.31616	0.1799261 93_at	93_at	687926 3', mRNA sequence. (from Genbank)
952	952 Melanoma	0.0886884	0.3863932	0.316049	RC_A 0.17988726 24 s	RC_AA3981 24 s at	Growth factor receptor-bound protein 14
953	953 Melanoma	0.0884562	0.3863059	0.316029	0.17981195 D50923	D50923_at	KIAA0133 gene
i	-	1					EST: zd41b11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
954	954 Melanoma	0.0881556	0.386303	0.316021	0.17971534 W68097 at	W68097_at	
955	955 Melanoma	0.0879364	0.3862831	0.315927	0.17964177 t	C15910_s_a t	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL)
956	956 Melanoma	0.0877927	0.3861978	0.315902	0.179552321	AA070545_a t	AA070545_a Zm70c03.r1 Stratagene neuroepithelium (#937231) Homo sapiens t cDNA clone 530980 5', mRNA sequence. (from Genbank)
						AA386297_a	
957	957 Melanoma	0.0876146	0.3860516	0.315902	0.1794887 t	+	(from Genbank)
958	958 Melanoma	0.0873856	0 3860243	0.315832	0.47940362	X13766_s_a	ricosco atod CNO
959	959 Melanoma	0.0873313	. 1	0.315712	0.17934053 D88153 at	D88153 at	Home saniens mRNA for HYA22 complete cds
			1			AA486144 a	
096	960 Melanoma	0.0871529	0.3859246	0.315686	0.17927803 t	+-	clone 840786 5', mRNA sequence. (from Genbank)
						070040	CT. +000,000 A Common fatal lines and and 1000 A 1100 O 111
961	961 Melanoma	0.087082	0.3859092	0.315593	0.17923926 36_at	A00 13	CDNA clone 428143 3', mRNA sequence. (from Genbank)
962	962 Melanoma	0.0870151	0.3857962	0.315522	0.1791759 Z34820 s	Z34820 s at	at Calcium channel, voltage-dependent. I type alpha 1C subunit
(RC_D60475 EST: Human fetal brain cDNA 3'-end GEN-111F09, mRNA sequence.
963	963 Melanoma	0.0863522	0.385725	0.315522	0.17908989		(from Genbank)
964	964 Melanoma	0.0862478	0.3857182	0.345/36	0.179000000 84	RC_AA4122	A COLL amount of A Manager and an animal of the state of
						AA45824E A	EST: 2048h03.r1 Stratagene endothelial cell 937223 Homo sapiens
965	965 Melanoma	0.0862031	0.385542	0.315356	0.17893206	t	t element; mRNA sequence. (from Genbank)
996	966 Melanoma	0.085889	0.3852078	0.315344	RC 0.17883709 78	RC_AA2331 78_at	Homo sapiens mRNA for KIAA0831 protein, complete cds
						RC AA0740	
296	967 Melanoma	0.0858335	0.3851854	0.315284	0.17876199 90_at	90_at	sapiens cDNA clone 531483 3', mRNA sequence. (from Genbank)
896	968 Melanoma	0.0850627	0.3851712	0.315166	0.1787029 t	AA033703_a t	EST: zf01d10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 375667 5', mRNA sequence. (from Genbank)

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							THE GOAL WALL COURT WOULD BEEN MADE
696	969 Melanoma	0.0849712	0.3851475	0.315104	RC_A 0.17861678 32_at	_AA0226 at	AA0226 EST: ze73a01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA at clone 364584 3', mRNA sequence. (from Genbank)
970	970 Melanoma	0.0847323	0.3850874	0.315063	0.17851534	Y09912_ma 1_at	AP-2 beta gene
971	971 Melanoma	0.0844758	0.3848748	0.315013	0.1784022 U41060_at	1060 at	Breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds
972	972 Melanoma			0.314762	0.1783561	RC_AA1949 98_at	Homo sapiens purineraic receptor P2Y5 mRNA complete cds
973	973 Melanoma	-+		0.314741	0.17833209 Y09022	3022 at	Not56-like protein
974	974 Melanoma	 -		0.314721	0.17821473 U38480	8480 at	Retinoid X receptor-gamma mRNA
975	975 Melanoma	0.0838402	0.3845255	0.314689	0.17813747 D85429	5429 at	DNAJ PROTEIN HOMOLOG 1
976	976 Melanoma	0.0837794	0.3844882	0.314605	RC_A 0.17810053126 at	RC_AA4787	EST: zv14d09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
977	977 Melanoma	0.083725	-	0.31454	0.17804712 S67156 at	7156 at	ASPA Aspartoacylase (aminoacylase 2 Canavan disease)
978	978 Melanoma	0.0836926	0.384462	0.314432		7012 at	Immunodiobulin lambda gene locus DNA clone-6106
979	979 Melanoma	0.083654	0.384456	0.314242	0.17792843	RC_AA4311 93_at	Homo sapiens mRNA for KIAA0544 protein partial cds
86	980 Melanoma	0.0836	0.3843976	0.314223	0.17786537 M95925 at	5925 at	Leucine zipper on the D14S46F locus mRNA
Š					RC	44890	EST: aa54d11.s1 NCI CGAP GCB1 Homo sapiens cDNA clone
22	ed I Melanoma	0.0834826	0.3843418	0.314181	0.17783083 09_at		IMAGE:824757 3', mRNA sequence. (from Genbank)
982	982 Melanoma	0.0833386	0.3841745	0.314112	RC_A 0.17760456 91_at	A4881	EST: ad08e05.s1 Soares NbHFB Homo sapiens cDNA clone 877664 3', mRNA sequence. (from Genbank)
							EST: ze97d11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
983	983 Melanoma	0.0832802	0.0832802 0.3844633	0.2440.64	RC_ 0.47750050	A0273	clone 366933 3' similar to contains Alu repetitive element;, mRNA
3	Micial III	0.0022002	0.3041033	0.314001	0.17/5295917		sequence. (from Genbank)
984	984 Melanoma	0.0831597	0.3841532	0.314041	RC_A 0.17743386 84_at	A1502	EST: zl07h04.s1 Soares pregnant uterus NbHPU Horno sapiens cDNA clone 491671 3', mRNA sequence. (from Genhank)
					AFFX-	-	(Allegano Hor) Constant
					≘ :	HUMGAPDH	
985	985 Melanoma	0.0831503	0.3841532	0.313964	/M3 0.1774302 st-2	3197_3_	Alveraldahirto 3 who conhote debindrous
					AFFX-	×	oyograndriyue-o-priospriate ueriyarogeriase
					SI.	HUMGAPDH	
986	986 Melanoma	0.0831503	0.3841521	0.313922	0.17741387 st	/M33197_3_ st	AFFX-HIMGAPDH/M33107 3 et (endoconous control)
1 286	987 Melanoma	0.0831186	0.3840401	0.313834	0 17733847 102704 at		EST: ye23a04.r1 Homo sapiens cDNA clone 118542 5: (from
					RC	A4787	EST: zv14g12.s1 Soares NhHMPu S1 Homo saniens cDNA clone
988	988 Melanoma		0.0829896 0.3839553	0.313796	0.17733108 40_at		753670 3', mRNA sequence. (from Genbank)

				RC AA1971	RC AA1971 EST: zq11a05.s1 Stratagene muscle 937209 Homo sapiens cDNA
elanoma	989 Melanoma 0.0829753 0.3839081	0.3839081	0.313721	0.17722821 80_at	clone 629360 3', mRNA sequence. (from Genbank)
990 Melanoma	0.0822569	0.3838808	0.313621	0.17719446 D13645_at	KIAA0020 gene
					SLC4A2 Solute carrier family 4, anion exchanger, member 2
elanoma	991 Melanoma 0.0818772 0.3838668	0.3838668	0.313557	0.17710419 U62531_at	(erythrocyte membrane protein band 3-like 1)
992 Melanoma		0.0817362 0.3838567	0.31351	0.17699933 L38025 at	CNTFR Ciliary neurotrophic factor receptor
993 Melanoma	0.081425	0.3838294	0.313457	0.17699103 L38517_at	Indian hedgehog protein (IHH) mRNA, 5' end
				AA284709 a	The second secon
994 Melanoma	0.0814158 0.3834817	0.3834817	0.313452	0.17693147 t	Kallikrein 3, (prostate specific antigen)
				RC AA2054	RC AA2054 EST: zq66b06.s1 Stratagene neuroepithelium (#937231) Homo
995 Melanoma		0.0813572 0.3834803	0.313435	0.17682509 37_at	sapiens cDNA clone 646547 3', mRNA sequence. (from Genbank)
				RC_AA0261	RC_AA0261 EST: ze94c06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
elanoma	996 Melanoma 0.0812518 0.3832463	0.3832463	0.313343	0.17674197 11_at	clone 366634 3', mRNA sequence. (from Genbank)
				RC_AA0260	RC_AA0260 EST: ze86b05.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
elanoma	997 Melanoma 0.0810807	0.383213	0.313267	0.17671172 54 at	clone 365841 3', mRNA sequence. (from Genbank)
998 Melanoma	0.0807698	0.3832115	0.313262	0.17665395 L35594_at	Autotaxin mRNA
			-	AA324364_a	AA324364_a EST: EST27175 Cerebellum II Homo sapiens cDNA 5' end similar to
999 Melanoma	0.0806223	0.3832029	0.313012	0.1766273 t	EST containing Alu repeat, mRNA sequence. (from Genbank)
				U68135_s_a	U68135_s_a U68135 Human cell line PCI-06B Homo sapiens cDNA clone SCC-
alanoma	1000 Melanoma 0.0806181	0.383182	0.313	0.17657281	S1c, mRNA sequence
***************************************	-	4		- Control of the Cont	

FIG. 8X

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

					<u>A</u>	AFFX-	
	Mesothelio					30_M_	(Jundan Const) also atalasses and AMP 1
~	ma	1.0591416	1.0591416 0.6999174	0.623343	0.47049877 at-2		Human 28S ribosomal KNA gene, complete cas. (Ironi Genidank)
					A	AFFX-	
	Mesothelio				2	M27830_M_	
N	2 ma	1.0591416	1.0591416 0.6458688	0.575521	0.43784672 at		AFFX-M27830 M_at (endogenous control)
	Mesothelio						
(1)	3 ma	1.0539508	1.0539508 0.6269065	0.552575	0.4221624 X	16662 at	0.4221624 X16662 at ANX8 Annexin VIII
	Mesothelio				<u>ır</u>	C_AA4196	RC_AA4196 EST; zv04b06,s1 Soares NhHMPu S1 Homo sapiens cuina cione
4	4 ma	0,992618	0.612074	0.540431	0.4113423 09_at	9_at	752627 3', mRNA sequence, (from Genbank)
	Mesothelio				LY.	C_AA2937	RC_AA2937 EST: zt56g08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
	5 ma	0.8888267	0.8888267 0.5970459	0.53064	0.40285575 96_at	6_at	clone 726398 3', mRNA sequence. (from Genbank)
	Mesothelio					171503 s a	N71503_s_a EST: yw32b10.r1 Homo sapiens cDNA clone 253915 5'. (from
v	6 ma	0.8654811	0.8654811 0.5931432	0.522774	0,39587444 t		Genbank)
	Mesothelio				L	RC_AA0378	
,	7 ma	0.8612852	0.8612852 0.5855894	0.517713	0.39051464 03 at	3 at	Glutamine-fructose-6-phosphate transaminase 2
	Mesothelio				<u></u>	C_AA4550	RC_AA4550 EST; aa04d11,s1 Soares NhHMPu S1 Homo sapiens cDNA clone
w	8 ma	0.8443461	0.8443461 0.5781475 0.512088	0.512088	0,38488322 78_at		812277 3', mRNA sequence. (from Genbank)
					The state of the s	The same of the sa	

FIG. 9/

and and a strength of the stre

- 1 -	Mooch olio				RC AA4062	EST: zu65e08.s1 Soares testis NHT Homo sapiens cDNA clone
	o ma	0.8403058	0.5759057	0.505169		742886 3', mRNA sequence. (from Genbank)
-	Mesothelio				A1502	EST: 2104g08.s1 Soares pregnant uterus NbHPU Homo sapiens
· ~	10 ma	0.8332273	0.5695669	0.501049	0.37639734 10_at	cDNA clone 491390 3', mRNA sequence. (from Genbank)
-	Mesothelio	000000	000000000000000000000000000000000000000	0 407700	0 37266138 KN0765 at	COMPLEMENT C3 PRECIIRSOR
	11 ma	0.8293908	- 1	0.48/1/22	0.37200130 NOZ703 at	
5 5	Mesothelio 12 ma	0.827219	0.5607175	0.49555	0.36919844 V00594 s_at Metallothionein isoform 2	Metallothionein isoform 2
: 5	Mesothelio				RC AA1956	RC AA1956 EST: zr33f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
. ⊏	13 ma	0.82658	0.5570877	0.492473	0.3661324 56 at	665217 3', mRNA sequence. (from Genbank)
5	Mesothelio				RC AA1956	EST: zr33f10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
⊱	14 ma	0.8225429	0.5529053	0.489945	0.36331722 60_at	665227 3', mRNA sequence. (from Genbank)
I≥	Mesothelio					EST: HUMGS0003801, Human Gene Signature, 3'-directed cDNA
Ξ	15 ma	0.7978091	0.5509036	0.487753	0.3606286 C01833_at	sequence, mRNA sequence. (from Genbank)
∑ [Mesothelio	0 7942148	0.5479719	0.484985	0.3579962 L33799 at	PCOLCE Procollagen C-endopeptidase enhancer
: ≥	Mesothelin	2		!	M62895 s a	
: E	17 ma	0.7825837	0.5463682	0.482761	1	Annexin II (lipocortin II) pseudogene 2
				and the same of th		EST: zt37a11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 724508 3' similar to contains Alu repetitive element; contains
≥	Mesothelio				RC_AA2916	element MER25 repetitive element;, mRNA sequence. (from
Ξ	18 ma	0.7629534	0.5449515	0.480798	0.3536204 44_at	Genbank)
≥	Mesothelio				_	
Ε	19 ma	0.7571154	0.5421202	0.478808	0.35162205 J04080_at	C1S Complement component 1, s subcomponent
≥ 8	Mesothelio 20 ma	0.7431973	0.5402978	0.477441	0.34978545 U27185 at	RAR-responsive (TIG1) mRNA
12	Mesothelio			-	RC_AA2341	EST: zr54f06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
:	21 ma	0.7386388	0.5377274	0.47298	0.3476147 90 at	667235 3', mRNA sequence. (from Genbank)
2	Mesothelio					
	22 ma	0.7328405	0.536799	0.471744	0.3454912 U63824_at-2	0.3454912, U63824_at-2 TEA domain family member 4
2	Mesothelio	0.790040E	0 5040040	0 474464	0 3428204 183824 of	Transcription factor BTEE-1 (BTEE1) mRNA
=1	23 IIId	0.7 320403		10.17.0	0.04506594 005064 81	Transcription reconstruction (March 1, 1971) Homos canions of NAA
≥ ≿	Mesothelio 24 ma	0.7216471	0.534914	0.468383	AA15689/_s 0.3425291 _at	EST: ZIZUDUT, IT Soares pregnant uterus norte o norte saprens conversione 502453 5', mRNA sequence. (from Genbank)
≥ ⊏	Mesothelio 25 ma	0.7209008	0.5338743	0.466288	0.34100002 X15882 at	COL6A2 Collagen, type VI, alpha 2
-2	Mesothelio		3]		ALMON (TRAININ)
	26 ma	0.7201456	0.5310615	0.464752	0.33956483 U08021 at	Nicotinamide N-metnyliransterase (Ivivivi I) ItikivA
≥ ⊏	Mesothelio 27 ma	0.7165751	0.5294145	0.463369	0.3380699 M14058_at	at C1R Complement component C1r
1						

	Mesothelio					AA115572 s	AA115572 s clone 491445 5' similar to TR:G895845 G895845 PUTATIVE P64
28	28 ma	0.6926372	0.5285939	0.462431	0.33655077	lat.	CLCP PROTEIN.;, mRNA sequence. (from Genbank)
	Mesothelio					M55998_s_a	
29	29 ma	0.6917406	0.5273998	0.461138	0.335557761	-	Alpha-1 collagen type I gene, 3' end
30	Mesothelio	0.6803457	0 5247797	0.450744	0.00410040 \$460400	ţ	O city on the filter and the feet of the city of the c
3		0.0030407	- 1	41.7867.0	0.33412012	ָם,	IGEBEO INSUIITEIKE GLOWITH TACTOL DIFFICING PROTEIT O
Č	Mesothelio	7,10,10		000	100000		Transforming growth factor-beta induced gene product (BIGH3)
م	31 ma	1917/90	0.58236.0	0.45833	0.3327401	0.3327401 M/7349 at	mKNA
	Mesothelio					X74929_s_a	
32	32 ma	0.6682161	0.5225286	0.457361	0.33140004 t		KRT8 Keratin 8
	Mesothelio						The state of the s
33	33 ma	0.6650274	0.5218657	0.456506	0.33014134 X56667	X56667_at	CALB2 Calbindin 2, (29kD, calretinin)
	Mesothelio						S100A10 S100 calcium-binding protein A10 (annexin Il ligand,
34	34 ma	0.6600438	0.5208061	0.454849	0.32891425 M38591	M38591_at	calpactin I, light polypeptide (p11))
	Mesothelio				And the second s		EST: vi83a11.r1 Homo sapiens cDNA clone 145820 5', (from
35	35 ma	0.6511369	0.5193346	0.453717	0.32773528 R79356	R79356 at	Genbank)
	Mesothelio	And the state of t					
36	36 ma	0.6490868	0.6490868 0.5186078	0.452831	0.32669944 U77594_at		Tazarotene-induced gene 2 (TIG2) mRNA
	Mesothelio					X12876_s_a	
37	37 ma	0.6456585	0.5181995	0.451232	0.3253647 t		KRT18 Keratin 18
	Mesothelio					RC_AA4789	RC_AA4789 Disabled (Drosophila) homolog 2 (mitogen-responsive
38	38 ma	0.6436112	0.5175271	0.449982	0.32408893 71	71_s_at	phosphoprotein)
	Mesothelio				No. of the second secon		
39	39 ma	0.6390519	0.5152585	0.448872		0.3232682 M11718_at	COL5A2 Collagen, type V, alpha
	Mesothelio						EST: yh82a08.r1 Homo sapiens cDNA clone 136214 5'. (from
40	40 ma	0.6375759	0.515186	0.447571	0.32227367 R33735_at		Genbank)
	Mesothelio					A4239	EST: zv79g03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
41	41 ma	0.6253181	0.5146735	0.446496	0.3215576 87_at		clone 759892 3', mRNA sequence. (from Genbank)
	Mesothelio					A4914	EST: ab01d12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
42	42 ma	0.6253093	0.6253093 0.5128632	0.446151	0.32042876 63_at		clone 839543 3', mRNA sequence, (from Genbank)
	Mesothelio						Company of the Compan
43	43 ma	0.6244977	0.5115336	0.444976	0.31962454 V00594_at		Metallothionein isoform 2
	Mesothelio						
44	44 ma	0.6022893	0.5113515	0.444402	0.31864458 U03877_at	U03877_at	HEAT SHOCK 70 KD PROTEIN 1
	Mesothelio				•	RC_AA4294	
45	45 ma	0.5995887	0.5111262	0.44345	0.31794432 73_at		CD63 antigen (melanoma 1 antigen)
	Mesothelio					A4051	EST: zu52h04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
46	46 ma	0.5993412	0.5102298	0.442973	0.31701964 99_at	99 at	clone 741655 3', mRNA sequence. (from Genbank)

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a bsothelio		Mesothelio					RC_AA2106	EST: zr88b05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
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Control Cont	9	Mesothelio					RC_AA4105	EST: zv16h06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
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orthelio		desothelio						Illiman linocortin (LID) 2 neardogage mPNA complete ade lite
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0.552521 0.49959 0.42858 0.3042381 61 at sothelio 0.5410206 0.498832 0.428373 0.30358905 X53587 at	<u>~</u>	1esothelio				LC.		EST: zu99d05.s1 NCI CGAP GCB1 Homo sapiens cDNA clone
sothelio 0.5410206 0.498832 0.428373 0.30358905 X53587 at	63 п)a	0.552521	0.49959	0.42858	0.3042381 6	at	MAGE:746121 3', mRNA sequence, (from Genhank)
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	044 [1	la l	0.5410206	0.498832	0.428373	0.30358905 X	at	TGB4 Integrin beta-4 subunit

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10	Mesothelio 65 ma	0.5389456	0.4987521	0.427308	0.30303353 15_at	KC_AA0374 15_at	KC_AA0374 EST: 2k33a09.s1 Soares pregnant uterus Nortzo Horno sapiens 15_at cDNA clone 484600 3', mRNA sequence. (from Genbank)
 	Mesothelio					RC AA0042	EST: zh97f02.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429243 3' similar to contains element MER22 repetitive
	66 ma	0.5375664	0.4984164	0.42658	0.3024114 74		element ;; mRNA sequence. (from Genbank)
+	Mesothelio					RC_AA1215	
	67 ma	0.5290971	0.4983387	0.426241	0.30173755	34_at	Ribosomal protein L24
 -	Mesothelio						
	68 ma	0.5285683	0.496771	0.425882	0.3010942 Y00503	Y00503_at	KRT19 Keratin 19
	Mesothelio						
=	69 ma	0.5278923	0.5278923 0.4963656	0.425264	0.3007496	0.3007496 X76029_at	NEUROMEDIN U-25 PRECURSOR
	Mesothelio					AB000220_a	
=	70 ma	0.5227398	0.4955348	0.424915	0.30012681		Semaphorin E
	Mesothelio						
	71 ma	0.5193663	0.4954979	0.424008	0.2994847 D00017	D00017_at	ANX2 Annexin II (lipocortin II)
	Mesothelio					RC_AA4872	EST: ab19f04.s1 Stratagene lung (#937210) Homo sapiens cDNA
	72 ma	0.5178543	0.4953613	0.423249	0.29888615 02_at	02_at	clone 841279 3', mRNA sequence. (from Genbank)
	Mesothelio						EST; yi56e02.r1 Homo sapiens cDNA clone 143258 5'. (from
	73 ma	0.5129159	0.4952377	0.423076	0.29839018	0.29839018 R73982_at	Genbank)
	Mesothelio					AA443499_f	
	74 ma	0.5123816	0.4942474	0.421875	0.29777405		Keratin 8
ļ	Mesothelio					RC_AA4238	
	75 ma	0.5096717	0.4936403	0.421006	0.2974624 84_at		Homo sapiens mRNA for KIAA0287 gene, partial cds
	Mesothelio			-		A1131	EST: zm27e01.s1 Stratagene pancreas (#937208) Homo sapiens
	76 ma	0.5087988	0.5087988 0.4932602	0.42067	0.29684785 66_at	66_at	cDNA clone 526872 3', mRNA sequence. (from Genbank)
	Mesothelio					AA292153_a	
	77 ma	0.5079263	0.4924502	0.420124	0.29637235 t	-	Growth arrest-specific 1
 -	Mesothelio					AA381902_a	EST: EST95112 Activated T-cells I Homo sapiens cDNA 5' end,
	78 ma	0.506678	0.4922077	0.419533	0.29579914 t	+	mRNA sequence, (from Genbank)
	Mesothelio					RC_AA4475	EST: zw90h07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
	79 ma	0.5061134	0.4911891	0.418903	0.29550776 04_at	04_at	clone 784285 3', mRNA sequence. (from Genbank)
	Mesothelio					AA046840_a	
=	80 ma	0.5039741	0.4904096	0.418557	0.29503757 t	ţ	CCAAT/enhancer binding protein (C/EBP), delta
	Mesothelio		ŀ			RC_AA2337	EST: zr44a07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
	81 ma	0.5032339	0.4901018	0.417974	0.29441684 63_at	63_at	666228 3', mRNA sequence. (from Genbank)
	Mesothelio						EST: Human aorta cDNA 5'-end GEN-345B11, mRNA sequence.
~	82 ma	0.5032095	0.4899276	0.417707	0.2940374 D62965	D62965_at	(from Genbank)
~	Mesothelio 83 ma	0 5031133	0 4893804	0.417361	0.29366824 M21389	M21389 at	KRT5 Keratin 5 (epidermolysis bullosa simplex, Dowling- Meara/Kobner/Weber-Cockavne types
1							

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septhelio 0.5016016 0.4893059 0.416528 0.2931924 2 2				-			AFFX- HUMRGE/M	
asothelio	ò	Mesothelio	-		0.7		10098_3_at-	
asothelio activities and southelio activities and southelio activities and southelio activities and southelio activities and activities and southelio activities and activities activities and activities	0	פ	01.001.00.0	- 1	0.416528	0.2931924	2	Human 18S rRNA gene, complete. (from Genbank)
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sothelio	38	ma				0.29273582		AFEX-HUMRGE/M10098 3 at (endodenglis control)
a 0.4985302 0.4866997 0.416095 0.29224983 M90657_at soothelio 0.4983092 0.4866791 0.415768 0.29178137 L13923_at soothelio 0.4899468 0.4857902 0.415072 0.29146454 67_at at soothelio 0.4899468 0.4850152 0.414634 0.2910173 L13698_at soothelio 0.4872159 0.4849082 0.413671 0.29027018 U77643_at sothelio 0.4872159 0.4822632 0.413671 0.29027018 U77643_at sothelio 0.4872159 0.4822632 0.413679 0.28975877 U77643_at sothelio 0.4872159 0.4822632 0.413679 0.28975877 U77643_at sothelio 0.4872159 0.4822632 0.413679 0.28975877 U77643_at sothelio 0.4872159 0.4805446 0.411895 0.28975877 X79882_at sothelio 0.4873745 0.4805446 0.411895 0.28975877 X79882_at sothelio 0.4873826 0.4804767 0.411201 0.28802437 t sothelio 0.4873826 0.4778755 0.409964 0.28685072 0.33464_s_at sothelio 0.4774815 0.4778755 0.409964 0.28685072 0.33464_s_at sothelio 0.477875 0.409964 0.28685072 0.33464_s_at sothelio 0.477875 0.409964 0.28685072 0.33464_s_at sothelio 0.477875 0.409964 0.28685072 0.33464_s_at sothelio 0.4778778 0.4778778 0.409577 0.286551568 t		Mesothelio					1	
sothelio	98	ma	-		0.416095	0.29224983		TUMOR-ASSOCIATED ANTIGEN L6
a 0.4983092 0.4866791 0.415768 0.29178137 L13923 at seothelio		Mesothelio						
seothelio	87	ma	-		0.415768	0.29178137	L13923_at	FBN1 Fibrillin 1 (Marfan syndrome)
a 0.4912033 0.4857902 0.415072 0.29146454 67 at ssothelio		Mesothelio	-		-		A4436	EST: zw86b07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
ssothelio	88	ma	-	- 1	0.415072	0.29146454		clone 783829 3', mRNA sequence. (from Genbank)
sothelio 0.4878193 0.4849082 0.414287 0.2906958 at AA477978.s asothelio 0.4872159 0.4832644 0.413671 0.29027018 0.77643_at-2 asothelio 0.48357745 0.4812809 0.412609 0.28975877 0.77643_at-2 asothelio 0.48357745 0.4812809 0.412609 0.289421 8C_AA6091 0.4835745 0.4812809 0.412609 0.289421 8C_AA6091 0.4835745 0.4812809 0.412609 0.289421 8C_AA6091 0.4835745 0.480546 0.411201 0.289421 8C_AA6091 0.4835745 0.480546 0.411201 0.289421 8C_AA6091 0.483586 s at at an accordance of the control o		Mesothelio						
sothelio	88	ma	0.4899468		0.414634	0.2910173	L13698 at	GAS1 Growth arrest-specific 1
sothelio		Mesothelio					AA477978 s	
sothelio a 0.4872159 0.4832644 0.413671 0.29027018 U77643_at-2 ssothelio 0.4872159 0.4822632 0.413579 0.28975877 U77643_at at-2 sothelio 0.4836731 0.4812809 0.412609 0.28914264 U40434_at sothelio 0.4808653 0.4804767 0.411201 0.28802437 t sothelio 0.4774815 0.478525 0.410118 0.28685072 J03464_sat sothelio 0.4778755 0.409964 0.28685072 J03464_sat sothelio 0.4778756 0.409964 0.28685072 J03464_sat sothelio 0.4778756 0.409964 0.28685072 J03464_sat sothelio 0.4778756 0.409964 0.28685072 J03464_sat sothelio 0.4778756 0.409964 0.28685072 J03464_sat sothelio 0.4778765 0.409964 0.28685072 J03464_sat sothelio 0.4778766 0.409964 0.28685072 J03464_sat sothelio 0.4778766 0.409964 0.28685072 J03464_sat sothelio 0.4778768 0.409977 0.28651568 t	96	ma	0.4878193		0.414287	0.2906958	at	Short-chain dehydrogenase/reductase 1
sothelio						Processing the state of the sta		
ssothelio 0.4872159 0.4822632 0.413579 0.28975877 U77643_at sothelio 0.4836731 0.4818311 0.413679 0.289421 85_at sothelio 0.4835745 0.4812809 0.412609 0.28914264 U40434_at sothelio 0.4810574 0.4805446 0.411895 0.28857827 X79882_at sothelio 0.4793426 0.478838 0.410784 0.28857827 X79882_at sothelio 0.4774815 0.478525 0.410784 0.28769788 U50330_at sothelio 0.4774815 0.4778755 0.409964 0.28685072 J03464_s_at sothelio 0.4778755 0.409964 0.28685072 J03464_s_at	9				0.413671	0.29027018	U77643 at-2	Secreted and transmembrane 1
10.4872159 0.4822632 0.413579 0.28975877 U77643_at		Mesothelio						
Southelio 0.4836731 0.4818311 0.413071 0.289421 85_at	92	ma	0.4872159		0.413579	0.28975877		K12 protein precursor mRNA
Scothelio		Cilo di Contra					1	EST: af12c06.s1 Soares testis NHT Homo sapiens cDNA clone
sothelio 0.4835745 0.4812809 0.412609 0.28914264 U40434_at sothelio 0.480653 0.4804767 0.411895 0.28914264 U40434_at sothelio 0.4808653 0.4804767 0.411201 0.28802437 t sothelio 0.4793426 0.478525 0.410118 0.2873057 L35545_at sothelio 0.4774815 0.4778755 0.409964 0.28685072 J03464_s_at sothelio 0.47737621 0.4774978 0.409577 0.28651568 t	S	Mesomello	700070		!		A6091	1031434 3' similar to SW:INO1_SPIPO P42803 MYO-INOSITOL-1-
sothelio	33	ma	0.4836/31		0.413071	0.289421		PHOSPHATE SYNTHASE;, mRNA sequence. (from Genbank)
sothelio 0.483:745 0.4812809 0.412609 0.28914264 U40434_at at sothelio 0.4810574 0.4805446 0.411895 0.28857827 X79882_at sothelio 0.4793426 0.478838 0.410784 0.2873057 L35545_at sothelio 0.4774815 0.4778755 0.409964 0.28651568 t sothelio 0.4737621 0.4774978 0.409577 0.28651568 t		Mesothelio						
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sothelio 0.4808653 0.4804767 0.411895 0.28857827 X79882 at sothelio 0.4808653 0.4804767 0.411201 0.28802437 t sothelio 0.4793426 0.478838 0.410784 0.28769788 U50330 at sothelio 0.4774815 0.478525 0.409964 0.28685072 J03464 s. at sothelio 0.4778755 0.409964 0.28685072 J03464 s. at sothelio 0.47787621 0.4774978 0.409577 0.28651568 t		Mesothelio						
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sothelio 0.4793426 0.478838 0.410784 0.287569788 U50330_at sothelio 0.4774815 0.4778755 0.409964 0.2873057 L35545_at sothelio 0.4763861 0.4778755 0.409964 0.28685072 J03464_s_at sothelio 0.4737621 0.4774978 0.409577 0.28651568 t		Mesothelio						
sothelio 0.4774815 0.478525 0.410118 0.2873057 L35545 at sothelio 0.4763861 0.4778755 0.409964 0.28685072 J03464 s. at sothelio 0.4737621 0.4774978 0.409577 0.28651568 t	97	ma	0.4793426	0.478838	0.410784	0.28769788	क्र	3MP1 Bone morphogenetic protein 1
Sothelio 0.47787625 0.410118 0.2873057 L35545_at acthelio 0.4778755 0.409964 0.28685072 J03464_s_at acthelio 0.4737621 0.4774978 0.409577 0.28651568 t	Č	Mesothelio						
sofhelio 0.4763861 0.4778755 0.409964 0.28685072 J03464 sat sothelio 0.4737621 0.4774978 0.409577 0.28651568 t	88	ma	0.4774815	0.478525	0.410118	0.2873057		Endothelial cell protein C/APC receptor (EPCR) mRNA
0.4763861 0.4778755 0.409964 0.28685072 J03464 s at at at at at at at at at at at at at		Mesothelio						
sothelio 0.4737621 0.4774978 0.409577 0.28651568 t	66	ma	0.4763861	0.4778755	0.409964	0.28685072		Sollagen, type I, alpha 2
0.473/621 0.4774978 0.409577 0.28651568 t		Mesothelio					/65292_s_a	
	198	ma	0.4737621	0.4774978	0.409577	0.28651568		4FL1 H factor (complement)-like 1

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Me	Mesothelio					THPO Thrombopoietin (myeloproliferative leukemia virus oncogene
101 ma	~-	0.4714901	0.4774398	0.40913	0.286142 U70136_at	
Me	Mesothelio					Г
102 ma	_	0.4702461	0.4769206	0.408089	0.28585374 M13955_at	
₩e	Mesothelio				RC_AA4959	
103 ma		0.4690899	0.4765172	0.40777	0.28563184 94_at	768514 3', mRNA sequence. (from Genbank)
						EST: zc03c04.s1 Soares parathyroid tumor NbHPA Homo sapiens
Me	Mesothelio				RC_AA0;	RC_AA0373 cDNA clone 321222 3' similar to contains Alu repetitive element;,
104 ma	-	0.4660687	0.4756764	0.40759	0.2851871 57 i at	mRNA sequence. (from Genbank)
₩	Mesothelio				RC_AA4500	00
105 ma	-	0.4624333	0.4755229	0.407197	0.28481406 06_s_at	Sulfotransferase, estrogen-preferring
Me	Mesothelio				RC AA3983	EST: zt62d05.s1 Soares testis NHT Homo sapiens cDNA clone 33 726921 3' similar to qb:M65290 INTERLEUKIN-12 BETA CHAIN
106 ma		0.4621536	0.4752841	0.406856	0.28464383	
Me	Mesothelio					
107 ma		0.4613135	0.4752674	0.406525	0.28434384 D62584_at	t Osteoglycin (osteoinductive factor)
Me	Mesothelio					
108 ma		0.4612729	0.4748662	0.405754	0.2839068 Z74615_at	t COL1A1 Collagen, type I, alpha 1
Me	Mesothelio					
109 ma		0.4606631	0.4747266	0.405528	0.28351343 L12350_at	t THBS2 Thrombospondin 2
Me	Mesothelio				RC_AA2;	RC_AA2783 EST: zt08d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
110 ma		0.4594612	0.4745681	0.405044	0.28319076 99_at	IMAGE:712521 3', mRNA sequence. (from Genbank)
Me	Mesothelio				RC_AA4656	92
111 ma		0.45913	0.4741481	0.404472	0.28281102 87_at	RNA binding motif, single stranded interacting protein 1
Me	Mesothelio				U51010_s_a	
112 ma		0.4583692	0.4740085	0.404313	0.2824474 t	Nicotinamide N-methyltransferase gene, exon 1 and 5' flanking region
Me	Mesothelio				RC_AA4061	
113 ma		0.4579493	0.4739832	0.403959	0.28218293 63_at	FSHD region gene 1
Me	Mesothelio				RC_AA1	55 EST: zl09g08.s1 Soares pregnant uterus NbHPU Homo sapiens
114 ma		0.4559823	0.4736125	0.403626	0.28172773 54 at	cDNA clone 501470 3', mRNA sequence. (from Genbank)
Me	Mesothelio			***	RC_AA1	RC_AA1906 EST: zp89g09.s1 Stratagene HeLa cell s3 937216 Homo sapiens
115 ma		0.455856	0.4718037	0.403307	0.28141677 76_at	cDNA clone 627424 3', mRNA sequence. (from Genbank)
Me	Mesothelio				RC_AA4(
116 ma		0.4552911	0.4713191	0.402801	0.28103325 92_at	
Me	Mesothelio				W58057_s	
117 ma		0.4528318	0.4711553	0.402516	0.28071174 at	Periplakin
Me	Mesothelio					
118 ma		0.4506959	0.4708276	0.402449	0.28039315 80_at	KIAA0331 gene product
Me	Mesothelio	11				
119 1118		0.448/1/4	0.4703919	0.402328	0.2800/892 H126/4 at	t KNA binding motif, single stranded interacting protein 1

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Mesothelio Mesothelio Mesothelio 121 ma	0.4482785	0.4698058	0.401566	0.27980366 D37965_at AA490685_ 0.279367 t	ro,	PDGF receptor beta-like tumor suppressor (PRLTS) EST: aa45b03.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
Mesothelio 122 ma	0.4478299	,	0.400739		A5999	EST: ag28h10.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1090915 3', mRNA sequence. (from Genhank)
Mesothelio 123 ma	0.4469251	0.4688821	0.400611	H 0.27883661	H47955_s_a	Homo sapiens mRNA for cartilage-associated protein (CASP)
Mesothelio 124 ma	0.4427893	0.4687813	0.400237	AF HI M 0.27847564 st	-FX- JMGAPDH I33197_3_	AFFX-HUMGAPDH/M33197 3 st (endogenous control)
Mesothelio 125 ma	0.4427893	0.4686248	0.399759	AFF HUN ///////////////////////////////////	X- MGAPDH 3197_3_	Glyceraldehyde-3-phosphate dehydrogenase
Mesothelio 126 ma	0.4424716	0.4685089	0.399613	0.2777363 M59815	at	C4A Complement component 4A
Mesothelio 127 ma	0.4407809	0.4675502	0.39909	H H 10 0.27749163	FFX- UMRGE/M 0098_5_at-	Human 18S rRNA gene, complete. (from Genbank)
Mesothelio 128 ma	0.4407809	0.4674844	0.398778	AFFX- HUMRGE/M 0.27716902 10098 5 at		AFEX-HUMRGE/M10098 5 at (endogenol)s
Mesothelio 129 ma	0.4398573	0.4674425	0.39874	RC_A 0.27682126 84 at	C_AA1478 4_at	RC_AA1478 EST: zl50b04.s1 Soares pregnant uterus NbHPU Homo sapiens 84 at cDNA clone 505327 3', mRNA sequence. (from Genbank)
Mesothelio 130 ma	0.439275	0.4671778	0.398498	A. 0.27652305	971_s	Homo sapiens mRNA for serine protease (TLSP), complete cds
Mesothelio 131 ma	0.4373124	0.4669934	0.398209	0.2761791 X13334 at		CD14 CD14 antigen
Mesothelio 132 ma	0.4372183	0.4668276	0.398136	0.2757815 R22139 at		EST: yh25b11.r1 Homo sapiens cDNA clone 130749 5'. (from Genbank)
Mesothelio 133 ma	0.4347976	0.466678	0.397539	0.275471 J03764 at		PAI1 Plasminogen activator inhibitor, type I
Mesothelio 134 ma	0.4337199	0.4665658	0.397285	RC_A 0.27523434 54 at	A4301	EST: zw59h08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774399 3', mRNA sequence. (from Genbank)
Mesothelio 135 ma	0.43283	0.4664007	0.396849	RC_A 0.27479455 60_at	A2364	EST: zr75h04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669271 3', mRNA sequence. (from Genbank)

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Mesothello						
136 ma	0.4277421	0.4656811	0.396524	0.27458873 K03430	ä.	C1QB Complement component 1, q subcomponent, beta polypeptide
Mesothelio					M13690_s_a	
137 ma	0.4233997	0.4654488	0.396135	0.27432048 t		C1NH Complement component 1 inhibitor (angioedema, hereditary)
Mesothelio	_				M98447_rna	
138 ma	0.4216149	0.4654255	0.395989	0.2740517 1_at		Keratinocyte transglutaminase gene
Mesothelio					44499	Homo sapiens mRNA for glycoprotein-associated amino acid
139 ma	0.4204468	0.4652267	0.395796	0.27387062 14_at		transporter y+LAT1
Mesothelio					46217	EST: af54e12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
140 ma	0.418851	0.4645197	0.39544	0.2736085		clone 1035502 3', mRNA sequence. (from Genbank)
Mesothelio					t	EST: zu42b02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
141 ma	0.4183705	0.4183705 0.4624448	0.395152	0.27318463 t	I	clone 740619 5', mRNA sequence. (from Genbank)
Mesothelio	0					
142 ma	0.4182154	0.4182154 0.4618441	0.394914	0.27290955 U53446_at		Mitogen-responsive phosphoprotein (DOC-2) mRNA
Mesothelio			-		RC_AA2523	EST: zs12g10.s1 NCI CGAP GCB1 Homo sapiens cDNA clone
143 ma	0.4175313	0.4616772	0.39463	0.27259552 95 at		IMAGE:685026 3', mRNA sequence. (from Genbank)
Mesothelio	0.414622	0.4614214	0.394423	HG2614	, 7	- Lohol Viii Alcho 1
Mesothelio	4		27	100707	ر ان	Congger, Type VIII, Aprila 1
145 ma	0.4145766	0.4612699	0.394323	0.272106951	0.5-105-101	IGEBP4 Insulin-like growth factor-hinding profein 4
Mesothelio	0 4141904	0.4604793	0 394092	RC_AA	1820	EST: zp62f10.s1 Stratagene endothelial cell 937223 Homo sapiens
Mesothelio		2011.001.0	3001000	0.51 13:00		CONA GIOITE UZ-40 1 0, HINNA SEQUENCE. (HOIH GEHORIK)
147 ma		0.4124289 0.4600243	0.393741	0.2716834 U66075 at		Transcription factor hGATA-6 mBNA
Mesothelio	+				RC AA0538	FST: 7e25h09 s1 Soares fetal heart NhHH10W Home caniene contact
148 ma		0.411295 0.4596118	0.393425	0.27147886		clone 360065 3', mRNA sequence, (from Genbank)
Mesothelio	0				3C AA1370	EST: zl02g02.s1 Soares pregnant uterus NbHPU Homo sapiens
149 ma	0.4109646	0.4109646 0.4594492	0.393041	0.27117264 73 at	73 at	cDNA clone 491186 3', mRNA sequence. (from Genbank)
Mesothelio	-					EST: yu83h04.r1 Homo sapiens cDNA clone 240439 5'. (from
150 ma	0.4106963	0.4590546	0.392806	0.27085504 H90124	at	Genbank)
Mesothelio						
151 ma	0.4101897	0.4589709	0.392596	0.27060622	F30851_i_at	0.27060622 T30851_i_at Homo sapiens clone 24775 mRNA sequence
Mesothelio		1			AA157623_s	
152 ma	0.4100129	0.458912	0.392312	0.27025464	at	KIAA0750 gene product
Mesothelio						
153 ma	0.4089626	0.4584708	0.391809	0.27006364 L13210_at		Mac-2 binding protein mRNA
Mesothelio		10000	1)83174_s_a	
154 ma	0.405/352	0.4057352 0.4580235	0.391417	0.26973784 t		CBP1 Collagen-hinding profein 1

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	Mesothelio					RC_AA2625	RC_AA2625 EST: zs22b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
155 ma	ma	0.4054766	0.4578699	0.391138	0.26942688 56_at		IMAGE:685913 3', mRNA sequence. (from Genbank)
	Mesothelio						
156 ma	ma	0.4047325	0.4575348	0.391059	0.26906043 U90913	at	Clone 23665 mRNA sequence
	Mesothelio						
157 ma	ma	0.4040333	0.4573097	0.390543	0.26897198 0351_3_st		AFFX-HSAC07/X00351_3_st (endogenous control)
	10 CH (C) (C)					AFFX-	
Me	Mesomello	0 4040333	0.4566076	0 300404	0.0686843	HSACU//XU	No info for gono
0001	Moodtolic	0.4040333	1	0.330404	0.200003		NO IIIIO IOI deile
159 ma	Mesomello	0.4007604	0.4565281	0.390192	0.2684282 76 at	Abuss	KIAA0331 gene product
	Mesothelio					A6211	EST: af61h05.s1 Soares NhHMPu S1 Homo sabiens cDNA clone
160 ma	ma	0.3997216	0.4563727	0.389836	0.2683481 69 at		1046553 3', mRNA sequence. (from Genbank)
	Mesothelio					A2814	EST: zt04c07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
161 ma	ma	0.3992522	0.4562641	0.389698	0.26807234 65_at		IMAGE:712140 3', mRNA sequence. (from Genbank)
	Mesothelio					A2365	EST: zr75g11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
162 ma	ma	0.3990413	0.4562237	0.389546	0.26789218 42_at		669284 3', mRNA sequence. (from Genbank)
							EST: zt03d07.r1 NCI CGAP GCB1 Homo sapiens cDNA clone
	Mesothelio					AA281694_a	AA281694_a IMAGE:712045 5' similar to TR:G409466 G409466 CG1 PROTEIN
163 ma	ma	0.398028	0.4560871	0.389379	0.267438 t	-	PRECURSOR. [2] TR:G296164;, mRNA sequence. (from Genbank)
	Mesothelio						
164	164 ma	0.3975346	0.4558353	0.388906	0.26728898 U89942_at		Lysyl oxidase-related protein (WS9-14) mRNA
	Mesothelio					AFFX- M27830_5_a	
165 ma	ma	0.3964796	0.4555971	0.388827	0.26700023		AFFX-M27830_5_at (endogenous control)
	:					AFFX-	
166 ma	Mesomello	0.3964796	0 4549846	0.388596	0.26667702 ₁₋₂	7830_5_a	Himan 28S ribosomal BNA gene complete cds (from Genhank)
	Mesothelio					AA4357	EST: zt79h07.s1 Soares testis NHT Homo sapiens cDNA clone
167 ma	ma	0.3962999	0.454874	0.388293	0.26649773 69	s at	728605 3', mRNA sequence. (from Genbank)
							EST: zv92d05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767241 5' similar to TR:E213399 E213399 TISSUE
	Mesothelio					AA418478_a	CARBOXYPEPTIDASE INHIBITOR.;, mRNA sequence. (from
168	168 ma	0.3939805	0.4548523	0.387803	0.26626006	+	Genbank)
169	Mesothelio 169 ma	0.3938985	0.4547785	0.387513	ן 0.26606774 t	U24389_s_a t	Lysyl oxidase-like protein gene
Mes	Mesothelio	0 3038608	0.4848408	0782040	0.26581.43	0.26581431144548 at	AOD1 Amisanoria 1 (channal forming integral protein 28kD)
0/1	Ша	0.3930090	- 4	- 1	0.2030143		Act : Aquaponii I (dianiia-loiniig iitegial pioteii, zono)

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

Mesothelio	io				ii taal taali 8" taali qaa ahii	That there that east that the third that
	0.3933392	2 0.4539185	5 0.386935	KC_A 0 2655198 74 at	KC_AA1364	
Mesothelio ma	0.3915184	4 0.4537064			RC_AA2554 32_at	
Mesothelio	0.3911737	7 0.4534501	0	0.2650505	AB002364_a	
Mesothelio		t			1	FST: Himan fetal ling SPAA 5:
ma Mesothelio	0.3908614	4 0.4529941	0.386238	0.2646919 D31294	D31294_at	(from Genbank)
)	0.3903879	9 0.4527878	0.386039	0.26459667 H42262	H42262 at	EST: yo63a04.r1 Homo saplens cDNA clone 182574 5'. (from Genhank)
ma	0.3902266	0.3902266 0.4526013	0.385761	0.264310031	(57351	RPS3 Ribosomal protein e3
Mesothelio ma	0.3898825	0.4521105	0.385573	0.2640924	AA203274_a	AA203274_a CDNA clone 446465 5' similar to contains element MER27 repetitive
Mesothelio ma	0.3867889			0.0830344	D21254_s_a	element;, mkNA sequence. (from Genbank)
Mesothelio		1		1100003:0		Cadnerin 11 (OB-cadherin, osteoblast)
Mesothelio	0.3865562	0.4516666	0.385119	0.26351938 L37882 at		Frizzled gene product mRNA
, [0.3860667	0.4516502	0.385014	0.26335284 1137283 at		Miorefikell
Mesothelio ma	0.3859107	0.4508272	0.387867	7 70000	Ø	micronalirassociated glycoprotein-2 MAGF-2 mRNA
Mesothelio			1001000	0.2031401	770000	FN1 Fibronectin 1
ma Mesothelin	0.3850843	0.4505113	0.384726	0.26282948 59 at	ال AA6211 9 at	59 at 1046544 3', mRNA sequence, (from Genhank)
	0.3828769	0.4502988	0.384253	0.2626094 25081 at		ABHO Anhair
Mesothelio	0.3811958	0.4500729	0.384044	RC_A 0.26247543.25.24	A3978	EST: zt47g02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
Mesothelio	0.2004442	7505077			327_i	cione 725522 3', mRNA sequence. (from Genbank) EST: zf65e11.r1 Soares retina N2b4HR Homo seging conto
Mesothelio	71 17	0.4491213	0.383866	0.26229405	-	381836 5', mRNA sequence. (from Genbank)
	0.3794902	0.4493083	0.383752	RC_A	A6003	1
	0 3791040	0.440000		0.002020		Endocytic receptor (macrophage mannose receptor family)
	2000	0.440332	0.3835	0.26184973 U73377	at	SKI V-ski avian sarcoma viral oncogene homolog
	0.3785763	0.4486814	0.383025	0.26169628 D57823	±	H-Sapiens mRNA for Sec23A instant 2240b
	0.3774908	0.4485579	0.382896	0.26139084 52	71010 04 0	dd9h17 (1148bb
١				10110000104:0	1010 dt-21	czorosocytot lo al-z/Peptidylprolyl isomerase C (cyclophilin C)

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Mesothelio						
190 ma	0.3774908	0.4485042	0.382475	0.26129478 S71018 at	S71018_at	Cyclophilin C [human, kidney, mRNA, 883 nt]
Mesothelio					RC AA1612	
191 ma	0.3765168	0.4484175	0.382411	0.26107258 92_s_at	92_s_at	Interferon, alpha-inducible protein 27
Mesothelio					RC_AA4875	EST: ab20h12.s1 Stratagene lung (#937210) Homo sapiens cDNA
192 ma	0.3753303	0.4482835	0.382331	0.26083657 57_at		clone 841415 3', mRNA sequence. (from Genbank)
Mesothelio	io 0.373353	0.4482321	0 382308	20000	A4103	EST: zv16e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
Mesothelio	1	ı	0.305.00	0.200000000 57 at	0001	733816 3', mKNA sequence. (from Genbank)
194 ma		0.3705493 0.4481449	0.38173	0.26035422,40.at	A4282	ES I: zw51d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
Mesothelio	+		2	0.40000442	40 at	Golfe (1997) 3, IIIRIVA Sequence. (Ifom Genbank)
195 ma	0.3699757	0.4475755	0.38142	0.2600308	_at	Homo sapiens agrin precursor mRNA, partial cds
Mesothelio					W38778 s	EST: zb27g04.r1 Soares parathyroid tumor NhHPA Homo saniens
196 ma	0.3692148	0.3692148 0.4473875	0.38125	0.25979215 at		cDNA clone 304854 5', mRNA sequence. (from Genbank)
Mesothelio	.0				HG2743- HT2846 c c	
197 ma	0.3680646	0.4467453	0.381,135	0.2594731	20107	Caldesmon 1, Alf. Splice 4, Non-Muscle
Mesothelio		0.3676729 0.4467103	0 380882	0.050000	06700_s_a	
Mesothelio	+-		700000	0.500000	1 A 4 4 7 E 4 0 0	COLSAT Alpha-1 type 3 collagen
199 ma	0.3667775	0.4459901	0.380444	0.25922918	AA 14/310_S	EST: ZISUCTZ.FT Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505366 51 mRNA ceruance (from Contract)
Mesothelio	0				AA393089 a	EST: #60b10 rd Source facilie NLT Lamb accient and all
200 ma	0.366183	0.4458225	0.380323	0.25888658		t 727579 5', mRNA sequence (from Genhank)
Mesothelio			0000		(51441_s_a	(1) 1001100
Mosotholi	0.3036273	0.4434646	0.380123	0.25863868 t		SERUM AMYLOID A PROTEIN PRECURSOR
202 ma	0.3656358	0.4448871	0.379825	RC_A 0.25832933 28_at	A4005	EST: zu70f09.s1 Soares testis NHT Homo sapiens cDNA clone 743369 3', mRNA sequence, (from Genbank)
Mesothelio	0				RC AA2269	=ST: 2r/8r03 et Ctratagona NIT3 politografia escalare
203 ma	0.3641193	0.444782	0.379658	0.2581616 68 at		Sapiens cDNA clone 663796 3' mRNA serillance (from Conhant)
Mesothelio	0 2624040	0000000			T	Company of the second of the s
Mesothelio		0.444/82	0.3/9348	0.25/93135 L36033_at		SDF1 Stromal cell-derived factor 1
205 ma	0.3613996	0.4444318	0.379111	0.2577622 U28369	at	Semaphorin V mRNA
Mesothelio 206 ma	0.3599863	0.4434809	0.378983	0.2573951 R77200 at		EST: yi65g05.r1 Homo sapiens cDNA clone 144152 5'. (from Genhank)
Mesothelio 207 ma	0.3596864	0.4430622	0.378786	0.257216161	HZ906_s_a	Clathrin, Light Polypeptide B. Alf. Splice 2
					-	

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AA094507_s EST: cp0543.seq.F Fetal heart, Lambda ZAP Express Homo sapiens AA465016_a|;contains element LTR3 repetitive element ;, mRNA sequence. (from HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "A RC_AA1016 | Homo sapiens herpesvirus entry protein B (HVEB) mRNA, complete EST: zx80d02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA sapiens cDNA clone 593840 3', mRNA sequence. (from Genbank) clone 810051 5' similar to TR:G1020091 G1020091 NEUROPSIN. EST: zs42g06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zo87a05.s1 Stratagene ovarian cancer (#937219) Homo Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-Homo sapiens serum-inducible kinase mRNA, complete cds Homo sapiens PNG pseudogene, complete sequence FGF9 Fibroblast growth factor 9 (glia-activating factor) AFFX-HSAC07/X00351_3_at (endogenous control) PPIB Peptidylprolyl isomerase B (cyclophilin B) 687898 3', mRNA sequence. (from Genbank) Low-Mr GTP-binding protein (RAB31) mRNA Homo sapiens clone 24742 mRNA sequence cDNA 5', mRNA sequence. (from Genbank) HSPB1 Heat shock 27kD protein 1 RAS-RELATED PROTEIN R-RAS hydroxylase), alpha polypeptide II FORM" PRECURSOR No info for gene Genbank) 0.25602996 0351 3_at-2 RC AA1668 RC_AA2358 U59877_s_a RC_AA4210 RC_AA1258 HSAC07/X0 0.25659284 M63835_at ਬ HSAC07/X0 aţ 0.25492033 M63573 at aţ Ħ 0.25570235 0351 3 at 0.25448275 D14838 at 0.2551188 M14949 0.256252 W49521 0.2570701 Z23090 0.25554204 C01721 0.2547859 03 f at AFFX-0.2553497 10 at 0.2546368 51 at 0.25397906|01 at 0.2537038 61 at ₩ 0.25694147 0.25640056 0.25418022 0.37818 0.37789 0.377562 0.376993 0.376849 0.377264 0.378631 0.376497 0.376394 0.376335 0.376185 0.375819 0.375668 0.375443 0.375166 0.375647 0.374856 0.3573782 0.4410614 0.3595741 | 0.4426197 0.3584483 0.4419668 0.359108 0.4422325 0.3590687 | 0.4419912 0.3536399 0.4405411 0.3528539 0.4402399 0.3462601 | 0.4391219 0.3536399 0.4407468 0.3526817 0.4399075 0.3468566 0.4391219 0.3446173 | 0.4382553 0.3441015 | 0.4379733 | 0.4397745 0.439612 0.346117 0.4384002 0.3495798 0.4394777 0.3497838 0.3496834Mesothelio Mesothelio 209 ma 210 ma 211 ma 214 ma 208 ma 212 ma 213 ma 215 ma 217 ma 218 ma 219 ma 220 ma 221 ma 222 ma 223 ma 224 ma

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Docket No.:

The detail of the print of the

Docke	t No.:	2825.2020	0-002
Title:	Genet	ic Markers	for Tumors
Invente	ors: Sri	dhar Rama	swamy, <i>et al</i> .

	Mecothelio				٥		EST: zw75d12.s1 Soares testis NHT Homo sapiens cDNA clone
225 ma	mesourcilo	0.3438057	0.4373981	0.374545	0.25346217 71 at	7473D	nozosa o similar lo contains element PTR/Tepetitive element;, mRNA sequence. (from Genbank)
	Mesothelio				AA44(AA446512 a	Zw67d05.r1 Soares testis NHT Homo sapiens cDNA clone 781257 5',
226 ma	ma	0.3435434	0.4373783	0.37439	0.25316134 t	ı	mRNA sequence. (from Genbank)
Me.	Mesothelio	0 3/3/00	0.4970064	7007760	HG544-		
777	Mesothelio	0.040132		0.374004	0.2330046Z F11344 at	L	Endotnellal Cell Growth Factor 1
228 ma	ma	0.3416644	0.3416644 0.4371724	0.373831	0.25282648 59 at	44013	Chromogranin A (parathyroid secretory protein 1)
	Mesothelio						EST: Human aorta cDNA 5'-end GEN-308H02. mRNA sequence
229 ma	ma	0.340757	0.436476	0.373435	0.25258577 D62633_f_at (from Genbank)	33 f at (from Genbank)
	Mesothelio				2	DC AA1820	7.1. mp. 2014 0.4 Other bearing and the lift in 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
230 ma	ma	0.3392169	0.3392169 0.4364047	0.373303	0.25240272 01 r at		CDNA clone 624811 31 mRNA sequence (from Genhank)
_	Mesothelio	The second secon			RC A	338	EST: zr47a02 s1 Soares NhHMPu S1 Homo saniens cDNA clone
231 ma	ma	0.3391393	0.4361565	0.373245	0.25227684 54 at		666506 3', mRNA sequence, (from Genbank)
	Mesothelio				RC A	RC AA0183 B	EST: ze41d12.s1 Soares retina N2b4HR Homo sapiens cDNA clone
232 ma	ma	0.3385454	0.4361417	0.3728	0.25199637 46_at		361559 3', mRNA sequence. (from Genbank)
Me: 233 ma	Mesothelio	0.3370938	0.3370938 0.4360204	0.372671	HG3494-0 0 2518249 HT3688	. to	Nirelear Easter N# 115
	Moodic					5	ממוסמו ו מסכו ו וו ווס
734 ma	Mesoureilo	0.3361548	0 4355957	0.372566	KC_A 0.25157008/45_2t	A2335	EST: zr30h12.s1 Stratagene NT2 neuronal precursor 937230 Homo
2	Mesothelio	210000		0,000	0.45 157 1000 45 at	A 4 500	Sapiens CLINA Gone 604967 3, MKNA Sequence. (from Genbank)
235 ma	ma	0.3359577	0.4354698	0.37239	0.251322191 at		Cone 809400 31 mRNA sequence (from Genhank)
-	Mesothelio						serio de la constanta de la co
236 ma	ma	0.3351829	0.4351678	0.372306	0.25119382 L41939 at-2		EphB2
1	Mesothelio				The second secon		
237 ma	ma	0.3351829	0.4350362	0.371858	0.25103143 L41939	, a	Receptor protein-tyrosine kinase (HEK5) mRNA, 3' end
	Mesothelio				AA150	J6 2.29	AA159673 a FST: zo80a02 r1 Stratagene overien cencer (#037240) Homo canione
238 ma	ma	0.3350738 0.4346767	0.4346767	0.371476	0.2506894 t	5,	cDNA clone 593162 5', mRNA sequence. (from Genbank)
	Mesothelio				RC_A	A4302	
239 ma	ma	0.3344775	0.4345905	0.371373	0.25047874 09_at		Homo sapiens LIM protein mRNA, complete cds
- ,070	Mesothello	70700000	0007				EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence.
740 IIIa	<u></u>	0.3320101	0.4344939	0.3/1108	0.2503522 D3141/ at		(from Genbank)
Me. 241 ma	Mesomello	0.3312918	0.4343924	0.370959	RC_A 0.25015047 79 at	A2923	EST: zt51h09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725921 3', mRNA sequence. (from Genbank)
Mes 242 ma	Mesothelio	0.3308044	0.3308044 0.4342115	0.370559	AA380	AA380393_a	EST: EST93352 Supt cells Homo sapiens cDNA 5' end, mRNA
274		4.0000000	0.4047113	0.070009	0.23004091		sequence. (irom Genbank)

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_	Mesothelio				RC_AA4177	111
243 ma	na	0.3307214	0.434191	0.37051	0.24973235 61_at	Homo sapiens clone 24416 mRNA sequence
	Mesothelio					AA120886_a EST: zk99g11.r1 Soares pregnant uterus NbHPU Homo sapiens
244 ma	na	0.3255457	0.4341651	0.370429	0.24952182	cDNA clone 491012 5', mRNA sequence. (from Genbank)
Mes 245 ma	Mesothelio	0.3250185	0.4330003	0020260	RC 0 24624624 46	
7	Acce 14 13	+	- 1	3.		1031/b2 3', mKNA sequence. (from Genbank)
Mes 246 ma	Mesotnello	0.3236072	0.4296275	0.9700E9		
1	Mesothelin		1	0.0	0.24910010 05/099 at	al APEG-1 mKNA
247 mg		0.3234028	0.4005405	000000		
1	Mesothelin	0.02070	- 1	0.303922	0.24033404	-
248 ma	nesoureilo na	0.3232438	0.4334988	0.369864	0.24873239 60 at	1990 EST: ar10g04.s1 Soares testis NHT Homo sapiens cDNA clone 1031286.31 mRNA ceruiance (from Cenhout)
2	Mesothelio				RC	
249 ma	Ja Ja	0.3231517	0.4334652	0.369814	0.24862197	antiden 2
2	Mesothelio					
250 ma	7a	0.3229977	0.4334141	0.369812	0.24830554 M94893 at	at TSPY Testis specific protein Y-linked
2	Mesothelio					T
251 ma	ງສ	0.3226399	0.4334072	0.369423	0.24812084 M97675	at Protein tyrosine kinase t-Ror1 (Ror1) mRNA
<u>2</u>	Mesothelio					
252 ma	Ja	0.3217647	0.4330064	0.369396	0.24798355 HT3165	at Tyrosine Kinase, Receptor Axl, Alt. Splice 2
	Mesothelio				C	
253 ma)a	0.3216868	0.4329847	0.369252	0.2477676 33 at	roz EST: Zpuddub.st Stratagene ovarian cancer (#93/219) Homo
2	Mesothelio					described and described of minds adductive. (Holl delibative)
254 ma	ງຊ	0.3178299	0.3178299 0.4328803	0.36904	0.24759671 1.20591	at ANX3 Annexin III (linocortin III)
2	Mesothelio					
255 ma	la	0.3175295	0.4327803	0.368648	0.2474494 Z74616	0.2474494 Z74616 s at COL1A2 Collagen tyne I alpha-2
2	Mesothelio				Z25821 ma	na Dodecenovl-Coenzyme A delta isomerase (3.2 trans-enovl-Coenzyme
256 ma	13	0.3172893	0.432263	0.368564	0.247156651 s at	
2	Mesothelio				RC AA3	RC AA3389 EST: EST44060 Fetal brain I Homo saniens cDNA 3' and mRNA
257 ma	ıg	0.3145921	0.4321356	0.368308	0.24703448 60_at	sequence. (from Genbank)
2	Mesothelio	· · · · · ·			HG862-	
258 ma	la	0.3130382	0.4320917	0.368208	0.24677531 HT862 s	at Transition Protein 2
Me	Mesothelio	0 0 0 0 4 1 4 1 10		0		
11 207	2	0/11710.0	0.4313920	0.368095	0.24668695 at	TAP binding protein (tapasin)
Me 260 ma	Mesouneilo	0.3111942	0.4318494	0,368035	RC_AA14 0.24640216 44 at	RC_AA1490 EST: zl45d09.s1 Soares pregnant uterus NbHPU Homo sapiens 44 at conversione 504881 3' mRNA sequence (from Conbon)
Σ	Mesothelio		3			
261 ma	la	0.3110852	0.4317474	0.367852	0.2462237 D12485_at	at Plasma cell membrane glycoprotein (PC-1) mRNA
						TOTAL PROPERTY DESCRIPTION OF THE PROPERTY OF

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sothelio					<u>X</u>	C_AA5983	RC_AA5983 EST: ae40d12.s1 Gessler Wilms tumor Homo sapiens cDNA clone
262 ma 0.3106881 0.4316641 0.36	0.4316641 0.3	0.3	0.36	6783	0.24611571 97	_at	898295 3', mRNA sequence. (from Genbank)
Mesothelio					<u> </u>	RC_AA6093	EST: af13g03.s1 Soares testis NHT Homo sapiens cDNA clone 1031572 3' similar to contains Alu repetitive element;, mRNA
263 ma 0.3089063 0.4315382 0.367609	0.4315382	0.4315382	0.36760	<u>0</u>	0.24600083 06_at		sequence. (from Genbank)
Mesothelio 0.3080049 0.4314415 0.367396	0.3080049 0.4314415	0.4314415	962386	L	0.2458277 W28414	4	EST: 46g7 Human retina cDNA randomly primed sublibrary Homo saniens cDNA mRNA sequence (from Genhank)
sothelio					Ō	Sa	EST: HUMGS0008391, Human Gene Signature, 3'-directed cDNA
265 ma 0.3077215 0.4312745 0.367349	0.3077215 0.4312745		0.367349		0.24565282 t		sequence, mRNA sequence. (from Genbank)
sothelio					R	A4814	EST: zv45a05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
266 ma 0.3076487 0.4308608 0.367075	0.3076487 0.4308608	0.4308608	0.367075		0.2454651 40_at		clone 756560 3', mRNA sequence. (from Genbank)
Mesothelio	0.3061175 0.4305389	0.4305389	0.366964		RC 0 245164 95	_AA6207	EST: af95b02.s1 Soares testis NHT Homo sapiens cDNA clone 1055499.3" mRNA secretore (from Genhank)
sothelio 0.3055421 0.4305275	0.3055421 0.4305275	0.4305275	0.366865		0.24489594 009770	at	Costeine-rich heart protein (hCRHP) mRNA
sothelio							
269 ma 0.3054353 0.4300905 0.366761	0.3054353 0.4300905	0.4300905	0.366761		0.24475668 X69910	ät.	P63 mRNA for transmembrane protein
Mesothelio 0.3033843 0.4299874 0.366548	0.3033843 0.4299874 0.366548	0.4299874 0.366548			0.24456517 X03350_at		ADH2 Alcohol dehydrogenase 2 (class I), beta polypeptide
Mesothelio 0.3031211 0.4299009 0.366409 0	0.3031211 0.4299009 0.366409	0.4299009 0.366409		0	RC_A 0.24445161 99_at	44588	EST: zx88d07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810829 3', mRNA sequence. (from Genbank)
Mesothelio 0.3027946 0.4297488 0.366333 0	0.3027946 0.4297488 0.366333	0.4297488 0.366333		0	U.244193661	U28694_s_a t	Chemokine (C-C motif) receptor 3
	20,000	0			A	A129547_a	AA129547_a EST: zn83f01.r1 Stratagene lung carcinoma 937218 Homo sapiens
othelio	0,3021324 0,4231100 0,300134	4610000			0.24401 123 [CDINA CIOTE 304735 3, HIRINA SEQUENCE. (HOLH GENDRIK)
0.3018513 0.4297033 0.366055	0.3018513 0.4297033 0.366055	0.4297033 0.366055		0	0.24401702 X51441	Ħ,	SERUM AMYLOID A PROTEIN PRECURSOR
Mesothelio 0.3018349 0.4294328 0.366008 0	0.3018349 0.4294328 0.366008	0.4294328 0.366008		0	0.24376348 D21255 at		CDH11 Cadherin 11 (OB-cadherin)
	0.3016914 0.4293107 0.365826	0.365826			A 0.243560751	σ,	Desmonlakin (DPI DPII)
sothelio	0 2012525 0 12002200 0 2055011	0 40000000		1	R	A4050	EST: zu19g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
othelio	0.3013330 0.4282300 0.303014	0.4292300 0.303014		2	0.24332042 49 at	A2916	738466 3, IIIKNA Sequence. (Irom Genbank) FST: 2445e11 s1 Soares overy frimor NhHOT Homo capiens CDNA
0.3000722 0.4291593 0.365541	0.3000722 0.4291593 0.365541	0.4291593 0.365541		0	0.2433352624_s_at) -	clone 725324 3', mRNA sequence. (from Genbank)
Mesothelio 0.2996498 0.4290913 0.365257	0.2996498 0.4290913	0.4290913	0.365257		RC 0.24327342 50	_AA0270 _at	EST: zk02g01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469392 3, mRNA sequence. (from Genbank)
Mesothelio 0.2995715 0.4284799 0.365113	0.2995715 0.4284799 0.365113	0.365113		_	0.24310869 Y00815	at	PTPRF Protein tyrosine phosphatase, receptor type, f polypeptide

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Docket No.:	2825.2020-002
Title: Genetic	Markers for Tumors
Inventors: Srid	har Ramaswamy, et al.

Mecotholio				LICE CO. III. AND THE CO.	- 1.	भूतम् भूतम् वत्त्री वत्त्री भूतम् भूतम्
281 ma	0.2993168	0.4283962	0.364948	0.24270055	H52862 at	T-plastin
Mesothelio					RC AA4528	
282 ma	0.2988851	0.428394	0.364857	0.24244279 55_at	55_at	Human mannose-specific lectin (MR60) mRNA, complete cds
Mesothelio					X60673_s_a	
200 IIIa	0.29//9/5	0.428258	0.364746	0.2423502	1	Adenylate kinase 3
Nesotnello 284 ma	0.2977417	0.428211	0.364509	0.24218814	M94065_s_a t	Dihydroorotate dehydrogenase
Mesothelio	The same of the sa					and a confirmage land
285 ma	0.2976749	0.4280612	0.364124	0.24208091 J03040 at	J03040 at	SPARC SPARC/osteonectin
Mesothelio					RC AA6095	
286 ma	0.2968232	0.4278942	0.364015	0.24190435 97 s at	97 s at	H.sapiens mRNA for galectin-8
Mesothelio 287 ma	0.2961833	0.4276793	0.363967	RC A 0 241727 38 at	RC_AA6001	Dihocomal protein Coo
Mesothelio		1		7.1.7.0	00 at	Nibosofilal protein SZU
288 ma	0.2957991	0.4276401	0.363836	0.24150997 R64459	R64459 at	OX-2 MEMBRANE GI VCOPPOTEIN DBECLIDSOD
Mesothelio					613	EST: 2x85a08 e1 Societo fotos Oktober
289 ma	0.2954979	0.4273034	0.363687	0.24144916 00 at		clone 796310 3', mRNA seguence (from Genhank)
Mesothelio						
290 ma	0.2951317	0.4272735	0.363419	0.2413078 Z48482 at	Z48482 at	MMP2 Matrix metalloproteinase 2
Mesothelio					RC AA4044	
291 ma	0.2943574	0.4272735	0.363102	0.24115908 26 at	26 at	Homo sabiens snurportin1 mRNA complete cds
Mesothelio					4A495758 s	AA495758 s EST: zw04d05.r1 Soares NhHMPu S1 Homo saniens cDNA clone
292 ma	0.2942408	0.4272478	0.363017	0.24086666	at	768297 5" mRNA sections (from Genhank)
Mesothelio					AA2837	FST: 718d04 e1 Soares overy times NHHOT Long against ANA
293 ma	0.2938848	0.4270558	0.362996	0.24081162 74 at		clone 713479 31 mRNA serience (from Carbart)
Mesothelio					The state of the s	EST: ww36d01 r1 Home conjone collaboration of 1200 of 1200 r1 th
294 ma	0.2937915	0.4269194	0.362802	0.2406264 N81162 at		Genbank)
Mesothelio					8	EST: 2542006 S1 Soares NhHMPh S1 Homo sanjons CDNA Slond
295 ma	0.2937113	0.4262981	0.36248	0.24039601 03 i at		687898 3', mRNA sequence, (from Genhank)
Mesothelio					RC AA2584	
296 ma	0.2933489	0.4259831	0.362187	0.2402035 82	s at	Homo sapiens mRNA for zinc finger protein complete cds
Mesothelio						con plaid too 'tipe of log
297 ma	0.292262	0.4255233	0.362161	0.24014857 U14407 at		L15 Interleukin 15
Mesothelio						
298 ma	0.292262	0.4253293	0.361853	0.23989204	J14407 at-2	0.23989204 U14407 at-2 Interleukin 15
Mesothelio					458509 cds	M58509 cds FDXR gene (adrenodoxin reductase) extracted from Human
299 ma	0.2911484	0.425132	0.361777	0.23972273 1_s_at	s at	adrenodoxin reductase gene
Mesothelio	1			<u> </u>	3C_AA2554	RC_AA2554 EST: zr83c09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
300 ma	0.2908772	0.4249571	0.361405	0.23955049 80 at	30 at	682288 3', mRNA sequence. (from Genbank)

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		_	_			
Me 301 ma	Mesothelio	0.2904261	0.4248895	0.361357	RC_AA2165 0.23939008 89 at	165 EST: zq94e07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 649668 3', mRNA sequence, (from Genbank)
	Mesothelio					+
302 ma	ma	0.2900542	0.4248895	0.361357	0.23922196 i at	
	Mesothelio		1			
303 ma	ma	0.2899059	0.4248767	0.361203	0.23908468 M86933_at	at AMELY Amelogenin (chromosome Y encoded)
	Mesothelio				RC_AA4784	
304 ma	ma	0.2895241	0.4248321	0.361068	0.23890056 11_at	cds
	Mesothelio				AA1741	AA174185_a Solute carrier family 9 (sodium/hydrogen exchanger), isoform 3
305 ma	ma	0.289039	0.289039 0.4247147	0.360984	0.23857582 t	regulatory factor 1
	Mesothelio					
306 ma	та	0.2880138	0.4246508	0.360765	0.23843938 M69023_at	at Globin gene
	Mesothelio	v			RC_AA4500	500 Homo sapiens cargo selection pretein TIP47 (TIP47) mRNA,
307 ma	ma	0.2878855	0.4238956	0.360589	0.2381562 45_at	complete cds
	Mesothelio					
308 ma	ma	0.287489	0.4238037	0.360492	0.23806638 U35139_at	at NECDIN related protein mRNA
	Mesothelio				RC_AA4192	
309 ma	ma	0.2870542	0.4237463	0.360457	0.23803474 00_at	KIAA0475 gene product
	:					
	Mesothelio	1		1	RC_AA4361	
310 ma	ma	0.2870087	0.423/195	0.36015	0.23/81359 /4_at	repetitive element;, mRNA sequence. (from Genbank)
	Mesothelio				M16474_s_a	Sa
311 ma	ma	0.2865384	0.4234672	0.36001	0.23762485 t	Butyrylcholinesterase, mRNA
	Mesothelio					ICAM1 Intercellular adhesion molecule 1 (CD54), human rhinovirus
312 ma	та	0.2851837	0.4234127	0.359979	0.23761922 M24283_at	at receptor
	Mesothelio				RC_AA4476	
313 ma	ma	0.284964	0.284964 0.4223645	0.359705	0,23733614 50_at	
	Mesothelio				W38597_s_	s_ EST: zb20c11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA
314 ma	ma	0.2849332	0.4222865	0.359699	0.23726723 at	
	Mesothelio		•		The state of the s	
315 ma	ma	0.2843717	0.4222146	0.359447	0.23711482 Y11709 at	at Extracellular matrix protein collagen type XIV, N-terminus
	Mesothelio					
316 ma	ma	0.2841564	0.4220865	0.359292	0.23703521 D78011	_at Dihydropyrimidinase
	Mesothelio					
317 ma	ma	0.2830383	0.4219773	0.3592	0.23688203 W67899	ੜ
	Mesothelio					
318 ma	ma	0.2829634	0.2829634 0.4217566	0.359142	0.23675115,302783	at normone binding protein p55)

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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Docket	t No.:	2825.2020-002
Title:	Geneti	c Markers for Tumors
Invento	ors: Sric	dhar Ramaswamy, et al.

Mesothelio						
319 ma	0.282797	0.421396	0.358936	0.2365317 C15160	at	Keratin 8
Mesothelio					HG2788-	
320 ma	0.2825536	0.4213612	0.358914	0.23646818 HT2896	äŧ	Calcyclin
Mesothelio			-		AA320369 s	And the second s
321 ma	0.2824925	0.4212976	0.358765	0.2363912		GLUT1 C-terminal binding protein
Mesothelio					00000	TOT
322 ma	0.2823211	0.4208453	0.358605	0.23622328 37 at	70040	CDNA clone 428719 3* mRNA sequence (from Genhan)
Mesothelio						EST: w38c10 r1 Homo saniens cDNA clone 273522 5' (from
323 ma	0.2814243	0.4207469	0.35844	0.23589112 N44757	at	Genbank)
					AFFX-	
Mesothelio					HUMGAPDH	
324 ma	0.2811649	0.4206722	0.358427	0.2356065 at		AFFX-HUMGAPDH/M33197 3 at (endogenous control)
Mesothelio					HUMGAPDH	
325 ma	0.2811649	0.4205172	0.358021	0.23548514 at-2	0 /610	Glyceraldehyde-3-phosphate dehydrogepase
						EST: zx10a05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
326 ma	0.2706657	73000010	750576.0	10000	486	clone 786032 3' similar to contains Alu repetitive element; mRNA
Mecotholio	1,500812.0	0.4203257	0.35/8/5	0.23530/// 2/ t at		sequence. (from Genbank)
327 ma	96770760	0.4200050	0.057700	1 0 0	_AA4280	EST: zw5/b01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
Mocotholio	0.2194130	0.4200859	0.35/1/23	0.23518856 69	at	clone 774121 3', mRNA sequence. (from Genbank)
328 ma	0.2700168 0.4100642	0.4400542	7027360	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	A2847	EST: zt24a09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
Mecotholio	0.2730100	0.4189343	0.337007	0.23511584 Z1 S	a, at	clone /14040 3', mRNA sequence. (from Genbank)
329 ma	0.2790019 0.4198158	0.4198158	0.357442	0.23497021 t	112903_S_a	ADH1 Alcohol dehydrogenase 1 (class I), alpha polypeptide
:						EST: af47g08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
Mesothello	1			<u> </u>	,_AA6216	done 1034846 3' similar to TR:G240986 G240986 LMW G-PROTEIN.
330 ma	0.2789257	0.4198058	0.357342	0.23492737 01	_at	., mRNA sequence. (from Genbank)
Mesomello	0 0787033	0.4406574	1		D62504_s_a	EST: Human aorta cDNA 5'-end GEN-292H10, mRNA sequence.
Contholio	0.21012.0	4/00614.0	0.33/23	0.234794211		(trom Genbank)
332 ma	0.2784993	0.4191384	0.357153	RC_A 0.23463072 82_at	A2840	EST: zs49b09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700793 3' mRNA sertience (from Genhank)
Mesothelio				d	\A399338 a l	AA399338 a FST: 749d10 r1 Spares ovary filmor NNHOT Homo capiens CDNA
333 ma	0.2780942	0.4188893	0.357132	0.23457842 t	5	clone 725683 5', mRNA sequence, (from Genbank)
Mesothelio 334 ma	0.9779908 0.4488893	0.4488873	0.957111	7 00244400		EST: Human aorta cDNA 5'-end GEN-331C09, mRNA sequence.
Id	0.2773300	0.4 100023	0.337114	0.23441109 D79819_at		(from Genbank)

The state of the s

	Mesothelio		-		1	VA431876_a	AA431876_a EST: zw51h07.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
335 ma	ma	0.277864	0.418596	0.356924	0.23436195		clone 773629 5', mRNA sequence. (from Genbank)
	Mesothelio					_AA2562	EST: zr80c01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
336	336 ma	0.2773325	0.4185888	0.356664	0.23414975 68	at	681984 3', mRNA sequence. (from Genbank)
	Mesothelio						EST: zd67d01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
337	337 ma	0.2767816	0.4184786	0.356579	0.23399428 W76492 at		clone 345697 5', mRNA sequence. (from Genbank)
	Mesothelio	(4	1		A4469	EST: zw85f08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
338	338 ma	0.2764948	0.418467	0.356322	0.23378077 68_at	38 at	clone 783783 3', mRNA sequence. (from Genbank)
	Mesothelio					AA478194_a	- Interest of the Control of the Con
339	339 ma	0.2760193	0.4183464	0.356215	0.23365131 t		Murine leukemia viral (bmi-1) oncogene homolog
	Mesothelio						
340	340 ma	0.2753549	0.4179443	0.356111	0.2334893 X51521	-at	VIL2 Villin 2 (ezrin)
	Mesothelio						
341	341 ma	0.2751349	0.4177954	0.355983	0.23332065 T50262_at		Human ribosomal protein L35 mRNA, complete cds
	Mesothelio			-		RC_AA4248	EST: zw04b04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
342	342 ma	0.2744901	0.417682	0.355905	0.23313068 13_at		768271 3', mRNA sequence. (from Genbank)
	Mesothelio					RC AA2517	
343	343 ma	0.2735335	0.4176089	0.355783	0.2330342 72 at	2 at	H.sapiens mRNA for HES1 protein
	Mesothelio						Control of the Contro
344	344 ma	0.2734388	0.4174465	0.35544	0.23292561 M55210 at		LAMC1 Laminin, gamma 1 (formerly LAMB2)
	Mesothelio					RC AA4320	EST; zw89c01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
345	345 ma	0.2731738	0.4174359	0.355271	0.23270084 74 at		clone 784128 3', mRNA sequence. (from Genbank)
	Mesothelio						
346	346 ma	0.2729727	0.4172877	0.355165	0.2325193 M11433	411433_at	RBP1 Cellular retinol-binding protein
	Mesothelio					7_xpt	HPR from Human haptoglobin and haptoglobin-related protein (HP
347	347 ma	0.2724803	0.4170156	0.355145	0.23242764 2_s_at		and HPR) genes./ntype=DNA /annot=mRNA
	Mesothelio				<u> </u>	4109	EST: zv39g09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
348	348 ma	0.27241	0.4169379	0.355086	0.23223045 54_at		clone 756064 3', mRNA sequence. (from Genbank)
	Mesothelio					AB002373_a	
349	349 ma	0.2722752	0.4167611	0.354783	0.23212373		KIAA0375 gene product
	Mesothelio					RC_AA1366	EST: zk99a04.s1 Soares pregnant uterus NbHPU Homo sapiens
350 ma	ma	0.2719807	0.4167071	0.354577	0.23202516 60 f at	30 f at	cDNA clone 490926 3', mRNA sequence. (from Genbank)
	Mesothelio						
351		0.2717615	0.4166851	0.354459	0.23187621 HT998_s	<u>,a</u>	Sulfotransferase, Phenol-Preferring
	Mesothelio						
352	352 ma	0.2714625	0.4166542	0.354303	0.2317313	(64177_f_at	0.2317313 X64177_f_at Metallothionein
	Mesothelio					189563_s_a	EST: HFBEST-40 Human fetal brain QBoqin2 Homo sapiens cDNA,
353 ma	ma	0.2711764	0.4166268	0.35413	0.2316397 t		mRNA sequence. (from Genbank)
Ĺ	Mesothelio	777		1	j i	RC_AA2810	
354 ma	ma	0.2711233	0.4165609	0.35406	0.231493/7/90_at	00 at	Homo sapiens mRNA for KIAA0524 protein, partial cds

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

	Mesothelio				-		
355	355 ma	0.2705316	0.4163262	0.354054	0.23132135 D31117	J31117_at	Ribosome binding protein 1 (dog 180kD homolog)
	Mesothelio				1	AA292234 a	EST: zt50h06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
356	356 ma	0.2698444	0.4163151	0.353716	0.23121814		clone 725819 5', mRNA sequence. (from Genbank)
	Mesothelio					X53002_s_a	
357	357 ma	0.2696341	0.4163128	0.353684	0.23109083 t		ITGB5 Integrin beta-5 subunit
L	Mesothelio	1					
328	358 ma	0.2695124	0.416113	0.353393	0.23097472 D78014 at	078014_at	Dihydropyrimidinase related protein-3
	Mesothelio					HG3227-	
329	359 ma	0.2692829	0.415942	0.353259	0.23085128 HT3404	HT3404_at	Guanine Nucleotide-Binding Protein Hsr1
Ме 360 ma	Mesothelio ma	0.2692072	0.2692072 0.4158708	0.353233	0.23066181 U33837_at	J33837_at	Glycoprotein receptor gp330 precursor, mRNA
** * * * * *							EST: zc44h06.r1 Soares senescent fibroblasts NbHSF Homo sapiens
	Mesothelio					0.00000	CLINA GIOTE JEST I SITTIFICATION OF TRANSPORTED AND USE TRAINING TO THE STATE OF TH
361	361 ma	0.2691709	0.415728	0.353207	0.23060541 at	w40000 s_ at	ırarısport protein precursor - mouse ;, mkivA sequence. (from Genbank)
							EST: zr78g10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
	Mesothelio				Andrew .	A2349	669570 3' similar to contains Alu repetitive element;, mRNA
362	362 ma	0.2688853	0.2688853 0.4155587	0.353138	0.2304331 25 at		sequence. (from Genbank)
5	Mesothelio	0		6		A2799	EST: zs88b05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
3	363 ma	0.2679166	0.4155543	0.353038	0.23023693 13_at		IMAGE:704529 3', mRNA sequence. (from Genbank)
700	Mesothello	0.000.000		0		31_cds	HPR gene (haptoglobin-related protein) extracted from Human
5	204 1119	0.2074019	0.4100900	0.333038	0.23004094 1_at		naptoglobin gene (alpha-2 allele)
Į.	Mesothello				pian	A4577	EST: zx87c05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
365	365 ma	0.2669676	0.2669676 0.4153308	0.352677	0.22978924 07_at)7_at	clone 810728 3', mRNA sequence. (from Genbank)
9	Mesothelio				4,8280		
366	366 ma	0.2659099	0.2659099 0.4149956	0.352549	0.22971031 L33881 at		PRKCI Protein kinase C, iota
	Mesothelio				<u></u>	V38597_i_a	EST: zb20c11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA
367	367 ma	0.2658401	0.2658401 0.4149952	0.352473	0.22962393 t		clone 302612 5', mRNA sequence. (from Genbank)
	Mesothelio				1	4A405548_a	AA405548 a EST: zw39f01.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
898	368 ma	0.2654928	0.4147382	0.352361	0.22946161		clone 772441 5', mRNA sequence. (from Genbank)
	Mesothelio					AA292158_s	EST: zt46c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
369	369 ma	0.2654812	0.4147237	0.35229	0.22931917	at	clone 725380 5', mRNA sequence. (from Genbank)
	Mesothelio				114	RC_AA2340	EST: zr74b02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
370	370 ma	0.2646896	0.4146949	0.352265	0.2292628 61	_at	669099 3', mRNA sequence. (from Genbank)
	Mesothelio					RC AA2280	
371	371 ma	0.2645322	0.4146686	0.352208	0.22898363 20_at	20_at	Splicing factor (CC1.3)
372	Mesothelio 372 ma	0.2644391	0.4146319	0.352189	0 22892465 1	4A092182_a	AA092182_a EST: II6255.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
			2	22.2	, , , , , , , , , , , , , , , , , , , ,		

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	Mesothelio		L				
373 ma	ma	0.2639977	0.4145599	0,352117	0.22876163 HT4215	HT4215_at	Phospholipid Transfer Protein
	Mesothelio					RC_AA4026	EST: zu49e02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
374 ma	ma	0.2638247	0.4142842	0.352091	0.22865224 37_at		clone 741338 3', mRNA sequence. (from Genbank)
	Mesothelio					A0404	EST: zk46h09.s1 Soares pregnant uterus NbHPU Homo sapiens
375 ma	ma	0.263732	0.4142569	0.351852	0.22840008 65_at	35_at	cDNA clone 485921 3', mRNA sequence. (from Genbank)
	Mesothelio			-	_	RC_AA4365	EST: zv08e10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
376 ma	ma	0.2622728	0.4141102	0.351821	0.2283448 60_at	30_at	753066 3', mRNA sequence. (from Genbank)
	Mesothelio					RC_AA4546	EST: zx99f06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
377 ma	ma	0.2620748	0,4140485	0.35164	0.22818822 54	54_at	811907 3', mRNA sequence. (from Genbank)
	Mesothelio						
378 ma	ma	0.2608421	0.4138808	0.351371	0.22810231 L11005_at	L11005_at	ALDEHYDE OXIDASE
	Mesothelio					D82226 s a	EST: similar to TAT-binding protein-2, mRNA sequence. (from
379 ma	ma	0.2602913	0.4134417	0.351323	0.22787218t		Genbank)
	Mesothelio					AA412620_s	EST: zt97b10,r1 Soares testis NHT Homo sapiens cDNA clone
380 ma	ma	0.259976	0.4132258	0.351218	0.22782445	ʻat	730267 5', mRNA sequence. (from Genbank)
	Mesothelio						
381 ma	ma	0.2597271	0.4131955	0.351182	0.22762097 D78611	D78611_at	MEST Mesoderm specific transcript (mouse) homolog
	Mesothelio						
382 ma	ma	0.2587902	0.2587902 0.4131866	0.351129	0.22741862 M62486 at		C4BPA Complement component 4-binding protein, alpha
	Mesothelio					211	EST: af61g05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
383 ma	ma	0.2579113	0.4130346	0.350854	0.22732015 62_s_at	62_s_at	1046552 3', mRNA sequence, (from Genbank)
	Mesothelio					RC_AA4428	EST: zv60g03.s1 Soares testis NHT Homo sapiens cDNA clone
384 ma	ma	0.2577417	0.4128937	0.350851	0.22721846 83_at	83 <u>_</u> at	758068 3', mRNA sequence. (from Genbank)
	Mesothelio					RC_AA3938	EST: zv64c05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
385 ma	ma	0.2572492	0.4128761	0.350594	0.22701173 03_at	03_at	clone 758408 3', mRNA sequence. (from Genbank)
	Mesothelio					AA247966_a	EST: k1064.seq.F Human fetal heart, Lambda ZAP Express Homo
386 ma	ma	0.2571623	0.4128408	0.350497	0.2268388 t	ť	sapiens cDNA 5', mRNA sequence. (from Genbank)
	Mesothelio					AA043021_a	
387 ma	ma	0.2563624	0.2563624 0.4128379	0.350494	0.22669156 t		UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4
	Mesothelio					RC_AA4314	EST: zw70f01.s1 Soares testis NHT Homo sapiens cDNA clone
388 ma	ma	0.2561876	0.4128003	0.350492	0.2266417154_at	54_at	781561 3', mRNA sequence. (from Genbank)
	Mesothelio					RC_AA4822	EST: ab15c03.s1 Stratagene lung (#937210) Homo sapiens cDNA
389 ma	ma	0.2561725	0.412762	0.350424	0.22647038	24_f_at	clone 840868 3', mRNA sequence. (from Genbank)
	Mesothelio					RC_AA4468	EST: zw90e07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
390 ma	ma	0.255707	0.4127204	0.350346	0.2263404 99_at	99 <u>_</u> at	clone 784260 3', mRNA sequence. (from Genbank)
	Mesothelio					R50008_s_a	
391 ma	ma	0.255569	0.4123099	0.350298	0.22612622 t		7-dehydrocholesterol reductase
302 ma	Mesothelio	0.2540791	0.4123089	0.350177	RC 0.22603863.62	RC_AA2561 62_at	EST: zr79b07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681877 3' mRNA segrence (from Genbank)
326	-110	0.5040131	. 1	0.000	0.44003000		

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	Mesothelio						SLC4A2 Solute carrier family 4, anion exchanger, member 2
393 ma	na	0.2539966	0.4119516	0.350086	0.22599895 U62531	at	(erythrocyte membrane protein band 3-like 1)
_	Mesothelio				A	AA389673_a	EST: M164 Fetal heart, Lambda ZAP Express Homo sapiens cDNA
394 ma	па	0.2536245	0.4117795	0.349921	0.2258484 t	1	5', mRNA sequence. (from Genbank)
_	Mesothelio				×	X16869_s_a	
395 ma	na	0.2526417	0.4112976	0.349691	0.22577219 t		Eukaryotic translation elongation factor 1 alpha 1
_ (Mesothelio	1000				_AA4321	EST: zw71g10.s1 Soares testis NHT Homo sapiens cDNA clone
396 ma	na	0.2523231	0.4111635	0.349443	0.22566217 86	at	781698 3', mRNA sequence. (from Genbank)
	:					HG3431-	
_	Mesothelio					HT3616_s_a	
397 ma	па	0.2522436	0.2522436 0.4111333	0.3494	0.22557667 t		Decorin, Alt. Splice 1
	Mesothelio				<u> </u>	A399299 a	AA399299 a clone 725992 5' similar to contains element PTR5 repetitive element;
398 ma	na	0.2520875	0.4111212	0.349393	0.22540876 t	l	mRNA sequence. (from Genbank)
4	Mesothelio						A TABLE OF THE PROPERTY OF THE
399 ma	na	0.251916	0.4106347	0.349298	0.22528914 X75342	'at	SHB SHB adaptor protein (a Src homology 2 protein)
_	Mesothelio						
400 ma	na	0.2516347	0.4106028	0.349045	0.22508854 X	.04011_at-2	0.22508854 X04011_at-2 Cytochrome b-245, beta polypeptide (chronic granulomatous disease)
	Mesothelio	1					
401 ma	na	0.2516347	0.2516347 0.4105609	0.348728	0.22501616 X04011_at		CYBB Chronic granulomatous disease
_	Mesothelio				i.C.	A1361	VAMP (vesicle-associated membrane protein)-associated protein A
402 ma	na	0.2512981	0.4105581	0.348501	0.22479467 30_at	0_at	(33kD)
2	Mesothelio						
403 ma	Па	0.2511897	0.4100671	0.348415	0.22470313 M37435_at		CSF1 Colony-stimulating factor 1 (M-CSF)
2	Mesothelio				L	12332	
404 ma	na	0.2507062	0.4098586	0.348254	0.22466822 57_at		Transforming growth factor beta 1 induced transcript 1
_	Mesothelio				ŧ.L	14901	EST: ab05f07.s1 Stratagene fetal refina 937202 Homo sapiens cDNA
405 ma	Па	0.2503646	0.4098494	0.348087	0.22452894 42 at		clone 839941 3', mRNA sequence. (from Genbank)
2	Mesothelio						
406 ma	na	0.2501709	0.2501709 0.4096539	0.347538	0.2244206 Y00318	at,	IF I factor (complement)
2	Mesothelio				Ľ.	RC_AA4908	
407 ma	na	0.2499502	0.4093384	0.347529	0.22433786 28_at	8 at	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
2	Mesothelio					-	
408 ma	na	0.2496551	0.4092615	0.347515	0.22427422 S77410_at		AGTR1 Angiotensin receptor 1
<u>جے</u>	Mesothelio				L.	A4795	EST: zu36h10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
409 ma	na	0.2492012	0.4089173	0.34739	0.22412626 33_at	3 at	clone 740131 3', mRNA sequence, (from Genbank)
2	Mesothelio				<u></u>	RC_AA5991	
410 ma	na	0.2491543	0.4089043	0.347381	0.22400711 44_at	4_at	Myosin phosphatase, target subunit 1
Me	Mesothelio	0.2490323	0.2490323 0.4086484	0 3/7330	A 00038/105	AA156670_s	Homo conjone' ocrip produces mDNA portiol ode
	5	0.4.100040	10100010	0.047.000	1	-	TOTILO Sapierio agriri precursor minara, partiar cus

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	Mesothelio					RC_AA4577	RC_AA4577 EST: zx87d04.s1 Soares ovary tumor NbHOT Homo saplens cDNA
412	412 ma	0.2489954	0.2489954 0.4085035	0.347076	0.22380021 18	at	clone 810727 3', mRNA sequence. (from Genbank)
	Mesothelio					14885_rna	Transforming growth factor-beta 3 (TGF-beta 3) exon 1 (and joined
413	413 ma	0.2482034	0.4084218	0.347049	0.22367676	1_s_at	CDS)
	Mesothelio					RC_AA1207	
414	414 ma	0.2480238	0.4081271	0.347048	0.22361214 83	83_at	Eukaryotic translation initiation factor 2, subunit 3 (gamma, 52kD)
415	Mesothelio 415 ma	0.2477716	0.2477716 0.4080536	0.346969	0.22338553 D53639	D53639 at	Ribosomal protein S26
	Mesothelio					118	EST: zt67a06.s1 Soares testis NHT Homo sapiens cDNA clone
416	416 ma	0.2477203	0.2477203 0.4078318	0.346805	0.2233027 09	ı ă ,	727378 3', mRNA sequence. (from Genbank)
	Mesothelio					RC AA2510	EST: zs02g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone MAGE 684062 3' similar to contains element CFR renetitive element
417	417 ma	0.2476606	0.2476606 0.4076881	0.346688	0.2231707 14_at	}	, mRNA sequence. (from Genbank)
	Mesothelio						
418	418 ma	0.2475363	0.4075764	0.346504	0.2230116 L04270_at	L04270_at	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR
	Mesothelio						
419	419 ma	0.2474755	0.4073702	0.346401	0.22287212 Z29083	Z29083_at	5T4 gene for 5T4 Oncofetal antigen
120	Mesothelio	0.0474586	0.4070858	0 3/6341	0 00064346 006074	C08074 24	EQT. similar to man an BNA contract (from Contract)
140	Mecotholio	0.241 1900		0.0400	0.222040	00021 1 at	DOE Discortal growth factor vaccular and otherial growth factor
421	421 ma	0.2463169	0.407275	0.346096	0.22253941 X54936	X54936 at	related protein
	Mesothelio						
422	422 ma	0.2450352	0.2450352 0.4072544	0.346001	0.22233939 U03057_at		Actin bundling protein mRNA
422	Mesothelio	0.0445443	9071706	0.375041	RC 0 22221208 14	_AA4969	Homo sapiens short form transcription factor C-MAF (c-maf) mRNA,
470	110	0.2440140	0.4071730	0.343341	0.22221200	4 9	complete cas
424	Mesothelio 424 ma	0.2442416	0.4068076	0.345919	0.2221232 Z71389_at	Z71389_at	Skin-antimicrobial-peptide 1 (SAP1)
	Mesothelio						Cancellous bone osteoblast mRNA for serin protease with IGF-binding
425	425 ma	0.2441866	0.4067788	0.345833	0.22194098 D87258_at	D87258_at	motif
	Mesothelio					RC_AA4497	EST: zx07e10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
426	426 ma	0.2436549	0.2436549 0.4067064	0.345551	0.22187173 49 at	49_at	clone 785802 3', mRNA sequence. (from Genbank)
	oile disconnection					7 707077 7	EST: zw82c11.r1 Soares testis NHT Homo sapiens cDNA clone
427	427 ma	0.2434348	0.4064515	0.345485	0.221703991	10101-4 1	t Anti-biol AntiGEN PRECURSOR.: mRNA sequence, (from Genbank)
	Mesothelio					AA247903_a	EST: j5812.seq.F Human fetal heart, Lambda ZAP Express Homo
428	428 ma	0.2423227	0.4064489	0.345308	0.22164738 t	1	sapiens cDNA 5', mRNA sequence. (from Genbank)
429	Mesothelio	0 2423147	0 4064195	0 345274	0.22157875 W26231 at	W26231 at	H.saniens mRNA for NRD1 convertase
	Mesothelio						
430	430 ma	0.2422528	0.2422528 0.4063329	0.345094	0.221495/6 043328	U43328_at	CRTL1 Cartilage linking protein 1

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al*.

	MACCALL						
431	ma	0.2421041	0.4063158	0.344922	0.22134243	0.22134243 J03241 s at	TGFB3 Transforming growth factor, beta 3
	Mesothelio				A CONTRACTOR OF THE CONTRACTOR	A4466	EST: zw89g02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
432	432 ma	0.241955	0.4063049	0.344886	0.22123498 50_at		clone 784178 3', mRNA sequence. (from Genbank)
	Mesothelio						
433	433 ma	0.2413752	0.4062403	0.344814	0.22118278	D50840_at-2	0.22118278 D50840_at-2 UDP-glucose ceramide glucosyltransferase
434	Mesothelio	0.2413752	0.4061826	0 3/456/	0 22411838 DE0840 at	D50840 at	of the state of th
2	Meentholic			1001100	0.22111030		Ceralline glucosylitatisterase
435	435 ma	0.2410928	0.4061479	0.344559	0.22093682 J04177 at		COL11A1 Collagen type XI alpha 1
	Mesothelio						
436	436 ma	0.2407925	0.4061341	0.344522	0.22075522 D86961 at		KIAA0206 gene. partial cds
	Mesothelio		l			RC_AA4856	
437	437 ma	0.2404071	0.4060069	0.344313	0.2207041 55_at	55_at	Human Iow-Mr GTP-binding protein (RAB31) mRNA, complete cds
	Mesothelio					AA234634_f	
438	438 ma	0.2403573	0.4057519	0.344154	0.22062474		CCAAT/enhancer binding protein (C/EBP), delta
	Mesothelio					M83667_ma	
439	439 ma	0.2401941	0.4057243	0.344011	0.220452891	s_at	NF-IL6-beta protein mRNA
	Mesothelio					A4259	EST: zw17h06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
440	440 ma	0.2398953	0.4056556	0.344005	0.22026935 06_at		clone 769595 3', mRNA sequence. (from Genbank)
							EST: zt32e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
							clone 724060 3' similar to TR:G1199669 G1199669 PROTEIN
	Mesothelio					AA2357	KINASE C-BINDING PROTEIN BETA 15.;, mRNA sequence. (from
441	441 ma	0.2397178	0.4055153	0.343983	0.22015002 37	_at	Genbank)
	Mesothelio					\A504595_a	EST: aa60g12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
442	442 ma	0.2396792	0.4053633	0.343776	0.22002147		IMAGE:825382 5', mRNA sequence. (from Genbank)
	Mesothelio						
443	443 ma	0.2383773	0.4051912	0.343764	0.21994853 U89606_at		Pyridoxal kinase mRNA
	Mesothelio			-	-	RC_AA2561	EST: zr79a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
444	444 ma	0.2378864	0.2378864 0.4049136	0.343732	0.21983626 53 s at		681880 3', mRNA sequence. (from Genbank)
,	Mesothelio					A3862	EST: EST07569 Fetal brain Homo sapiens cDNA 3' end, mRNA
445	445 ma	0.2364085	0.4046356	0.343486	0.21976471 64 at		sequence. (from Genbank)
446	Mesothelio	0.2363854	0.4043772	0.343225	A 21071101	A410325_a	EST: zv11e04.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
	Mesothelio			0.010200	101110	C AAR202	Coosts of minima sequence. (IIOIII Genibank)
447	447 ma	0.2357366	0.4039094	0.343106	0.21957351 89 at	1020	Homo sapiens clone 23887 mRNA segmence
	Mesothelio						
448	448 ma	0.2346154	0.4038987	0.342923	0.21950486 U76189_at		EXTL2 (EXTL2) mRNA, partial cds
Me Me	Mesothelio	0.2342022	0077007	0.00044	RC 0 2404E464 60	_AA2817	
244	1110	0.4245030		0.342911	0.21343104	s at	Human Hpast (HPAST) mKNA, complete cds

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				;	W. Carp	14. Charle Charle Or Carle Links	Entry The Three Th
45(Mesothelio	0.039880					
2	Morotholi	+	9 0.4037049	9 0.342818	_	0.21939255 X06256 at	(ITGA5 Integrin, alpha 5 (fibronectin recentor, alpha polymontide)
45	451 ma	0.2336102	2 0.4036565	5 0.342695		RC_AA4494	RC_AA4494 EST: zx05d07:31 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 42 at
	Mesothelio	0				1133202 6 2	done robot 3, Illrivia sequence. (from Genbank)
452	452 ma	0.2329444	4 0.4036079	9 0.342587	0.21908201	033202_s_d	
	Mesothelio						Mainte-D (maint) mrina
45.	453 ma	0.2321748	8 0.4036035	5 0.342412		0.21891865 U05291 at	FMOD Elbramadatt
	Mesothelio					RC. AAO318	FST: -1/12-04 -4 C-
454	454 ma	0.2319844	4 0.4035982	2 0.342316	0.2187156514 at	14 at	COLLAN Algorithms 120020 21
1	Mesothelio						CDIVA CIVILE 41 0638 3, mKNA sequence. (from Genbank)
455	455 ma	-	0.2319695 0.4035739	0.34231		0.21859495 M97630 at	Foundation
	Mesothelio					AA00776E 2	realismembrane receptor (ror2) mRNA
456	456 ma	0.2314104	1 0.403105	0.342241	0.218536421	t	throwal is a september of the collection of the
	Mesothelio	0				M42272 C	minary sequence, (from Genbank)
457	457 ma	0.2311485	0.4031004	0.342118	0.21836177	10116616.5.8	
	Mesothelio	-				OC AAREA	Alconiol denydrogenase 3 (class I), gamma polypeptide
458	458 ma	0.2310899	0.4026878	0.342	0.21827297 81 at	H4551	EST: aa15g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
-	Mesothelio					23	organo 3, IIIRINA sequence. (from Genbank)
459 ma	ma	0.2310309	0.4020965	0.341792	0.21812743 HT1153	HT1153 at	Nicleoside Dinhocophate Kirasa Nasoo 129
460 me	IMESOTABIO					AA214658 a	SZH-92HIGA WIII GAN WIII GAN GAN GAN GAN GAN GAN GAN GAN GAN GAN
2	Mana	0.2307408	0.4020499	0.341577	0.2180665		H beta 58 homolog
2	Mesomello						A POINT OF THE PROPERTY OF THE
401 1118	ma	0.230499	0.401907	0.341572	0.21788551 L09708 at	L09708 at	C2 Complement seems to a
	Mesothelio					N75870 c 2	oz sonipienieni component C2
462 ma	та	0.2301794	0.4018511	0.341387	0.21783352	141 301 0 S a	, , , , , , , , , , , , , , , , , , ,
	Mesothelio						Udal specificity phosphatase 1
463 ma	ma	0.2296507	0.4017795	0.341305	0.21767801	AAZ/9546 a	AAZ/9346_a EST: ZS86b06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
	Mesothelio					X04470 c c	INMAGE: 104339 5, mKNA sequence. (from Genbank)
464 ma	та	0.229372	0.4017411	0.341303	0.21742909+	B 6 0/440	יים כס מר
	Mesothelio				20031 11 200	1 4 4 4	RPL32 Ribosomal protein L32
465 ma	та	0.2291974	0.4016492	0.341281	0.21733332 05 at	A4015	EST: 2x60b05.s1 Soares testis NHT Homo sapiens cDNA clone
	Macatholic						EST: zy26h12 r1 Soares NhHMD: \$1 Long 6
466 ma	Tia	0.2288922	0.4016431	0.341244		AA422123_f	AA422123_f 754823 5' similar to contains Alu repetitive element: mRNA
	Mesothelio		1	0.041244	0.2112104	at	sequence. (from Genbank)
467 ma	na	0.2285914	0.4015709	0.340908	0.21708141 DR3475 at		718 804 80
<u> </u>	Mesothelio					-	NAMU I US gene
468 ma	па	0.2284748	0.4013893	0.340908	0.21694946 43 at	חכנישט	687.07 3' mDNA common females and cone
							of of this is sequence. (If om Genbank)

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

Meso	Mesothelio				R	RC AA0565	EST: zi66a02.s1 Stratagene colon (#937204) Homo sapiens cDNA
469 ma	•	0.2283897	0.4013639	0.340857	0.21685775 88	at	clone 509546 3', mRNA sequence. (from Genbank)
Meso	Mesothelio					AA458761_i	Transcription factor AP-2 alpha (activating enhancer-binding protein 2
470 ma		0.2283637	0.4013563	0.340729	0.21672162	at	alpha)
Meso	Mesothelio						
471 ma		0.2282104	0.4013358	0.3407	0.21651788 U09278_at	109278_at	Fibroblast activation protein mRNA
Meso	Mesothelio	00027760		0.240640	R 202020E 0		VINC. FLOOD
4/2 IIIa		0.4411899	0.4013133	0.340042	0.21040/05/30	u at	Homo sapiens clone 23851 mKNA sequence
Meso	Mesothelio	0 0277600	0 224600	0000000	1100000000		O 1 13 13 13 13 13 13 13 13 13 13 13 13 13 13
4/3 1114		0.22/4000	0.4011342	0.340303	0.2162828 U19/18 at	i	MFAP2 Microfibriliar-associated protein 2
Meso	Mesothelio	7077000		2	R	2783	EST: zs80f03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
4/4 ma		0.22/40/	0.4009159	0.340445	0.21620809 29_t_at	9_t_at	IMAGE:/03805 3, mRNA sequence. (from Genbank)
Meso 475 ma	Mesothelio ma	0.2272256	0.4008453	0.340368	0.2161225 X04741	04741 at	UBIOLITIN GARBOXYI -TERMINAI HYDROI ASE ISOZYME 11
Meso	Mesothelio		1				
476 ma		0.2271608	0.4008043	0.340186	0.21593271 D90224_at	90224_at	TXGP1 Tax-transcriptionally activated glycoprotein 1 (34kD)
Meso	Mesothelio				_ &	RC AA0749	EST: zm82b10.s1 Stratagene ovarian cancer (#937219) Homo
477 ma		0.227099	0.227099 0.4007765	0.34001	0,21587294 19 at		sabiens cDNA clone 544411 3', mRNA sequence, (from Genbank)
Meso	Mesothelio	0000044	000000000000000000000000000000000000000		N 1	A4315	EST: zw79e12.s1 Soares testis NHT Homo sapiens cDNA clone
4/8 ma		0.2266117	0.4006988	0.34	0.21583039 71	1_at	782446 3', mRNA sequence. (from Genbank)
Meso	Mesothelio						EST: zc20b05.r1 Soares senescent fibroblasts NbHSF Homo sapiens
479 ma		0.2265718	0.4006097	0.339973	0.21567237 W39573_at		cDNA clone 322833 5', mRNA sequence. (from Genbank)
Meso	Mesothelio	0 0065000		100000	R 020212000	A2821	EST: zt02b01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
400 1118		797697770	0.4005808	0.338835	0.21547976 4U at	u_at	IMAGE:/11913 3, mKNA sequence. (from Genbank)
Meso 481 ma	Mesothelio	0.2260045	0 4004966	0.339869	0.21533905\W26649_at		Zinc finaer protein 140 (clone pHZ-30)
Meso	Mesothelio				8	-	EST: zu12e03 s1 Soares testis NHT Homo saniens cDNA clone
482 ma		0.2255955	0.400438	0.339705	0.21529225 89	at	731644 3', mRNA sequence. (from Genbank)
Meso	Mesothelio						
483 ma		0.2254329	0.2254329 0.4003266	0.339406	0.21497512 J05633_at	05633_at	ITGB5 Integrin beta-5 subunit
Meso 184 ma	Mesothelio	0.2241578	97760070	0.020405	R 000001	RC_D59894	EST: Human fetal brain cDNA 3'-end GEN-073B05, mRNA sequence.
Meso	Mesothelio	0.5211310		0.000		A A 26.20	FST: 777 and st Sparse NHLMD; St Home savious above alone
485 ma		0.2237888	0.4001212	0.339354	0.21484278 43	at	6688243' mRNA sequence (from Genhank)
Meso	Mesothelio						
486 ma		0.2236281	0.4000667	0.339313	0.2146696 U27655	127655_at	RGP3 mRNA
Meso 487 ma	Mesothelio	0 2227389	0.2227389 0.3998457	0.339278	RC 0 21457149 34	RC_AA3996	EST: zt93e08.s1 Soares testis NHT Homo sapiens cDNA clone
2011		0.5221 000	10100000	0.000210	0.041 1041.2.0		1 20020 0, IIINNA OCHUGING. (IIOIII OCIIDAIN)

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Docket	No.:	2825.2020-002
Title:	Geneti	c Markers for Tumors
Invento	ors: Sric	dhar Ramaswamy, et al.

	MACCALL						
485	Wesomello 488 ma	0.220808	0 3007965	7770000		RC_AA2363	RC_AA2363 Homo sapiens 3-phosphoglycerate dehydrogenase mRNA, complete
<u> </u>	Mesothelio			ر د د	0.2 1440304 05 S at	17	COS
486	489 ma	0.2218874	0.3997648	0.338991	0.21440908	AA43047 I_s	EST: 2X74g11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809540.5' mRNA sequence (from Canhark)
	Mesothelio	-				1	order of the state
490	490 ma	0.2217476	0.3996199	0.338851	0.21436471 U55853	U55853_at	130 kD Golgi-localized phosphoprotein (GPP130) mRNA
491	Mesothelio	3777760 U		7 0000	OLLUON NO O	T	Homo sapiens 130 kD Golgi-localized phosphoprotein (GPP130)
7	1110		0.3894132	0.33884	0.21425/2	0.2142572 U55853 at-2	mRNA, complete cds
492	Mesothello	0.2246582	0 3000000	702020	200	A357394_a	
70	Mosotholio	-	ì	0.338791	U.Z1410935 t		sequence. (from Genbank)
403	A03 ma	0.0945707		00000			
ř	Mana		0.3992518	0.338039	0.21399806 Y09022 at		Not56-like protein
494	Wesounello 494 ma	0.2203614	0.3991641	0.338591	0.2138821 t	M23892_s_a t	Al OX15 Arachidonata 15-linovymanasa
	Mesothelio					RC AA4179	RC AA4179 FST: 2v97cf3 s1 Soares NhHMDii S1 Home sanions abnin alexantering
495	495 ma	0.2203567	0.3985607	0.338348	0.21379384 70 at	70 at	767716 3. mRNA seguence (from Genhank)
	Mesothelio					M19309 s a	
496	496 ma	0.2201312	0.3985315	0.338226	0.21372181	f ·	TNNT1 Troponin T1, skeletal, slow
7	Mesothelio	1				X79683_s_a	
49/	497 ma	0.2195137	0.3981684	0.338199	0.2134969	ţ	LAMB2 Laminin, beta 2 (laminin S)
,	Mesothelio					\A216017_a	EST: hp0234.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
498	498 ma	0.2189459	0.3980964	0.338072	0.21342461 t		cDNA 5', mRNA sequence. (from Genbank)
	Mesothelio			-			EST: zc45b12.r1 Soares senescent fibroblasts NbHSF Homo sapiens
499	499 ma	0.2186447	0.3980737	0.338057	0.21333252 W52431 at		CDINA GIOTE 523247 3 SHITIIBIT TO SW.:WDNM_RAT P14730 WDNM1 PROTEIN 73 DIR-G07807 - mDNA 50% 10000 (45000 0 00000)
	Mesothelio					1	100 Let 1 1 100 00 1, Hinney Sequence, (HOIII GENDANK)
200	500 ma	0.2184503	0.3978872	0.337763	0.21330836 49	at	Homo sabiens chromosome 19, cosmid R33729
	Mesothelio						
201	501 ma	0.2181622	0.3978508	0.337742	0.2131824 D49950		at-2 Interleukin 18 (interferon-aamma-inducing factor)
1	Mesothelio						Coope Buspan
502	502 ma	0.2181622	0.3975223	0.337737	0.21315591 D49950	äţ	Liver mRNA for interferon-damma inducing factor(IGIE)
C	Mesothelio	00001					
503	ous ma	0.2179292	0.3974858	0.337643	0.21298145 R93659	at	Homo sapiens mRNA for KIAA0871 protein, complete cds
504	iviesomelio 504 ma	0.2177952	0.3967421	0.337613	0.21286994 294662	to	EST: yq42d12.r1 Homo sapiens cDNA clone 198455 5'. (from
	Mesothelio				1.0000	<u> </u>	EST: vi34d06 r1 Homo capione cDNA along 144494 F1 (2
505 ma	ma	0.2177161	0.3963943	0.33742	0.21272859 R66239	at	Genbank)
Mes 506 ma	Mesothelio ma	0.2176677	0.3961885	0.337368	0.2125208 R21443 at	, t e	Human pre-B cell enhancing factor (DREE) mPNA complete ede
						7	The second of th

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	Mesothelio					C00225_s_a	C00225_s_a EST: HUMGS0005889, Human Gene Signature, 3'-directed cDNA
507 ma	ma		0.2174594 0.3961577	0.337204	0.212401781		sequence, mRNA sequence. (from Genbank)
	Mesothelio		1	1		AA033703_a	AA033703_a EST: zf01d10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
508 ma	ma	0.2170233	0.3958407	0.337034	0.21230745 t	-	clone 375667 5', mRNA sequence. (from Genbank)
	Mesothelio					RC_AA4565	
509 ma	ma	0.2161591	0.3958302	0.336945	0.21222529 83_s_at	83_s_at	Human PL6 protein (PL6) mRNA, complete cds
	Mesothelio						
510 ma	та	0.2157186	0.3957498	0.336935	0.21208715 U40572	U40572_at	Beta2-syntrophin (SNT B2) mRNA
	Mesothelio						
511 ma	ma	0.2153397	0.3957498	0.336914	0.21207146	M23161_at-2	0.21207146 M23161_at-2 Human transposon-like element mRNA
	Mesothelio				A A THE RESIDENCE OF THE PARTY		
512 ma	ma	0.2153397	0.3956994	0.336914	0.21193664 M23161_at		Transposon-like element mRNA
	Mesothelio						The state of the s
513 ma	ma	0.215177	0.3956912	0.336877	0.2118418	L37868_s_at	0.2118418 L37868_s_at POU-domain transcription factor (N-Oct-3)
	Mesothelio						
514 ma	ma	0.2150646	0.3953228	0.336802	0.21173024	M20030_f_at	0.21173024 M20030_f_at Small proline rich protein (sprII) mRNA, clone 930
						HG3044-	
	Mesothelio					HT3742_s_a	
515 ma	ma	0.214339	0.3949409	0.336794	0.2116793	-	Fibronectin, Alt. Splice 1
	Mesothelio						EST: yy62b11.r1 Homo sapiens cDNA clone 278109 5. (from
516 ma	ma	0.2142871	0.3947811	0.336638	0.21148464 N95507	N95507_at	Genbank)
	Mesothelio					RC_AA2274	
517 ma	ma	0.2136581	0.3942333	0.336604	0.21138994 48_at	48_at	Homo sapiens mRNA for KIAA0456 protein, partial cds
	Mesothelio					X07438 s a	
518 ma	ma	0.213595	0.3941188	0.336591	0.21127711		DNA for cellular retinol binding protein (CRBP) exons 3 and 4
	Mesothelio		ı			74440	EST: zv45f09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
519 ma	ma	0.2133301	0.3939915	0.336587	0.21115571 54_at		clone 756617 3', mRNA sequence, (from Genbank)
	Mesothelio					RC_AA1499	
520 ma	ma	0.213175	0.3938974	0.336563	0.21102558 40_at	40_at	GLUT1 C-terminal binding protein
							EST: zq39h04.s1 Stratagene hNT neuron (#937233) Homo sapiens
	Mosotholio			-			CDINA Clone 632.119 3' Similar to contains Alu repetitive
524 ma	Ma	0.2428176	0.3934979	0 336474	0.2108815538 at	W 1000	elenien, conains elenement mort repennye elenem, mirany
5	Mesothelio			1	20001.2:0	AOREO	ECT. +f62,004 of Correst ratios NOb ALID Lionas conjune aDMA alona
522 ma	ma	0.2122943	0.3934718	0.336363	0.21079014 08	at	L-31. 202904:31 Soares retira nzb4tin trombosapiens conversioned 381558 3', mRNA sequence, (from Genbank)
	Mesothelio						
523 ma	ma	0.2117215	0.3934179	0.336189	0.21069182 U28811	-at	Cysteine-rich fibroblast growth factor receptor (CFR-1) mRNA
i.	Mesothelio			I			Chimeric mRNA derived from AML1 gene and MTG8(ETO) gene,
224 ma	ma	0.2114994	0.3932855	0.336152	0,21059/65 D14822 at		partial sequence

	Mesothelio					RC_AA4890	
525 ma	ma	0.2114889	0.3932436	0.33608	0.21049662 12		Human pre-B cell enhancing factor (PBEF) mRNA, complete cds
	Mesothelio					RC_AA4820	
526 ma	ma	0.2114278	0.3931314	0.335977	0.2103492 10	10_at	Homo sapiens mRNA for KIAA0747 protein, partial cds
	cilodtocof					DC AA9694	EST: zs21f07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685861 3' similar to SW:YB9B_YEAST P38334
527	ma	0.2109894	0.3929205	0.335861	0.21016462 11	at	REGION.; mRNA sequence. (from Genbank)
	Mesothelio		1	NAME OF TAXABLE PARTY O	The state of the s		
528 ma	ma	0.2108305	0.3928882	0.335856	0.21014549 X66945_at		FGFR1 Basic fibroblast growth factor (bFGF) receptor (shorter form)
	Mesothelio					A2349	EST: zr78h09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
529 ma	ma	0.2106664	0.3925149	0.335753	0.20998912 45_at	45_at	669569 3', mRNA sequence. (from Genbank)
	Mesothelio					AA401047_a	
530 ma	ma	0.2100579	0.3925138	0.335667	0.20994061		Homo sapiens mRNA for neuropsin, complete cds
	Mesothelio					RC_AA4875	EST: ab23g01.s1 Stratagene lung (#937210) Homo sapiens cDNA
531 ma	ma	0.2099166	0.3924354	0.335613	0.20980108 76	_at	clone 841680 3', mRNA sequence. (from Genbank)
	Mesothelio						Phosphotyrosine independent ligand p62 for the Lck SH2 domain
532 ma	ma	0.2098505	0.3923666	0.335597	0.20973511 U46751	U46751_at	mRNA
	Mesothelio						
533 ma	ma	0.2088933	0.3922677	0.335511	0.20962076 D87465_at		KIAA0275 gene
	Mesothelio					AF006088_a	
534 ma	ma	0.2088825	0.3921462	0.335393	0.20957813 t		Arp2/3 protein complex subunit p16
	Mesothelio						
535 ma	ma	0.208203	0.3921398	0.33539	0.20944118 L37347_at	L37347_at	NRAMP2 Natural resistance-associated macrophage protein 2
	Mesothelio						
536 ma	ma	0.2078574	0.3919636	0.335345	0.20935881 J04164_at	J04164_at	RPS3 Ribosomal protein S3
	Mesothelio						
537 ma	ma	0.2077247	0.3917378	0.33529	0.20916462 M32053_at	M32053_at	H19 RNA gene
	Mesothelio					AA397724_a	
538 ma	ma	0.2075718	0.3916083	0.335238	0.20905395 t		Ash2 (absent, small, or homeotic, Drosophila, homolog)-like
	Mesothelio						
539 ma	ma	0.2074651	0.3915875	0.335,168	0.20895852 D16532_at	D16532_at	VLDLR Very low density lipoprotein receptor
Me	Mesothelio	77377000	00000	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	~Y 000000 0		120004
010	Mecotholio	0.20/43/7	0.3913039	0.333117	0.20002047	<u>।</u> वा	KIAAUD / I gene product
541 ma	mesouneme	0.2063453	0.3910105	0.335019	0.20875412 250022	Z50022 at	Surface alycoprotein
	Mesothelio						A CONTRACTOR OF THE PROPERTY O
542 ma	ma	0.206067	0.3909571	0.335006	0.20866536 U01062_at	U01062_at	ITPR3 Inositol 1,4,5-triphosphate receptor, type 3
E 4.2	Mesothelio	0.2057022	20060020	0.324048	A 0 208572004 +	A351461	EST: EST59216 Infant brain Homo sapiens cDNA 5' end similar to
243 III	IIa	0.2031.923		0.334340	0.2003/204		Sittilial to periorit, titrays sequence, (itotil Genbain)

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Docket	No.:	2825.20	020-002
Title:	Geneti	ic Marke	ers for Tumors
Invento	ors: Sri	dhar Ran	maswamy, <i>et al</i> .

	IN Account						
544	Mesoureno 544 ma	0.2054123	0.3908607	0.334815	0.20848213	KC_AA4122 84 s at	Human poliovirus receptor mRNA, clone H20A
	Mesothelio					AA296821_a	EST: EST112387 Aorta endothelial cells Homo sapiens cDNA 5' end,
545	545 ma	0.2053218	0.3908163	0.334677	0.20841846	+	mRNA sequence. (from Genbank)
	Mesothelio					A4528	EST: zx36d03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
546	546 ma	0.2041049	0.3908101	0.33461	0.20833303 29_at		clone 788549 3', mRNA sequence. (from Genbank)
547	Mesothelio 547 ma	0.2036573	99066	0 334605	0 00834555 M&4089 at		, i i i i i i i i i i i i i i i i i i i
	Monostholic	0.5000010	0.0000	0.001000	0.20031333		rivioti Fiavin-containing monooxygenase 1
5.48	Mesoureilo 548 ma	0.2036435	0.2036435 0.3006347	0.22420E	0.0004646	A0539	EST: ze75c02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
	Mesotholio	0.5000450	0.3900317	0.334200	0.2001013 17 at		Gione 364802 3', mKINA sequence. (from Genbank)
549	Mesou reno 549 ma	0.2032492	0.2032492 0.3906317	0.33422	0.20814091 X89066_at		TRPC1 Transient receptor potential channel 1
				-	Transmission of the second of	and different contractions and the second contractions and the second contractions and the second contractions and the second contractions are second contractions and the second contractions are second contractions and the second contractions are second contractions and the second contractions are second contractions and the second contractions are second contractions and the second contractions are second contractions and the second contractions are second contractions are second contractions and the second contractions are second contractions and the second contractions are	EST: zl73e05.s1 Stratagene colon (#937204) Homo sapiens cDNA
	Mesothelin						clone 510272 3' similar to TR:E243948 E243948 CHROMOSOME VII
550	550 ma	0.2031317	0.3902877	0.334201	0.20799284 39_at	1000	READING FRAME ORF TGLU34C.;, mRNA sequence. (from Genbank)
L	Mesothelio					A4050	EST: zt06e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
5	551 ma	0.201605	0.390279	0.334157	0.20782875 04_at		IMAGE:712348 3', mRNA sequence. (from Genbank)
1	Mesothelio					VA464468_a	EST: zx84d05.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
22	552 ma	0.2015334	0.3902004	0.334137	0.20773098 t		clone 810441 5', mRNA sequence. (from Genbank)
553	Mesothelio 553 ma	0.2007246	0.3901786	0 33/108	778787000	AA233231_a	AA233231_a EST: zr69c12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
	Mesothelio		- 1	2000		1157843 c a	Human phosphatidylingiful 3 kingra dalta catalytic subunit mDNA
554	554 ma	0.1999803	0.3899444	0.33408	0.207610881		complete cds
	Mesothelio						
355	555 ma	0.1998984	0.3898961	0.334006	0.20747742	J03077_s_at	0.20747742 J03077_s_at PSAP Sulfated glycoprotein 1
556	Mesothelio 556 ma	0.1991575	0.3897548	0.333888	0.20743416 t	AA236610_a t	AA236610_a Zr99c11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
	1. A						EST: ze35e10.s1 Soares retina N2b4HR Homo sapiens cDNA clone
557	557 ma	0.1988742	0.3897381	0.333658	12072459 60		361002 3' similar to contains Alu repetitive element;, mRNA
	Mesothelio				0.2012100	ชี	sequence: (non Genbank)
558	558 ma	0.1988557	0.3896993	0.333617	0.20715865 Z21217	aţ	KIAA0008 gene product
559	Mesothelio 559 ma	0.198782	0.3896819	0.333428	RC A	A2848	EST: zt23a03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
	Mesothelio					544 a	Solice Loose of thinks Sequence. (Horn Gendalin.)
560 ma	ma	0.1986974	0.3896152	0.333328	0.20690812		Matrix metalloproteinase 21
Me 561 ma	Mesothelio ma	0.1986462	0.3896053	0.333328	0.20676218†	\52656_s_a	EST: yz06a09.r1 Homo sapiens cDNA clone 282232 5'. (from Genhank)

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	Mesothelio				2	M35410_s_a	
562	562 ma	0.1983917	0.3895016	0.333283	0.20672001 t	;	Insulin-like growth factor binding protein 2 (36kD)
	Mesothelio						
563	563 ma	0.1980007	0.3894578	0.333217	0.20664987 H52836	at	Yo22e10.r1 Homo sapiens cDNA clone 178698 5'. (from Genbank)
	Mesothelio					D51370	EST: Human fetal brain cDNA 3'-end GEN-031A12, mRNA sequence.
564	564 ma	0.1978949	0.3892011	0.332941	0.2065955	at	(from Genbank)
	Mesothelio						EST: yt02a04.r1 Homo sapiens cDNA clone 223086 5'. (from
265	565 ma	0.1977138	0.3890399	0.332792	0.20655228 H86648_at		Genbank)
	Mesothelio				<u>x</u>	_AA2332	EST: zr48d01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
266	566 ma	0.1977069	0.3889526	0.332741	0.20650889 58	8_at	666625 3', mRNA sequence, (from Genbank)
	Mesothelio				œ	RC_AA4486	EST: zx11g04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
267	567 ma	0.1974199	0.3883913	0.332594	0.20632608 88_at	8_at	clone 786198 3', mRNA sequence. (from Genbank)
	Mesothelio						
268	568 ma	0.1973655	0.3883345	0.332457	0.20618044 J04456_at		LGALS1 Ubiquinol-cytochrome c reductase core protein II
	Mesothelio						
269	569 ma	0.1968024	0.3882178	0.332368	0,2060999 L32976_at	32976_at	Protein kinase (MLK-3) mRNA
	Mesothelio						
220	570 ma	0.1968024	0.3880515	0.332365	0.20598094 L	32976_at-2	0.20598094 L32976_at-2 Mixed lineage kinase 3
	Mesothelio						
571	571 ma	0.1967201	0.3878915	0.332349	0.2058916 X51630	51630_at	WT1 Wilms tumor 1
	Mesothelio						
572	572 ma	0.1962218	0.3874916	0.332244	0.20574267 L16895	16895_at	LOX Lysyl oxidase
	Mesothelio						
573	573 ma	0.1957652	0.3874026	0.332045	0.20566025 M61916_at	161916_at	LAMB1 Laminin B1 chain
	N A				<u> </u>	070400	EST: zu42c09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
574	Mesomello 574 ma	0 195733	0.3873881	0.331748	0 2055847†	A4/6129_a	AA4/8129_a Glone / 40656 5 Similar to SW.:Bi3_MOUSE F26662 BRAIN PROTEIN +
5	Mesothelio					D45917 s a	The state of the s
575	575 ma	0.195714	0.3873186	0.331626	0.20550896		TIMP-3, partial cds (C-terminus region)
	Mesothelio					RC AA6100	EST: af08h02.s1 Soares testis NHT Homo sapiens cDNA clone
226	576 ma	0.1953356	0.3873185	0.331391	0.2054044 86_at	6 at	1031091 3', mRNA sequence. (from Genbank)
	Mesothelio						EST: zb65h10.r1 Soares fetal lung NbHL19W Homo sapiens cDNA
277		0.1952033	0.387284	0.331359	0.20528395 W24957	V24957_at	clone 308515 5', mRNA sequence. (from Genbank)
578	Mesothelio 578 ma	0.1938937	0.3872666	0.331327	0.2052298 U97519	197519 at	Podocalvxin-like
	Mesothelio		1				
579	579 ma	0.193278	0.3872604	0.33131	0.20502394 X64878_at	.64878_at	OXTR Oxytocin receptor
580	Mesothelio 580 ma	0.1932006	0.3872537	0.331248	RC 0.20490564 08	RC_AA4521 08_at	Transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. RC_AA0252 EST: ze74d01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA 897608 3' similar to WP:F10G7.4 CE02628 DNA DOUBLE-STRAND EST: Human placenta cDNA 5'-end GEN-502F04, mRNA sequence. AA096094_s EST: I8200.seq.F Fetal heart, Lambda ZAP Express Homo sapiens EST: ae33c05.s1 Gessler Wilms tumor Homo sapiens cDNA clone EST: HUMGS0005644, Human Gene Signature, 3'-directed cDNA MMP2 Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, adipose tissue), complete cds EST: HUMGS0003737, Human Gene Signature, 3'-directed cDNA at cDNA 5', mRNA sequence. (from Genbank)
RC_AA1366 EST: zk99a04.s1 Soares pregnant uterus NbHPU Homo sapiens RC_AA4782 Human apM2 mRNA for GS2374 (unknown product specific to Insulin-like growth factor binding protein-2 [human, placenta, cDNA clone 490926 3', mRNA sequence. (from Genbank) BREAK REPAIR;, mRNA sequence. (from Genbank) Homo sapiens mRNA for cytochrome b5, partial cds clone 364705 3', mRNA sequence. (from Genbank) Ras GTPase-activating-like protein (IQGAP1) mRNA Prostate carcinoma tumor antigen (pcta-1) mRNA sequence, mRNA sequence, (from Genbank) sequence, mRNA sequence. (from Genbank) 0.2037366 S37730_s_at Genomic, 1342 nt, segment 4 of 4] Cellular Retinol Binding Protein Ij Metallothionein-le gene (hMT-le) AGTR1 Anglotensin receptor 1 KIAA0246 gene, partial cds 72kD type IV collagenase) Selenium binding protein 1 PTMS Parathymosin (from Genbank) 0.20424563|91_at D13814 s a RC_AA1890 0.20351024 79_at ਲ Ħ, 0.20407999|HT4580_at 0.20451282 M55593 at aţ 0.20421125|D78676 at 0.20324661|M10942_at 0.20359865|L78132_at at 0.20319045 L33075 at 0.20471369 M24398 0.2048273 D87433 HG4310-0.20464611 C02053 0.20386317 60_i_at 0.20340508|98_s_at 0.2033644 C01782 0.20485955|96 at 0.2043922 15 at 0.20407383|t 0.20395282 0.331201 0.330973 0.3311 0.33101 0.330898 0.330681 0.330608 0.330751 0.330595 0.3305390.330513 0.3303890.330274 0.330255 0.330352 0.330076 0.330015 0.3299490.329909 0.1918052 0.3869906 0.1914123 0.3868948 0.1931225 0.3872353 0.1916117 0.3869688 0.1913175 0.3868339 0.1928806 0.3872264 0.1925956 0.3870134 0.1908514 0.3866944 0.1908042 0.3865404 0.1905037 0.3865145 0.1900148 0.3864979 0.1896491 0.3864979 0.1890415 0.3864113 0.1883227 0.3863119 0.386116 0.1874569 0.3853968 0.3862024 0.1879949 0.3858351 0.1878685 0.3857179

2825.2020-002

Docket No.:

FIG. 9G2

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0 1873512 0	0	0.3853352	0.329886	0.20307983 S78569 at		LAMA4 Laminin, alpha 4
	1	0		0.00000		obs stalemos OFFICO and MIND
0.1869947		0.3852638	0.32968	0.20297918 W27325	, m	Homo sapiens minima for 170, complete cus
0.1869064		0.385242	0.329593	0.20280015 303474	at	SERUM AMYLOID A PROTEIN PRECURSOR
0.1868855	ŀ	0.3850896	0.329423	0.20276515 U85773_at		Phosphomannomutase 2
1	1				60	EST: zt36b07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
0.1867134		0.3849286	0.329416	0.20264563 04_at		clone 724405 3', mRNA sequence. (from Genbank)
	i			<u> </u>	RC_AA0373 c	EST: zc03c04.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321222 3' similar to contains Alu repetitive element;,
0.1858333		0.1858333 0.3849052	0.329401	0.2025336 57_f_at		mRNA sequence. (from Genbank)
	1		-	يك	_AA6090	EST: af10e04.s1 Soares testis NHT Homo sapiens cDNA clone
0.1856962		0.3846811	0.329306	0.20247835 45	.at	1031262 3', mRNA sequence. (from Genbank)
0 1856397		0.3844618	0.329289	RC_A 0.20236593.93.at	A2912	EST: zs18d11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:685557 3'. mRNA sequence. (from Genbank)
				4	A6099	EST: af18a06.s1 Soares testis NHT Homo sapiens cDNA clone
0.1852401		0.3844458	0.328857	0.20223911 88_at		1031986 3', mRNA sequence. (from Genbank)
0.1850165	10	0.3844308	0.328761	0.20221132 J02854	, m	20-kDa myosin light chain (MLC-2) mRNA
0.184947		0.3842261	0.328747	0.20207407 R67128	ă Ţ	KIAA0331 gene product
		1	And the second s			
0.1845868		0.3841472	0.328726	0.20191963 HT417	လ	at Cathepsin B
0.1842545	10	0.3841435	0.328629	0.20187184 C01714_at		Homo sapiens serum-inducible kinase mRNA, complete cds
,0444040	-	70207060	11 11 OCC 0	0.0040404 \\ \(\text{\text{\cond}} \)		UCE Honotonite arough factor (honomaintin A. ecatter factor)
0.1041733	\sim	0.3040734	0.520333	0.60102.0	C	
0.1836578	8	0.3838438	0.328521	0.201773791		
		1			U66711_ma	
0.1836305	20	0.3834631	0.328487	0.20164914 1_s_at	1_s_at	Ly-6-related protein (9804) gene
0.1835091		0.3829757	0.328288	0.20160782 D42073_at	742073_at	Reticulocalbin
	1				AA293544_a	
0.1829329	6	0.3828857	0.328148	0.201560881		D component of complement (adipsin)
0.1828559	59	0.3828296	0.328092	M9 0.20144865 t-2	M91556_s_a t-2	Sodium channel, voltage-gated, type VI, alpha polypeptide
	ı.		1			

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-	Mesothelio					/191556_s_a	
619 ma	na	0.1828559	0.3828063	0.328067	0.20136723 t		SCN6A Sodium channel, voltage-gated, type VI, alpha polypeptide
	Mesothelio					AA4561	
620 ma	na	0.182582	0.3827744	0.32797	0.20129631 47	at	General transcription factor IIIA
-	Mesothelio					A4518	EST: zx16e06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
621 ma	na	0.1825701	0.3827287	0.327925	0.20118895 77_at		clone 786658 3', mRNA sequence. (from Genbank)
	Mesothelio					A2050	
622 ma	na	0.1824623	0.3826162	0.327896	0.20101675 72_at		ATPase, Ca++ transporting, plasma membrane 1
	Mesothelio					623	EST: zr44g03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
623 ma	ma	0.1820259	0.3826037	0.327689	0.20099492 51_f_at		666292 3', mRNA sequence. (from Genbank)
Ī	Mesothelio					RC_AA4912	
624 ma	па	0.1817187	0.3825004	0,327652	0.20090656 61	कं	Homo sapiens clone 23923 mRNA sequence
_	Mesothelio	The state of the s	Į.			A1509	EST: zl47e06.s1 Soares pregnant uterus NbHPU Homo sapiens
625 ma	na	0.1812172	0.3824107	0.327616	0.20085259 28_at	28_at	cDNA clone 505090 3', mRNA sequence. (from Genbank)
	Mesothelio					RC AA1289	EST: zn90a05.s1 Stratagene lung carcinoma 937218 Homo sapiens
626 ma	na	0.180924	0.3823892	0.327543	0.20075068 02_at	02_at	cDNA clone 565424 3', mRNA sequence. (from Genbank)
	Mesothelio					M28213_s_a	
627 ma	ma	0.1809178	0.3823841	0.327461	0.20070113 t		RAB2 RAB2, member RAS oncogene family
Me 628 ma	Mesothelio	0.1805072	0.3822286	0.327332	0.20060998	AA328993_s	EST: EST32546 Embryo, 12 week I Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)
020	5	0.10001.2	- 1	2001-200	22222	ź,	CCT: - x71000 c1 Coarse NhHMD1 C1 Home canions cDNA clone
	Mesothelio					RC_AA2629	668834 3' similar to TR:G969170 G969170 PX19.;; mRNA sequence.
629 ma	ma	0.1803827	0.3821041	0.327331	0.20057136 69 f at	69_f_at	(from Genbank)
	Mesothelio					RC_AA4469	
630 ma	ma	0.1798011	0.3820793	0.327218	0.20051731 26 s at	26_s_at	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4
-	Mesothelio						
631 ma	ma	0.1793241	0.3817459	0.327103	0,20039591 M63896_at	M63896_at	Transcriptional enhancer factor (TEF1) DNA
	Mesothelio	,					Laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD),
632 ma	ma	0.1793036	0.3815177	0.327043	0.20026253 L34155	L34155 at-2	epilegrin)
	Mesothelio			1			
633 ma	ma	0.1793036	0.3815156	0.327026	0.20015667 L34155_at	L34155_at	Laminin-related protein (LamA3) mRNA
	Mesothelio					RC_AA1316	EST; zi34f04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA
634 ma	ma	0.1780946	0.3813306	0.327018	0.2001186992	92_at	clone 503839 3', mRNA sequence. (from Genbank)
	Mesothelio						Transcript ch138 [human, RF1,RF48 stomach cancer cell lines,
635 ma	ma	0.1780903	0.3812982	0.32691	0.19999103 S77393	S77393_at	mRNA, 235 ntj
	Mesothelio						
636 ma	ma	0.1774533	0.3811724	0.326891	0.19991837 U20499_at	U20499_at	Estrogen suitotransferase mKNA
1	Mesothelio	7007		*00000	0.40000000	N910/1_s_a	EST: 2a1 /t10.r1 Soares tetal liver spieen TNFLS Horito sapiens convey
03/ ma	Ша	0.1774591	0.3001201	0.320031	0.13305025	1	

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N72380_s_a EST: yv38f12.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA AA095022_a EST: cp2494.seq.F Fetal heart, Lambda ZAP Express Homo sapiens RC_AA2269 EST: zr21b01.s1 Stratagene NT2 neuronal precursor 937230 Homo 743586 3' similar to SW.JANA_DROME P20348 SEX-REGULATED sapiens cDNA clone 664009 3', mRNA sequence. (from Genbank) RC AA4173 |730942 3' similar to contains element MER31 repetitive element;, Homo sapiens inner mitochondrial membrane translocase Tim23 RC_AA5212 EST: aa79e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 0.19925913 90_at IMAGE:827164 3', mRNA sequence. (from Genbank) EST: zu05a12.s1 Soares testis NHT Homo sapiens cDNA clone EST: zu72g10.s1 Soares testis NHT Homo sapiens cDNA clone (TIM23) mRNA, nuclear gene encoding mitochondrial protein, PROTEIN JANUS-A PRECURSOR: ;, mRNA sequence. (from done 245039 5', mRNA sequence. (from Genbank) Transforming growth factor beta-activated kinase 1 CALM1 Calmodulin 1 (phosphorylase kinase, delta) cDNA 5', mRNA sequence. (from Genbank) COMP Cartilage oligomeric matrix protein Insulin-like growth factor 1 receptor mRNA sequence. (from Genbank) 0.19944473 L35240_at-2 | Enigma (LIM domain protein) MGP Matrix protein gla KIAA0057 gene complete cds Enigma gene Genbank) RC AA4609 RC_AA4427 0.19854918 X53331_at RC_AA6094 RC_AA4323 RC_AA1556 0.19861484 D31762_at аţ 0.19973671 M19311 at 0.19931161|L35240_at 0.19874278 68 i at 0.19910164|L32137_ 0.19834757 69 at 0.19897059|22 at 0.19899285 73 at 0.19965887 62 at 0.19916373 33 at 0.19837253 0.19882444 0.32522 0.3251950.325407 0,325312 0.325725 0.325681 0.32544 0.326033 0.326018 0.326799 0.326386 0.32615 0.326073 0.325951 0.326705 0.326462 0.32688 0.1750197 0.3792232 0.1755718 0.3797453 0.1755296 0.3797176 0.1753673 0.3796374 0.1753 0.3795107 0.1750296 0.3793477 0.1761463 0.3800141 0.1760845 0.3799084 0.1758694 | 0.3798092 0.380611 0.1765347 0.3802867 0.1766856 0.3804237 0.176487 0.3801666 0.1761882 0.3800408 0.3801205 0.1764312 0.3801171 0.1770483 0.3806177 0.176487 0.176779 Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio Mesothelio 650 ma 651 ma 652 ma 653 ma 654 ma 643 ma 648 ma 649 ma 644 ma 646 ma 640 ma 641 ma 642 ma 645 ma 647 ma 638 ma

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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	,,						
655	Mesothelio 655 ma	0.174399	0.3791791	0.325056	0.19818458	RC_AA2583 83_at	Ash2 (absent, small, or homeotic. Drosonhila homolog). like
656	Mesothelio 656 ma	0.1743555	0.3790249	0.324918	U956 0.198128131 at	U95626_ma 1_at	Ccr2 gene (ccr2a) extracted from Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5), and ccr6 (ccr6) genes, and lactoferrin (lactoferrin)
	Mesothelio						(denomic clones lambda-ISK2-T2 HSE78TT: ADMA alcass no ra 4 ex
657	657 ma	0.1734003	0.3789631	0.324858	0.19800977 J00277	J00277_at	(generally concess ranged at 12, 1337 of 1, cDNA clones R5-[3,4, b]) c-Ha-ras1 proto-oncogene, complete coding sequence
658	Mesomello 658 ma	0.1730158	0.3787981	0.324854	0.197943661	X01677_s_a t	Glyraraldahyda 3 nhoonhoto dobooboo
	Mesothelio						Ciycelalueliyue-o-pilospilate defiyarogenase
629	659 ma	0.172954	0.3786646	0.32485	0.19782118	.34774 s at	0.19782118 L34774 s at Opioid-binding protein/cell adhesion molecule like
Mes	Mesothelio	1728227	0.3786100	0.004706	1000	3C_AA4364	RC_AA4364 EST: zv08f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
	Mesothelio	0.11			U.19775350/77 at	/ at	753057 3', mRNA sequence. (from Genbank)
661 ma	ma	0.1726466	0.3784561	0.324724	0.19763532 X77744	(777744_at	F11 mRNA
	Mesothelio			_	L	BC 001100	EST: zv03a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
662 ma	ma	0.1725055	0.3784482	0.324681	0.19758083 86 at	3	sequence. (from Genbank)
Me: 663 ma	Mesothelio	0.1722005	0.3783300	0.324670	RC A	A3982	EST: zt59f03.s1 Soares testis NHT Homo sapiens cDNA clone
	Mesothelio			5	0.137400034	AUAAG	7.2053 3, mKNA sequence. (from Genbank) EST: त्राहें होगह ूर्व १०००
664 ma	ma	0.1721294	0.3781903	0.324465	0.1973531 01 at	2440	CDNA clone 486729 31 mBNA control (from Carlette)
	Mesothelio		4			A0858	der et de la seguence (iron Genbank)
665 ma	ma	0.1719806	0.3781803	0.324394	0.19732334 51	at	Homo sapiens clone 24658 mRNA segments
	Mesothelio					-	ממוס בדססס ווו אואר פפלתפווכפ
666 ma	ma	0.1719037	0.3779434	0.324271	0.19729023 X00949 at		Prepro-relaxin H1
Me 667 ma	Mesothelio ma	0.171875	0.3779163	0.324155	RC_A 0.1971219525 at	A3938	
	Mesothelio		1		7		Horno saprens miking for leptin receptor gene-related protein
668 ma	ma	0.1717139	0.1717139 0.3779119	0.324137	0.19704229 L07515	at-2	numan neterochromatin protein homologue (HP1) mRNA, complete at-2 cds. (from Genhank)
(Mesothelio	<u>-</u>					Vicini Conscient
669 ma	Magathalia	0.1717139	0.3777939	0.324052	0.19698034 L07515 at		HETEROCHROMATIN PROTEIN 1 HOMOLOG
670 ma	Mesomello	0.1714479	0.3776662	0.323953	0.196867961	AA402538_a	- Industrial chromosomes to see the
	Mesothelio						Tourn septems an universitie 13, cosmid RZ6445
671 ma	ma	0.1713939	0.377657	0.323953	0.19671832 X01630 at		ASS Argininosuccinate synthetase
Me: 672 ma	Mesothelio	0 1713/157	0.3776600	1 200	2	_	EST: zt79c09.s1 Soares testis NHT Homo sapiens cDNA clone
-	Mesothelio	200	0.07 7 0000	0.323343	0.19008/02/39 at	4000	/285603', mRNA sequence. (from Genbank)
673 ma	na	0.1710866 0.3773328	0.3773328	0.323858	0.19651799 98 at	A4299	EST: zw65e01.s1 Soares testis NHT Homo sapiens cDNA clone 781080 3', mRNA sequence. (from Genhank)

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L						W weet fails day	Undi Uncer black arealy that 25 Units death that 2 Units death
	Mesothelio						
9	6/4 ma	0.1710471	0.3772689	0.323795		0.19646917 M11749. at	THY-1 MEMBRANE GI YCOBBOTEIN BEECH BESSE
9	Mesothelio 675 ma	0.1701795	0.3772266	0.323793	0.1963923	AB002337_a	KIAAA330 goog groding
-	Mesothelio					RC AA4765	EST: 2x03b04 64 Socias total fatica Nicologo
9	676 ma Mecotholia	0.1700468	0.3771604	0.323609	0.19624177 82	82_at	clone 785359 3', mRNA sequence (from Genhank)
<u>ن</u> 	Mesoullelle		0				EST: yj83f12.r1 Homo sapiens cDNA clone 155375 F. (from
	Mosofbolio		0.109847 0.3770596	0.323553	0.19616893	0.19616893 R69417 at	Genbank)
9	Mesouneik 678 ma) 0 169529	0.378050	07,000		RC_AA4821	
	Mesothelio	_	- 1	0.32333	0.19607806 27	27_at	Homo sapiens mRNA for PAK4 protein
65	679 ma	0.1690904	0.3768851	0 303840	405070	RC_AA2922	
	Mesothelio	+-	1	0.02500	0.19095651 28 at		STAT induced STAT inhibitor 3
ĕ	680 ma	0.1690471	0.3768125	0.323385	0 19589542 40 24	A1303	EST: zo19g09.s1 Stratagene colon (#937204) Homo sapiens cDNA
	Mesothelio			200	7+000001:0	0000	Glone 38/392 3', mRNA sequence. (from Genbank)
8	681 ma	0.1688984	0.3767556	0.323307	0.19584116 1	77242323_d t	EST. Zfo4gu7.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
9	Mesomelio						EST: vc40f01 r1 Homo sapiens cDNA close 82464 r1 :- ::
3	Mesothelia	0.1688756	0.3767038	0.323221	0.19575141 T68246 at	T68246_at	contains PTR5 repetitive element : (from Genhank)
89	683 ma	0.1687327	0.3764948	0 323110	RC A	A4914	EST: ab04a05.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
				2	0.13003000		clone 839792 3', mRNA sequence. (from Genbank)
				10 Page 194			EST: zt51f09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725897 3' similar to SW:ATF4 MOUSE Q06507 CYCL IC-AMP.
	Mesothelio					$\overline{}$	DEPENDENT TRANSCRIPTION FACTOR ATF-4 ;contains Alu
89	684 ma	0.1686777	0.3764804	0.323131	0.19551757 28 at	4343	repetitive element; contains element MER22 repetitive element;,
	Mesothelio					1767	TOT: 20 00 1
88	685 та	0.1684962	0.3763945	0.323126	0.19535476 20 at	4101	ES1: ZW9ZgU6.S1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
(Mesothelio						ordie 104414 3, mKNA sequence. (from Genbank)
89	686 ma	0.1683016	0.3763241	0.323097	0.19520125 Z18951 at		CAV Caveolin caveolae matoin 22kB
Ċ	Mesothelio					1	carcolli, carcolae plotelli, ZZRU
20	bor/ma	0.1676102	0.3761976	0.323042	0.19514242 D28124 at		Unknown product
688	688 ma	0.1675837	0.3760434	0.32303	Α 0.19506693 t	ro.	Section Princes O other 4
	Mesothelio				And the second s		EST: zw52e11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
989	689 ma	0.1674299 0.3757714	0.3757714	0.322895	0.19493578 30 at	A4339	NC_A44339 Gione 173708 3' similar to contains Alu repetitive element;, mRNA 30 af
069	Mesothelio 690 ma	0.1670877	0 375606	07.000		2301_a	cyconice. (II of III of II of II of II of II of II of II of II of II of II of II of
	Mesothelio	1	0.01	0.32279	0.194830021		Human mRNA for KIAA0303 gene, partial cds
691	691 ma	0.1663516	0.375599	0.322638	0.19477801	AA482319_1 E at	ES1: ab15c03.r1 Stratagene lung (#937210) Homo sapiens cDNA
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	42345	C02099_s_a EST: HUMGS0006419, Human Gene Signature, 3'-directed cUNA sequence, (from Genbank)	DC AA1355 FST - MODING ST Spares pregnant uterus NbHPU Homo sapiens	11000	A2927	f IMAGE:701798 3, mRNA sequence. (irom Genbank)	98 at Tissue specific mRNA	E	Osteopontin gene			AA5996 Homo sapiens TCFL5 mKNA for transcription ractor-like 3, complete		116	at 754497 3', mRNA sequence. (from Genbank)			RC_AA1341 cDNA clone 503382 3' similar to TR:G971709 G971709 LEUCINE	AMINOPEPTIDASE; mRNA sequence. (from Genbank)		AA427379 a EST: zw52h08.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA		EST: ze74h03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	RC_AA0253 clone 364757 3' similar to contains OFR.t1 OFR repetitive element ;,		RC_AA4127 Homo sapiens putative cyclin G1 interacting protein mRNA, complete		826	at Clone 724208 5, MKNA sequence. (IIIOIII Gendain)	AA405288_a clone 724553 5' similar to contains Alu repetitive element; contains	element LTK5 repetitive element,, IIIKNA sequence. (nom Censam)
0.19466743 U83411_at	RC_A 0.19462407 61_at	C020		0.1945371 39_at	P.C.	0.19444753 17_at	0 19431947 X67698	1120	0.19426782 1_at	RC	0.19418511 79 s at	RC PC	0.19408143 53_s_at	RC	0.19395018 21_at	0.19389415 L09260 at		RC.	0.1938167 38_at	0,19370669 U07919 at	AA4	0.193516t		RC,	0.19344762 51_at	S.	0.19334777 22 s at	S.	0.19333446 13 at	AA.	0.19330108 t
0.322569	0.322499	0 322480	0.02470	0.322383		0.322347	0.322295	0.0	0.322185		0.322051		0.321858		0.321831	0.321809			0.321784	0.321751		0.321657			0.321369		0.321329		0.321326		0.321175
0.3755322	0.3754666	0 3753200	0.57 35239	0.3752501		0.3751435	0.3750957		0.3750265	And the second s	0.3750138		0.3749325		0,3748867	0.3748223			0.3747199	0.3747064		0.3747011			0.3743643		0.3738854	1	0.3738823		0.1615035 0.3738562
0.1662612	ı	1	- 1	0.1655708		0.1653273	0.4652006		0.1647305		0.1646477		0.1643827		0.1642591 0.3748867	0.1632671			0.1631031	0 1627993		0.1627977			0.1627709		0.1617806		0.1616822		0.1615035
sothelio	sothelio	sothelio		sothelio	sothelio		Mesothelio	Acceptacio	ma	Mesothelio	na	Mesothelio	na	Mesothelio	na	Mesothelio	5	Mesothelio	ma	Mesothelio	Mesothelio	ma		Mesothelio	ma	Mesothelio	ma	Mesothelio	ma	Mesothelio	ma
Me: 692 ma	Mes 693 ma		694 ma	Me: Me: 695 ma	8	696 ma	Me.	1 180	698 ma		699 ma		700 ma		701 ma	Mei 707	10		703 ma	Mes 704 ma	5	705 ma			706 ma		707 ma		708 ma		709 ma

							EST: zu62d03.s1 Soares testis NHT Homo sapiens cDNA clone 742565 3' similar to SW:YEY6 YEAST P40093 HYPOTHETICAL 38.2
	Mesothelio					RC_AA4013	KD PROTEIN IN BEM2-SPT2 INTERGENIC REGION: mRNA
71(710 ma	0.160909	0.3738555	0.321168	0.19323151 45	s at	sequence. (from Genbank)
777	Mesothelio	7				RC_C20974	
=	711 ma	0.1608695	0.3738073	0.321153	0.19314803		Vanin 1
7.40	Mesothelio	0000	01001	0		_AA4432	EST: aa14d01.s1 Soares NhHMPu S1 Horno sapiens cDNA clone
7	Magathalia	0.1008500	U.1008500 U.3/36539	0.321123	0.19307591 12	12 at	813217 3', mRNA sequence. (from Genbank)
713	Mesoureiro 713 ma	0.1607781	0.3735802	0.324002	0 10305/87	AA252929_a	UOA historia formila a sur la constanta de la
	Mesothelio			7001-700	10100001.0		EST. HIMASONO3865 Ulman Cana Signature 31 ft. 12 Paris
714	714 ma	0.1607056	0.3735255	0.32105	0.19291717 C01877	C01877_at	EST: HOMISSOUSSOS, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)
	Mecothelio						EST: ab36c09.s1 Stratagene HeLa cell s3 937216 Homo sapiens
715	715 ma	0.1606276	0.373473	0 321047	RC_A 0 19289306 18 at	A4804	CDNA clone 842896 3' similar to SW:DYHC_ANTCR P39057 DYNEIN
	Mesothelio		1		000000000000000000000000000000000000000	2212 2	DE LA CITATIV, CILIARY: ,, IIIRNA Sequence. (Irom Genbank)
716	716 ma	0.1605957	0.1605957 0.3734498	0.321008	0.19283643		COT. 2049 For Source felling NZD4FIK HOMO Sapiens CDNA Clone 381764 5' mRNA seguence (from Cenhank)
	Mesothelio					RC AA6088	
717	717 ma	0.1603726	0.1603726 0.3734496	0.320939	0.19267048 50_at	50_at	EIF4E-like cap-binding protein
	Mesothelio		4		1	AA328684 a	EST: EST32211 Embryo. 12 week I Homo saniens cDNA 5' and
718	718 ma	0.1600236	0.1600236 0.3732539	0.320913	0.19252278		mRNA sequence. (from Genbank)
	Mesothelio					M13452 s a	
719	719 ma	0.1599198	0.3732411	0.320662	0.19247916	1	LMNA Lamin A
1	Mesothelio					H89551 s a	EST: yw28e07.r1 Homo sapiens cDNA clone 253572 5' (from
720	720 ma	0.1596973	0.3731312	0.320526	0.19243203 t	1	Genbank)
í	Mesothelio					3C_D20297	RC_D20297 EST: Human HL60 3'directed Mbol cDNA. HUMGS01271_clone
721	721 ma	0.1593922	0.3730203	0.320457	0.19233853	at	pm2024, mRNA sequence. (from Genbank)
1	Mesothelio					RC_AA6001	
77)	722 ma	0.1591617	0.37299	0.320448	0.19226988 40_at	10_at	Deleted in oral cancer-1
9	Mesothelio					A4606	EST: zx64b12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
123	723 ma	0.1589988	0.372941	0.320427	0.19216892 59_at		clone 796223 3', mRNA sequence. (from Genbank)
724	Mesotnello 724 ma	0 1587076	0.3728561	0 320340	400440	182319_j	EST: ab15c03.r1 Stratagene lung (#937210) Homo sapiens cDNA
	Mesothelio			0.020040	1	ָּם,	clone 840868 5, mKNA sequence. (from Genbank)
725	725 ma	0.1583093	0.3728167	0.320073	0.19204576	.08096 s at	0.19204576 L08096 s at CD70 CD70 antigen (CD27 ligand)
7.76	Mesothelio	7 4 5000000	7004040	0000		L08096_s_at-	
/ 20 1118	IIIa	0.1303093	0.1303093 0.3727327	0.320000	0.19198087/2		I umor necrosis factor (ligand) superfamily, member 7

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					M. Mark Brit W. Step South		મ માં મુખ્યમ પ્રત્યો મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી મામલી
							EST: zx36d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
				-	-		clone 788551 3' similar to TR:G595950 G595950 PROTEIN N-
	Mesothelio				Ж.	_AA4528	TERMINAL ASPARAGINE AMIDOHYDROLASE.;, mRNA sequence.
727 ma	ma	0.1583065	0.3726967	0.320006	0.19179444 30	at	(from Genbank)
	Mesothelio				R	RC_AA4466	EST: zw89h10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
728 ma	ma	0.1576646	0.372281	0.319961	0.1917312 66_at	6_at	clone 784195 3', mRNA sequence. (from Genbank)
	Mesothelio					rna	6-16 gene (interferon-inducible peptide precursor) extracted from
729 ma	ma	0.1576219	0.3722671	0.319946	0.19163463 1_s_at		Human interferon-inducible peptide (6-16) gene
	Mesothelio						
730 ma	ma	0.1575477	0.3722461	0,319918	0.19150676 U61262	161262_at	NEO1 Neogenin (chicken) homolog 1
	Mesothalio						EST: H. sapiens putatively transcribed partial sequence, UK-HGMP
731 ma	ma	0.1573079	0.3721707	0.319754	0.19142288 Z21081 at		sequence ID AAADIMBX; single read, mKNA sequence. (from Genbank)
	Mesothelio			The state of the s		1	
732 ma	ma	0.1571627	0.3721646	0.319649	0.19136856 L10844 at	10844 at	CDC42 Cell division cycle 42 (GTP-binding protein, 25kD)
	Mesothelio				<u>x</u>	RC AA4780	
733 ma	ma	0.156899	0.3720034	0.319635	0.19129904 17_at	7_at	Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
	Mesothelio				R	3402	EST: EST45737 Fetal kidney III Homo sapiens cDNA 3' end, mRNA
734 ma	ma	0.1565195	0.3718828	0.319561	0.19119152 93_at		sequence. (from Genbank)
1	Mesothelio				R	1020	EST: zl79f12.s1 Stratagene colon (#937204) Homo sapiens cDNA
735 ma	ma	0.1561409	0.1561409 0.3717813	0.319359	0.19110376 98_at		clone 510863 3', mRNA sequence. (from Genbank)
ļ	Mesothelio			-	₹	AA477031_a	EST: zu38c01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
736 ma	ma	0.1560452	0.3716324	0.319217	0.19106494 t		clone 740256 5', mRNA sequence. (from Genbank)
	Mesothelio						
737 ma	ma	0.1553954	0.371482	0.319086	0.19095929 X06614_at	06614_at	Receptor of retinoic acid
Me: 738 ma	Mesothelio ma	0.1551423	0.3714087	0.318994	RC_A 0.19087234.18.at	RC_AA3983	KIAA0331 gene product
					A	AFFX-	Action bloader
Î	Mesothelio	1			<u> </u>	0X/	
/39 ma	ma	0.155034	0.155034 0.3712879	0.318924	0.19075368 0351 M	st	AFFX-HSAC07/X00351_M_st (endogenous control)
					Ā	AFFX.	
	Mesothelio					HSAC07/X0	
740 ma	ma	0.155034	0.3712511	0.318891	0.19072299 03	351 M st-2	0.19072299 0351 M st-2 No info for gene
777	Mesothelio	7.00	0000710				EST: yb76c11.r1 Homo sapiens cDNA clone 77108 5' similar to
/4 I III 8	ma	0.15469//	0.3770883	0.31884	0.19063099 1505/6 at		SP:VE85_LAMBD P03755 EA8.5 GENE. (from Genbank)
Mes 742 ma	Mesothelio	0.1546808	0.370976	0.318681	RC_A	A4516	EST: zx44b03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
	Mesothelio			200000	0000000	A6217	EST: SPEARS of MINING Sequence. (MOM Genoalik)
743 ma	ma	0.1546719	0.3709493	0.318648	0.19052623 62_at	71 702	1030857 3', mRNA sequence. (from Genbank)

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					11111. 1111.		Toold three trials reads most facility the state of the s
	Mesothelio						
744 ma	ma	0.1545339	0.1545339 0.3708064	0.318621	0.19048376 M12125 at	M12125_at	Skeletal beta-tropomyosin
	Mesothelio						
745 ma	ma	0.1541821	0.370778	0.318591	0.19046527 L22548 at	. 22548_at	COL18A1 Collagen, type XVIII, alpha 1
	Mesothelio						
746 ma	ma	0.1539157	0.3706593	0.318505	0.19025284 M27492_at	M27492_at	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR
	Mesothelio						
747 ma	ma	0.1538554	0.3706252	0.3184	0.19022676 D88153_	D88153_at	Homo sapiens mRNA for HYA22, complete cds
	Mesothelio						ITGB1 Integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen
748 ma	ma	0.1534408	0.3705863	0,318399	0.19016187 X07979_at	X07979_at	CD29 includes MDF2, MSK12)
	Mesothelio					RC AA4565	The state of the s
749 ma	та	0.1533933	0.3705222	0.318289	0.19005607 88_at	88_at	Homo sapiens BC-2 protein mRNA, complete cds
	Mesothelio						
750 ma	ma	0.1532873	0.3704566	0.318209	0.19001427 D84239	D84239_at	IgG Fc binding protein
	Mesothelio						
751 ma	ma	0.1532873	0.3704194	0.318161	0.18984726	D84239 at-2	0.18984726 D84239_at-2 IgG Fc binding protein
	Mesothelio					The state of the s	Homo sapiens mRNA for smallest subunit of ubiquinol-cytochrome c
752 ma	ma	0.1531884	0.3703296	0.318111	0.18982284 D31286	D31286_at	reductase, complete cds
Me	Mesothelio	0.4594006	90000260		. 101010010	0.00.02	
3		0.1551220	0.1331220 0.3/02900	0.318039	0.189/0/84 23/9/6 at	١,	L I BP2 Latent transforming growth factor beta binding protein 2
, L	Mesomello	7	0			A1000	
/54 ma	ma	0.1528485	0.3/02906	0.31/893	0.18972875 26_at	26_at	clone 510832 3', mRNA sequence. (from Genbank)
	Mesothelio						
755 ma	ma	0.1528481	0.3702314	0.317798	0.18969578 X73478 at	X73478_at	HPTPA mRNA
J.	Mesothelio					RC_AA0349	EST: zk25e01.s1 Soares pregnant uterus NbHPU Homo sapiens
756 ma	ma	0.1520649	0.3700841	0.317688	0.18966319 25_at	25_at	cDNA clone 471576 3', mRNA sequence. (from Genbank)
	Mesothelio						The state of the s
757 ma	ma	0.1518661	0.3700409	0.317639	0.18951707	U77845_at-2	0.18951707 U77845_at-2 Human hTRIP (hTRIP) mRNA, complete cds
	Mesothelio						
758 ma	ma	0.1518661	0.3700409	0.317511	0.18939087 U77845_at	U77845_at	HTRIP (hTRIP) mRNA
	Mesothelio						
759 ma	ma	0.1517683	0.3700068	0.317475	0,18935347 U92074_at	U92074_at	RAD51 (S. cerevisiae)-like 1
1	Mesothelio	0				AA1133	l
/on ma	ma	0.1509183	0.3699558	0.317415	0.1892641287	87_at	cDNA clone 563578 3', mRNA sequence. (from Genbank)
	Mesothelio					M11717_rna	
761 ma	ma	0.1507523	0.3697926	0.317383	0.18918574 1	1_at	Heat shock protein (hsp 70) gene
Me 762 ma	Mesothelio	0 1503657	0.1503657 0.3606068	0.347997	f 0 1801101	AA043160_a	AA043160_a EST: zk48g01.r1 Soares pregnant uterus NbHPU Homo sapiens
104		0.1000001	0.000000		1001.0		ים ויסטום אוסטוט

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Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. EST: aa94h04.s1 Stratagene fetal retina 937202 Homo sapiens cDNA EST: ag23d09.s1 Jia bone marrow stroma Homo sapiens cDNA clone element L1 L1 repetitive element;, mRNA sequence. (from Genbank) element THR repetitive element;, mRNA sequence. (from Genbank) 0.18789992 52_at | mRNA sequence. (from Genbank) EST: Human Down syndrome region, YAC 152F7, mRNA sequence. EST: zu50g01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA AA011479_a EST: zi01b10.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens clone 838999 3' similar to contains Alu repetitive element; contains AA386297_a EST: EST185039 Brain IV Homo sapiens cDNA, mRNA sequence. RC_AA4010 |ctone 741456 3' similar to contains Alu repetitive element; contains EST: af18h05.s1 Soares testis NHT Homo sapiens cDNA clone cDNA clone 429499 5', mRNA sequence. (from Genbank) 1071185 3', mRNA sequence. (from Genbank) Homo sapiens clone 24619 mRNA sequence Glyceraldehyde-3-phosphate dehydrogenase Small proline-rich protein 2 (SPRR2B) gene Transforming growth factor-beta-2 mRNA Golgi SNAP receptor complex member Pinin, desmosome associated protein mRNA sequence. (from Genbank) Axin (AXIN) mRNA, partial cds from Genbank) (from Genbank) Prefoldin 1 Axin AA285290_a AA400333_a AF009674_a 0.18854679|L05188 f at AF009674_a /M33197_M_ | RC_AA4872 0.18895793|97 at RC_AA5994 HUMGAPDH 0.18838218 | 14 at 0.18842697 M19154 at 0.1883156 D45333 at 0.18891975|U69114 at 0.18781441 98 f at AFFX-0.18885572|34 at 0.18769458 st-2 0,18808661|t-2 0.18834558 1 0.18879592 0.18824713 0.18865359 0.18810296 0.316411 0.316404 0.317218 0.317179 0.317112 0.317056 0.317004 0.316981 0.316793 0.316694 0.316631 0.316437 0.31637 0.31637 0.316299 0.316577 0.1498383 0.3695536 0.1497794 0.3693826 0.1497228 0.3693816 0.1482684 0.3689131 0.368808 0.1480379 0.3684416 0.1479324 0.3683705 0.1476634 0.3681735 0.1502544 0.3696044 0.1484581 0.3693137 0.1484308 0.3690531 0.1479324 0.3683169 0.1497865 0.3693851 0.1481102 0.3684657 0.1477969 0.3682683 0.1477346 0.3681783

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	Mesothelio			-	7	AFFX- HUMGAPDH	
779	779 ma	0.1476634	0.3680417	0.316258	0.18759729 st	st	AFFX-HUMGAPDH/M33197 M st (endogenous control)
780	Mesothelio	0.4479670	1	070070	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	A0194	EST: ze58g01.s1 Soares retina N2b4HR Homo sapiens cDNA clone
3	Mesothelio	0.141.3010	0.3078473	0.316246	0.18/52535 98_at	yg_at	363216 3', mRNA sequence. (from Genbank)
781 ma	ma	0.1472232	0.3679125	0.316225	0.18750322 Y00281	700281 at	RPN1 Ribonhorin 1
	Mesothelio					360	EST: zu03c01.s1 Soares testis NHT Homo saniens cDNA clone
782	782 ma	0.1471884	0.3678747	0.315958	0.18736114 05 at		730752 3', mRNA sequence. (from Genbank)
783 ma	Mesothelio	0 1469105	778782	0.215017	F 0 40700E	A4969	EST: aa42f08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
	Mesothelio		1	118816.0	N.10123301_al	A4438	623523 3, mRNA sequence. (from Genbank) EST: zw88e11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
/84 ma	ma	0.1468581	0.3678202	0.3159	0.18722205 28 at		clone 784076 3', mRNA seguence, (from Genhank)
Me: 785 ma	Mesothelio ma	0.1466967	0.3677664	0.315844	RC_AA4	096	EST: zv72c09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
	Mesothelio				200	25.0	GOT:00-04 3, IIIKINA Sequence. (Irom Genbank)
786 ma	ma	0.1464503	0.3677286	0.315727	0.1870555 t	74403303 a	E31: zxs0e01.71 Soares ovary tumor NbHOT Homo sapiens cDNA clone 811032 5', mRNA sequence. (from Genbank)
	Mesothelio					-	EST: zf21b01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
787 ma	ma	0.1464263	0.3677156	0.315715	0.18704283 75_at	A0554	clone 377545 3' similar to SW:V1P_RAT P80144 MYOTROPHIN ;, mRNA sequence. (from Genbank)
	Mesothelio					C AA1025	RC AA1025 EST: zn42d02 s1 Stratagene endothelial cell 037223 Homo canions
788 ma	ma	0.1464106	0.367512	0.31569	0.18698433 81	1 at	cDNA clone 550083 3", mRNA sequence (from Genhank)
1	Mesothelio	1			X.	A2912	(Allegation Hot) Conscionation
789 ma	ma	0.1462587	0.3674645	0.315682	0.18683857 69 at	9 at	Homo sapiens mRNA for KIAA0776 protein, partial cds
790 ma	Mesomello ma	0.1459198	0.3674036	0.315666	0.18679723 t	A451640_a	AA451640_a EST: zx43d06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA t
	Mesothelio			The state of the s			EST: ww36a09.r1 Homo sapiens cDNA clone 254368 5' (from
791 ma	ma	0.1455774	0.3673827	0.315628	0.18678425 N71232 at		Genbank)
792 ma	Mesothello	0.1455075 0.3673371	0.3673371	0.315513	RC_A 0.18671526.70.34	A2331	
	Mesothelio			0.0010.0	0.1001.1001.		iiileiileukiii 13 receptor, alpha 1
793 ma	ma	0.1454725	0.3672379	0.31546	0.18654309 J04162 at		FCGR3 Fc fragment of log-low affinity IIIa recentor for (CD16)
	Mesothelio					T	de la company de la company ma, receptor for (CD10)
794 ma	na	0.1454179 0.3672225	0.3672225	0.315427	0.18653782 IL 10 at		No info for gene
	othelio				A	81_a	
em ce/		0.1453689	0.3670139	0.315347	0.18641892 t		Human mariner-like element-containing mRNA, clone pcHMT1
Me: 796 ma	Mesothelio ma	0.1453478	0.3669868	0.315273	RC_A 0.1863160917 at	C_AA2629 7	RC_AA2629 EST: zs26e11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
							The second of the sequence (HOLLI GELDALIK)

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Me	Mesothelio						she of large Alder Artery
797 ma		0.1451573	0.3669825	0,315266	0.18629725	U90546_at-2	0.18629725 U90546_at-2 Human butyrophilin (BTF4) mKNA, complete cds
Me	Mesothelio	0 4464679	0 3669467	0 345994	0 18623957 1 190546 at		Butyrophilin (BTF4) mRNA
/ yo ma		0.1451373	0.3000407	0.010224	0.10023337	1	
Mes 799 ma	Mesothelio	0.1445275	0.3668164	0.315051	0.18619058 Z26317 at		DSG2 Desmoglein 2
200	olothon		ì			AA296994 <	AA206004 s Homo saniens mRNA for putative seven transmembrane domain
IME	Mesoureno	0 4444054	0 386818	0 314038	0 18611146	24	none adplicing in which parameters are accounted in
OUU IIIC	1 ootholio	0.1444001	0.0000.0	0.01		A A A A A 7 F	EST: ah23e01 s1 Stratagene lung (#937210) Homo sapiens cDNA
801 ma	Mesouneilo	0.1438183	0.3665991	0.314911	0.18603478 58 at	2	clone 841656 3', mRNA sequence. (from Genbank)
			1				EST; af12d09.s1 Soares testis NHT Homo sapiens cDNA clone
Me	Mesothelio					RC AA6091	1031441 3' similar to TR:G988221 G988221 TBC1.;, mRNA
802 ma		0.1433477	0.366464	0.314905	0.18598638 95_at	95_at	sequence. (from Genbank)
ME	Mesothelio			-		AA053853_a	AA053853_a EST: zf52d01.r1 Soares retina N2b4HR Homo sapiens cDNA clone
803 ma	m.	0.1430161	0.366379	0.314704	0.18590131	-	380545 5', mRNA sequence. (from Genbank)
M	Mesothelio					AA2916	EST: zt45f05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
804 ma	m	0.1429838	0.3663466	0.314658	0.18586475 29	101	clone 725313 3', mRNA sequence. (from Genbank)
ğ	Mesothelio					RC_AA5987	
805 ma	co.	0.1426572	0.366249	0.314334	0.18575393 25_at	25 <u>at</u>	Endothelial differentiation-related factor 1
Me	Mesothelio	0.1422785	0.3661376	0.31431	0 18571821	0 18571821 W49745 at	Homo saniens FK506-binding protein (FKBP63) mRNA, partial cds
ME	Mecothelio	201	- 1				FST: 21/44n09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
807 ma	9	0.1420904	0.3658996	0.31426	0.18568048 29 at		clone 740896 3', mRNA sequence. (from Genbank)
Ž	Mesothelio						
808 ma	a	0.1420582	0.3658615	0.31426	0.18556799 T30851	- 18	s_at Homo sapiens clone 24775 mRNA sequence
Ĭ	Mesothelio						above school and the school of
809 ma	a	0.1420529	0.1420529 0.3658107	0.314221	0.18545656 R74226	R74226_at	Homo sapiens mKNA for A I P synthase subunit e, complete cds
Ž	Mesothelio	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1		7	10 40 61	Comment (all descent files)
8 IU ma	a	0.1410984	0.1416964 0.3037403	0.314100	0.10330109 U34333 at	034333 at	Radical IIIIge (Diosopriila) Ilvinorog
Me:	Mesonieno	0.1416609	ก 3656623	0.314074	0 18534394		Tumor rejection anticen (ang6) 1
110	a opotholio	0.11	- 1		0.1000	-1	
812 ma	Mesonieno ma	0.1413069	0.3655205	0.314035	0.18529645	0.18529645 M59911_at	ITGA3 Integrin alpha-3 subunit
N S	Mesothelio	0.4440010	f .	0 242040	RC A	RC_AA0652	RC_AA0652 EST: zm51f01.st Stratagene fibroblast (#937212) Homo sapiens
813/ma		0.1412030	0,3034361	0.513815	0,10317002	1140405 2 2	CDIVA GIOLIE JESTITI SI, IIIIMA Sequence: (IIIMI General)
∑ <u>X</u>	Mesothelio	0 444569	0.365/1504	0.343885	0 1850062	U19495_S_a	Intercrine-alpha (hIRH) mRNA
0 14 1119	d	0.141.000	1	_	100000	RC AA4647	
Me 815 ma	Mesomello ma	0.1410309	0.365438	0.313669	0.18497877 22	22_s_at	
				,			

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	Mesothelio				ጸ	C_AA3991	RC_AA3991 EST: zt57a02.s1 Soares testis NHT Homo sapiens cDNA clone
816 ma	та	0.1409987	0.3654273	0.313565	0.18486263 64	4_at	726410 3', mRNA sequence. (from Genbank)
	Mesothelio					U57847_s_a	
817 ma	ma	0.1409784	0.3652456	0.313491	0.18484572 t		Ribosomal protein S27 (metallopanstimulin 1)
Mes 818 ma	Mesothelio	0 1409545	0.3649857	0.313453	A 0 18482298	AA313977_s	Homo sapiens RNA polymerase II transcription factor SIII p18 subunit
2	Monothalia		- 1		11	a.	יייייייייייייייייייייייייייייייייייייי
819 ma	Mesomello ma	0.1406066	0.3649317	0.313408	0.18473002 W26054	/26054_at	EST: 18d8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
	Mesothelio						EST: zd52c12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
820 ma	ma	0.1406014	0.1406014 0.3648743	0.313358	0.1847259 W73751	at	clone 344278 5', mRNA sequence. (from Genbank)
	Mesothelio						Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid debudraceases complex made average processes
821 ma	ma	0.1404219	0.3647515	0.313243	0.18466003 X66785 f	66785 f at	at disease)
Met 822 ma	Mesothelio	0 1401071	0.3647273	0 242408	0 40464004 DE4400		Tob Committee
770	110	701010	I	0.010100	0.10404224 D	T	I UD Tarrilly
R23 ma	Mesoureno	0 1400013	0.3646945	0 040004		AA480073_a	EST: zv42a08.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
070	=	0.1400213	- 1	0.313031	0.184318/41		cione / 562/8 5, mKINA sequence. (from Genbank)
824 ma	Mesomello	0 1400193	0.3646337	0 312817	0 1844767 96	_AA4477	EST: aa20g11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
	Moootholia			0.015017	0.10110	at A A O TO O	o Locolo J. Hinning Sequence. (Holli Genoalik)
825 ma	ma	0.1397843	0.3645709	0.312782	0.18446559 62	_AA2590 _at	EST: zs3Un07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686749 3', mRNA sequence. (from Genbank)
	Moootholio				<u> </u>		EST: zo20g08.s1 Stratagene colon (#937204) Homo sapiens cDNA
826 ma	ma	0.1395858	0.3645709	0.312723	0.18433616 54	_AA 1325	clone 587486 3' similar to SW:MIJCE_MOUSE P21271 MYOSIN-LIKE PROTFIN + mRNA secilence (from Genhank)
	Mesothelio					AA0853	Homo saniens mRNA for .IM4 protein complete CDS (clone IMAGE
827 ma	ma	0.1395484	0.3644692	0.312657	0.18423387 99 at		546750 and LLNLc110F1857Q7 (RZPD Berlin))
C	Mesothelio	0000					
828 ma	ma	0.139493	0.364239	0.31249	0.18416665 Z24727_at	1	TPM1 Tropomyosin alpha chain (skeletal muscle)
820 ma	Mesothello	0 1303076	0 36404	0 240 480	0.40405204	04750 04	EST: HUMGS0003683, Human Gene Signature, 3'-directed cDNA
	Mesothelio	0.000		0.0	10000101	01100 at	sequerice, IIINNA sequerice. (IIOIII Gerinalik)
830 ma	ma	0.1393451	0.3639538	0.312433	0.18404976 L33801 at	33801 at	Protein kinase mRNA
Me. 831 ma	Mesothelio ma	0.1390674	0.363888	0.312413	0.18397096 68	-	EST: aa33d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815051 3" mRNA sequence (from Genhank)
	Mesothelio			and the same and t		1	
832 ma	ma	0.1390434	0.3638184	0.312221	0.18386336 D14660	14660_at	PUTATIVE 60S RIBOSOMAL PROTEIN
Me	Mesothelio	0 4 30 400	0024600	007070	770710070		
3	Mesothelio	0.100	1	0.012100	0.103/4041 UZU040 al		ZINF 134 ZING IINgel protein 134 (phz-9z)
834 ma	na	0.1387472	0.3637558	0.312167	0.18373337 M12529_at		APOE Apolipoprotein E

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Mesothelio				RC_AA036	RC_AA0395 EST: zf08d12.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
835 ma	0.138579	0.1385799 0.3636716	0.312115	0.18373168 95_at	
Mesothelio	 			RC_AA4165	
836 ma	0.1385695	5 0.3635986	0.312085	0.18365657 51_at	!
Mesothelio			24.00.44	RC_AA2812	
837 ma	0.1385294	4 0.3635841	0.312041	0.183626//45 at	IMAGE: 705133 3; MKNA sequence. (non Genbank)
Mesothelio				RC AA0170	EST: ze33e11.s1 Soares retina N2b4HK Homo sapiens cDNA clone 360812 3' similar to contains Alu repetitive element: mRNA
838 ma	0.1381553	3 0.3633605	0.312027	0.18351926 83_at	
170	110			0000	O TOT
839 ma	0.1381341	1 0.3633239	0.312027	0.18344453 08 at	
					EST: zn17h01.s1 Stratagene neuroepithelium NT2RAMI 937234
Mesothelio		1000000	0.000	RC_AA084	RC_AA0841 Homo sapiens cDNA clone 547729 3', mRNA sequence. (from
840 ma		0.1377120 0.3629905	0.312019	0,18343467 U4 at	Genbank)
841 ma		0.1374714 0.3629862	0.311751	0.18312952 07_at	Homo sapiens clone 23837 mRNA sequence
Mesothelio	elio			RC_AA1914	4
842 ma	0.1374435	5 0.3627804	0.311641	0.1830097 54_at	FGF intracellular binding protein
Mesothelio	elio 0 1371823	3 0 3626934	0.341622	0.1829947 X03168 at	VTN Vitronectin (serum spreading factor, somatomedin B,
Mesothelio				- 13	T
844 ma	0.1366761	1 0.3625163	0.311564	0.18294007 L14837_at	TJP1 Tight junction protein 1 (zona occludens 1)
Mesothelio	elio				
845 ma	0.1365293	3 0.3625107	0.311499	0.1828005 U95006_at	
Mesothelio		0 2000 0	117777	RC_AA0322	
846 ma	4	0.136349 0.3624749	0.317474	0.182/488/150_at	CUIVA CIONE 4/1011 3, MKIVA Sequence. (Ifom Genbank)
Mesothelio 847 ma		0.1362507 0.3624749	0.311464	KC_AA6217 0.18263337 79 at	Homo sapiens clone 23899 mRNA sequence
Mesothelio	+			The state of the s	
848 ma	0.1360817	7 0.3624114	0.311369	0.18258612 Z95636_at	
Mesothelio 849 ma	elio 0.1360424	4 0.3624096	0.311263	RC_AA4307 0.18253212 38 at	77 EST: zw32c02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770978 3', mRNA sequence. (from Genbank)
Mesothelio		1	1		
gon ma	0.1358195	5 0.3023553	0.31115	U.18236U65 22 at	Solute carrier family 22 (organic cation transporter), member 3
Mesothelio 851 ma	relio 0.1355915	5 0.3623509	0.311125	0.18231326 M77235_at	Cardiac tetrodotoxin-insensitive voltage-dependent sodium channel talpha subunit (HH1) mRNA
Mesothelio	lelio	0 3693033	0 311100	0 48221447 T83444 at	Homo eaniens mRNA for KIAA0887 protein partial ode
002 111	0.13300		0.311122	0.10221441 100444 0	-

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sothelio	856	ma	0.1347012	0.3621258	0.31085			alpha)
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sothelio 0.133933 0.3620499 0.310727 0.1816921 RC_AA4279 RC_AA4970 sothelio 0.1329128 0.3620499 0.310727 0.1816921 64_at 1 sothelio 0.1329128 0.3620499 0.310656 0.1815934 15_at 1 sothelio 0.1327154 0.3619533 0.310644 0.18145964 71_at 1 sothelio 0.1324424 0.3618533 0.310644 0.18145964 71_at 1 sothelio 0.1329748 0.3618313 0.310644 0.18144707 X95735_at 3 sothelio 0.1309748 0.3617846 0.310552 0.1813661 64_at 8C_AA486 sothelio 0.1309566 0.361748 0.310453 0.18102998 98_at sothelio 0.1309566 0.361748 0.31037 0.18102998 98_at sothelio 0.1297913 0.3617042 0.310193 0.18094808 D38305_at sothelio 0.1296342 0.3616667 0.310117 0.180	3	Mesothelio	0 4220080	0 3820840	0.310799	0 18170764 N4		EST: yy23a03.r1 Homo sapiens cDNA clone 272044 5. (from Genbank)
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sothelio 0.1301341 0.3617042 0.310321 0.18094808 D38305 at sothelio 0.1297482 0.3617042 0.310193 0.1808627 X76105 at sothelio 0.1297482 0.3616875 0.310183 0.18078786 35 at sothelio 0.1296342 0.3616667 0.310117 0.1807498 at sothelio 0.1294733 0.3616667 0.309979 0.18069968 34 at	ğ	Mesothelio	0.1306207	·		0.18102998	C_AA4056 3_at	EST: zu66e10.s1 Soares testis NHT Homo sapiens cDNA clone 742986 3', mRNA sequence. (from Genbank)
sothelio 0.1297913 0.3617042 0.310193 0.1808627 X76105_at sothelio 0.1297482 0.3616875 0.310183 0.18078786 35_at sothelio 0.1296342 0.3616667 0.310117 0.1807498 at sothelio 0.1294733 0.3616667 0.309979 0.18069968 34_at	398	Mesothelio 8 ma		1	0	0.18094808 D	38305_at	Tob
sothelio RC_AA6096 sothelio 0.1297482 0.3616875 0.310183 0.18078786 35 at L41919 rna1 L41919 rna1 sothelio RC_AA4602 RC_AA4602 0.3616667 0.309979 0.18069968 34 at	98	Mesothelio		1	0	0.1808627	76105 at	DAP-1 mRNA
sothelio 0.1296342 0.3616667 0.310117 0.1807498 at RC_AA4602 sothelio 0.1294733 0.3616667 0.309979 0.18069968 34 at at	87	Mesothelio	-	•	0	0.18078786	tc_AA6096 5_at	EST: at15h11.s1 Soares tesus Inflit Hollio Sapiens Cours Cons. 1031781 3', mRNA sequence. (from Genbank)
sothelio 0.1294733 0.3616667 0.309979 0.18069968 34 at	87	Mesothelio 1 ma		1	0	0.1807498	41919 ma' at	
	87	Mesothelio 2 ma				0.18069968	RC AA4602	

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Mesothelio 873 ma	0.1293987	0.3616236	0.309932	RC_A 0.1806564 72 at	A2624	RC_AA2624 EST: zs17g03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 72_at IMAGE:685492 3', mRNA sequence. (from Genbank)
Mesothelio 874 ma		0.3615972	0.30993	0.18060285 W01296_at		EST: yz94g12.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone 290758 5', mRNA sequence. (from Genbank)
Mesothelio 875 ma	0.1291995	0.361521	0.309884	0.18055838 Z34820		s_at Calcium channel, voltage-dependent, L type, alpha 1C subunit
Mesothelio		ł				
876 ma	0.1286409	0.3615159	0.309726	0.18047541 X66839	at	MaTu MN mRNA for p54/58N protein
Mesothelio			0 30072	0 18038265 10/15/82 at		NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4 (15kD,
Mocotholio	0.1200174	0.3012/31	0.00312	0.10030203	σ	FST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence.
878 ma	0.1283925	0.3612652	0.309704	0.18035804	8	(from Genbank)
Mesothelio	0				A1349	EST: zo23g08.s1 Stratagene colon (#937204) Homo sapiens cDNA
879 ma	0.1282987	0.3612469	0.309673	0.18030137 68_at		clone 587774 3', mRNA sequence. (from Genbank)
Mesothelio	0 1289456	0.361207	0.309601	RC_A 0.18026473.18.at	A2794	EST; zs85d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE-704269.3' mRNA secilence_(from Genbank)
Mesothelio	-				A2841	Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA)
881 ma	0.1281267	0.3611771	0.309541	0.1801558 43	äţ,	mRNA, complete cds
						EST: ze41a07.s1 Soares retina N2b4HR Homo sapiens cDNA clone
Mesothelio					RC_AA0171	361524 3' similar to contains element PTR7 repetitive element ;,
882 ma	0.1279139	0.3610486	0.309501	0.1800725 46 at	46_at	mRNA sequence. (from Genbank)
Mesothelio					AA446990_a	AA446990_a EST; zw90b07,r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
883 ma	0.127893	0.3609966	0.309345	0.18005331		clone 784213 5', mRNA sequence. (from Genbank)
					- Andrews	EST: zo36a01.s1 Stratagene endothelial cell 937223 Homo sapiens
						cDNA clone 588936 3' similar to SW:YBF7_YEAST P34222
Mesothelio			-		AA1431	HYPOTHETICAL 23.1 KD PROTEIN IN SHP1-SEC17 INTERGENIC
884 ma	0.1278207	0.3609622	0.30933	0.17998809 90	s at	REGION. ;, mRNA sequence. (from Genbank)
Mesothelio					A6000	EST: ag29h10.s1 Jia bone marrow stroma Homo sapiens cDNA clone
885 ma	0.1274802	0.3609615	0.309231	0.17994206 12_at	12_at	1091011 3', mRNA sequence. (from Genbank)
Mesothelio						
886 ma	0.1273314	0.3609431	0.309144	0.17978294 T55959	S	at TYRO protein tyrosine kinase binding protein
Mesothelio			0	1		
887 ma	0.12/2465	0.3606437	0.309042	0.17974265	0.17974265 WZ3469 at	Vesicle trafficking protein seczzo
Mesothelio	0 197944	0.3808044	0 308088	0 17068707	AA151795_s	AA151795_s Homo sapiens signal peptidase complex 18 kDa subunit mKNA,
Masch	\perp	- 1	2000	10000110	,	
889 ma	0.1270613	0.3604923	0.308902	0.17960605 Y08639_at	Y08639_at	Nuclear orphan receptor ROR-beta
Mesothelio	 	0 1270314 0 3604004	0.308818	RC 0 17954895 06	RC_AA3986	EST: zt74a08.s1 Soares testis NHT Homo sapiens cDNA clone 228054.3' mRNA sequence (from Genbank)
030 1118	0.1210314	1000000	3	١		

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	Mesothelio	- 0					FCT: Homo conjunction
88	891 ma	0.1267453	3 0.3601458	0.308799	0.1795266144367 at	144367 at	single-page common meanly frameworth (randomly primed, normalized),
	Mesothelio	0				5	americ pass sequence, mixiva sequence. (from Genbank)
83	892 ma	0.126685	0.3599991	0.308788	0.17942157 139060	L39060 at	Transcription factor St 1 mDN A
	Mesothelio		ł	-			Transcription racio of Hilling
3	Macotholio	0.120085	0.3599644	0.308788	0.17939046 L39060	L39060_at-2	Homo sapiens transcription factor SL1 mRNA, complete cds
89	894 ma	0.1262371	0.3599457	0.308731	0 17931265 578187		M DUACET TO THE COLLEGE TO THE COLLE
	Mesothelio	0			2001200	מוסוסו שו	M-FINASE INDUCER PHOSPHALASE 2
89	895 ma	0.1261937	0.3599069	0.308609	0.17919485 U12595 at	U12595 at	Tumor necrosis factor type 1 receptor associated protein (TRAP1)
836	Mesothelio 896 ma	0.125905	0.3597957	0.308567	0 47040704	RC_AA0530	
	Mesothelio	_		100000	0.17.913704 Z1 at	zı al	SCO1 (yeast homolog) cytochrome oxidase deficient 1
.68	897 ma	0.1256268	0.3596991	0.308504	0.179005681147624 24	147621 24	Minopological Management
	Mesothelio				0000	041 021 at	nucleolar autoantigen Nobs mRNA
89	898 ma	0.1253305	0.3594312	0.30842	0.17898133 W27873 at		Himon ekolotol minolo 4 o La Landa 6
	Mesothelio						FST: 245503 c4 Society 1.3 KD MKINA for tropomyosin
368	899 ma	0.1251713	0.3593925	0.308346	0.17888178 19	at	Cone 726293 31 mRNA sequence (from Contrary)
5	Mesothelio					A2582	EST: 2835004.s1 NCI CGAP GCR1 Homo canions COMA class
N N	Soo ma	0.1248676	0.3593658	0.308332	0.17877924 03 at		IMAGE:687222 3', mRNA sequence. (from Genhank)
901	IMESULITERIO 901 ma					AA402298_s	
000	Manathalia	0.1247353	0.3593054	0.308309	0.1787499		Actinin, alpha 4
000	OU2 ma	0 40 44000	I C		<u> </u>	A4482	EST: zw83h07.s1 Soares testis NHT Homo saniens CDNA clone
308	9	0.124/023	0.3593051	0.308239	0.17864318 82 at		782845 3', mRNA sequence. (from Genbank)
	Mesothelio				•		3-beta-hydroxysteroid dehydrogenase gene extracted from Human
903	903 ma	0.1244502	0.3591977	0.30816	0.1786131 1 at	144_rna	type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta
							Normer as gene
							22.3. Contains three novel genes one similar to C. elagas Veans 4
	Mocotholic						and one similar to (predicted) plant, worm, yeast and archaea
904	904 ma	0.1240703	0.3590309	0 308433	R 20000001	AA2434	bacterial genes, and the first exon of the KIAA0319 gene. Contains
	Mesothelio	1	00000	0.000133	0.17033823 97	at	ESTS, GSSs and putative CpG islands
905 ma	ma	0.1240644	0.3589746	0.308064	0.17850018 66	_AA3937	EST: zv64f06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
	Mesothelio					j.	date (30433 3 , IIIRNA sequence. (Irom Genbank)
906 ma	ma	0.1236625	0.3588665	0.308029	0.17842485 M83088 at		PGM1 Phoenhood ingenity of 1
1	Mesothelio						ora i rosprogracor ludose i
907 ma	ma	0.1235042 0.3588092	0.3588092	0.307938	0.17831104 R39394 at		Homo sapiens mRNA for E1B-55kDa-associated protein

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908	Mesomello 908 ma	0.1234809	0.3587831	0.307886	0.17825784	AA464013_a t	AA464013_a EST: zx82d05.r1 Soares ovary tumor NbHOT Homo sapiens cDNA t
	Mesothelio		ŀ				
909	909 ma	0.1234238	0.3587174	0.307844	0.17815654 U37690_at	U37690_at	RNA polymerase II subunit (hsRPB10) mRNA
	Mesothelio						
910	910 ma	0.1232986	0.3587139	0.307749	0.17811759 M97815	M97815 at	CRABP2 Cellular refinoic acid-binding protein 2
	Mesothelio					HG174-	7 HOLD RELIEF
911	911 ma	0.1229773	0.3587134	0.30773	0.1779859 HT174 at	HT174 at	Desmonlakin I
	Mesothelio			- Constant		RC AA2274	
912	912 ma	0.1226119	0.3586837	0.307628	0.17790654 63 at	63 at	Homo sanjens mBNA for KIAA0859 profesio complete ade
	Mesothelio						advantage of the second protein, complete cas
913 ma	ma	0.1224362	0.3586761	0.307569		0.1778632 U28386 at	RCH1 RAG (recombination activating gene) cohort 1
Me: 914 ma	Mesothelio ma	0.122195	0.35865	0.307477	0.17779882	RC_AA6098	EST: af08d11.s1 Soares testis NHT Homo sapiens cDNA clone
	Mesothelio			A.J.		RC AA488	FST: 2255210 ct NO! CCAD CCD4 11
915 ma	ma	0.1220511	0.3586392	0.307347	0.17779456 43 at	43 at	HOLD Sapiens CUNA GOOD HOLD Sapiens CUNA GONE
	Mesothelio					RC AA2783	EST: 708c05 st NCI CGAP GCR4 Home conjunctional
916 ma	ma	0.1215292	0.3586242	0.307231	0.1777433 91 at	91 at	IMAGE:712520 31, mRNA sequence (from Genhank)
	Mesothelio					A1470	EST: 2032a02.s1 Stratagene colon (#937204) Homo saniens cDNA
917 ma	ma	0.1214902	0.3585805	0.307114	0.17763695 67 at		clone 588554 3', mRNA sequence, (from Genhank)
3	Mesothelio					A0215	EST: ze67c01.s1 Soares retina N2b4HR Homo saniens cDNA clone
918 ma	ma	0.1212508	0.3585594	0.307005	0.17756614 92_at		364032 3', mRNA sequence. (from Genbank)
2	Mesothelio					_AA4476	EST: zw97a02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
3131118		0.121142	0.3585175	0.306978	0.17747997 17	_at	clone 784874 3', mRNA sequence. (from Genhank)
Mes 920 ma	Mesothello	0 1211297	0.358/470	0 306071	0 47740000	A0248	EST: ze79b09.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
	Mesothello		0.11	1,6000.0	0.111422US 00 al	oo al	clone 365177 3', mRNA sequence. (from Genbank)
921 ma	O a local	0.1206806	0.3584403	0.30689	C AA1 0.17735139 18 s at	KC_AA1483	Himan mRNA for KlAA0060 cond.
	Mesothelio					H53657 s a	the state of the s
922 ma	na	0.1200143	0.1200143 0.3583807	0.306671	0.17726841	i	Homo sapiens mRNA for KIAA0511 protein partial cds
Me 923 ma	Mesothelio	0 110001	0.000000			459216_s_a	
2	Mocotholio	0.113031	0.3303032	0.300099	0.1//1/841 t		GABRB1 Gamma-aminobutyric acid (GABA) A receptor, beta 1
924 ma	Official	0.1197425	0.3583282	0.306668	RC_A 0.17710753 62 at	3C_AA4114 32 at	RC_AA4114 EST: zv30g03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA 62 at clone 755188 3' mRNA semience (from Genhank)
1	sothelio				*	4A011243 s	AA011243 s EST: ze19d03.r1 Soares fetal heart NhHH19W Homo saniens CDNA
925 ma		0.1196871	0.3582468	0.306555	0.17701708	at	clone 359429 51, mRNA sequence (from Genhank)
Mes 926 ma	othello	0.1195219	0.3582159	0.306384	0 17600334 D30440 04		
	othelio			100000	11000011	$\neg \vdash$	o protein-coupled receptor
927 ma		0.1192552	0.358186	0.306384	0.1769431 X93510 at		37 kDa LIM domain protein

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				***************************************	Name of the last o		
	Mesothelio						EST: zc12e07.r1 Soares parathyroid tumor NbHPA Homo sapiens
928 ma	ma	0.1192548	0.358097	0.306246	0.17685503 W37660	N37660 at	mRNA sequence. (from Genbank)
	Mesothelio						
929 ma	ma	0.1188443	0.3580616	0.30622	0.17678544 S57235_	at-2	CD68 antigen
	Mesothelio						
930 ma	ma	0.1188443	0.3580124	0.306215	0.17672476 S57235 at	357235_at	CD68 CD68 antigen
	Mesothelio						EST: zd78h06.r1 Soares fetal heart NbHH19W Horno saniens cDNA
931 ma	ma	0.1187804	0.3578187	0.306186	0.17665581 W79496	N79496_at	clone 346811 5', mRNA sequence, (from Genbank)
	Mesothelio						
932 ma	ma	0.1187195	0.3577879	0.306076	0.17651887 L44497 at	.44497 at	Small inducible cytokine A5 (RANTES)
	Mesothelio					6	EST: zw82d03.s1 Spares testis NHT Homo saniens cDNA clone
933 ma	ma	0.1186495	0.3577812	0.306061	0.17646107 94	at at	782740 3' mRNA sectionce (from Genhank)
	Mesothelio	-				-	
934 ma	та	0.1184462	0.3576656	0.305854	0.17638555 L42621 at		Lv-9 mRNA
	Mesothelio						
935 ma	ma	0.1184462	0.357582	0.305843	0.1763528	0.1763528 L42621 at-2	Lymphocyte antigen 9
							EST: aa90h11.s1 Stratagene fetal retina 937202 Homo saniens cDNA
Me	Mesothelio			1 1 1		AA4569	clone 838629 3' similar to contains Alu repetitive element;, mRNA
യാവ	IIIa	U.1184227	0.3575677	0.305/55	0.1762782281	at	sequence. (from Genbank)
1	Mesothelio	0			L	A2812	EST: zs94f04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
937 ma	ma	0.1183584	0.3575545	0.305717	0.17623325 60_at		IMAGE:705151 3', mRNA sequence. (from Genbank)
(Mesothelio					U53831_s_a	
938 ma	та	0.1179122	0.3575407	0.305648	0.17621173 t		Homo sapiens interferon regulatory factor 7B mRNA, complete cds
	Mesothelio				14	A3984	EST: zt62a05.s1 Soares testis NHT Homo saplens cDNA clone
939 ma	та	0.1177467	0.3574895	0.305626	0.17613311 23_at		726896 3', mRNA sequence, (from Genbank)
_	Mesothelio						
940 ma	ma	0.1176955	0.357475	0.305526	0.17611235 U52840_at		Cri-du-chat region mRNA, clone CSA1
	Mesothelio				ı.C.	RC AA5041	
941 ma	па	0.117556	0.3574715	0.305503	0.1760122 45_at		Human Chromosome 16 BAC clone CIT987SK-A-635H12
	Mesothelio						
942 ma	na	0.1175122	0.3574573	0.305498	0.1758089 D17516_at		PACAP receptor
	Mesothelio					M55682 s a	
943 ma	na	0.1174797	0.357405	0.305441	0.17573658 t		CRTM Cartilage matrix protein
-	Mesothelio						EST: 31f8 Human retina cDNA randomly primed sublibrary Homo
944 ma	na	0.1174023	0.3573946	0.305438	0.17572148 W27435 at		sapiens cDNA, mRNA sequence. (from Genbank)
Me. 945 ma	Mesothelio	0.1173181	0.3573315	0.305419	RC 0 17E680E 94	_AA2876	EST: zs53f07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
	Mesothelio		2	0.000	0.11.00030.0	א מו	IMAGE: 701221 3, MKNA sequence. (from Genbank)
946 ma		0.1172893	0.3572818	0.305364	0.1755497 X90857	at	-14 gene, containing clobin regulatory element

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

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-	Mesothelio						
47	947 ma	0.1172746	0.1172746 0.3572787	0.3051	0.17553464	0.17553464 M16973 at	C8B Complement component 8, beta polypeptide
	Mesothelio						EST: EST188361 HCC cell line (matastasis to liver in mouse) II Homo
48	948 ma	0.1172237	0.3572785	0.305047	0.1754986	_at	sapiens cDNA 5' end, mRNA sequence. (from Genbank)
	Mesothelio						ID4 Inhibitor of DNA binding 4, dominant negative helix-loop-helix
<u>⊋</u> †	949 ma	0.11/0895	0.3572647	0.305047	0.17542727 U28368	U28368_at	protein
- 10	Mesothelio 950 ma	0.116983	0.3572566	0.304943	0 17533398 32866 at	1.32866 at	Effortor roll protonen roomtor 4 (EDD 4)
1	Mesothelio		1		20000	RC AA4294	EST: 7W34015 s1 Sogres overy timer NHLOT Lows control DNA
1	951 ma	0.1168641	0.3572474	0.30494	0.17528553 78 at	78 at	clone 771176.3' mRNA seguence (from Conhonk)
Ī	Mesothelio						Service of the way sequence, (Foll Collibatin)
23	952 ma	0.1164243	0.3570024	0.304918	0.17520262	0.17520262 W16804 at	NCK adaptor protein 1
	Mesothelio 953 ma	0 1158706	0.3569776	0.304862	0 47546069	-	
21	Mesothelio		- 1	0.304002	0.17318083	M13004 C C	Interreron-Induced leucine zipper protein (IFP35) mRNA, partial cds
<u>4</u>	954 ma	0.1158272	0.3569629	0.30477	0.175125021	W15334 8 a	BCI 2 B-cell CH /lymphoma 2
_	Mesothelio						
5	955 ma	0.1155963	0.3569373	0.304748	0.1750764	0.1750764 D84454 at	UDP-dalactose translocator
	Mesothelio						Dispose in the property of the
9	956 ma	0.1154589	0.3568518	0.304526	0.17504567 X76534 at		NMB Neuromedin B
	Mesothelio	T 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	i c		The state of the s	5 cds	
7	207 IIIa	0.1154283	0.356/81	0.304526	0.17492838 10_at		Human V beta T-cell receptor (TCRBV) gene locus
	Mesothelio						EST: 27e5 Human retina cDNA randomly primed sublibrary Homo
-	958 ma	0.1153941	0.3567528	0.304378	0.17485286 W27327_at		sapiens cDNA, mRNA sequence. (from Genbank)
	Mesothelio					BC AA2808	EST: zs99b05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
6	959 ma	0.1152854	0.3567329	0.304354	0.17471334 10 at		TUMOR 10 KD PROTEIN :: mRNA seguence (from Genhank)
=	Mesothelio						EST: zm27d08.s1. Stratagene pancreas (#037208) Homo capions
0	960 ma	0.115184	0.3566887	0.30434	0.17464292		cDNA clone 526863 3', mRNA sequence, (from Genbank)
	Mesothelio	0.4464005	000000	000000	1	A2912	EST: zs18d06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
- -	lid Mooth-lis	0.1131823	0.350628	0.304268	0.17458712 72 at	72_at	IMAGE:685547 3', mRNA sequence. (from Genbank)
	Mesomello 962 ma	0.1146084	0.3565882	0.304211	0.174560071	AA292171_a	AA292171_a EST: 2t50d08.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
=	Mesothelio		The same of the sa			3C AA4546	EST: 2x99f01.s1 Soares NhHMPr. S1 Homo saniens CDNA clone
3	963 ma	0.1145436	0.3565616	0.304105	0.17452978 51	, te	811897 3. mRNA seguence (from Genhank)
_	sothelio			-			
4		0.1143449	0.3562443	0.304056	0.1744562 U62800_at	U62800_at	CST6 Cystatin M
Me 965 ma	sothelio	0.1142265	0.3559554	0.304054	0.174381021	AA055019_a	AA055019_a EST: zf16g06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
							Section (Indiana)

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966 ma	ma	0.1141428	0.3559169	0.304024	RC_A 0.17430581 62_at	KC_AA2851 62 at	RC_AA2851 EST: 2s48e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 62_at IMAGE:700738 3', mRNA sequence, (from Genbank)
0	Mesothelio		1			A0547	EST: zk69h02.s1 Soares pregnant uterus NbHPU Homo sapiens
967 ma	Macotholio	0.1139822	0.3556997	0.303989	0.17426912 04_at		cDNA clone 488115 3', mRNA sequence. (from Genbank)
968 ma	ma	0.1139767	0.3556572	0.303974	0.174232231.05148	1 05148 at-2	7-eta-Chain (TCD) accordant proton proton (CC) (CC)
	Mesothelio		ŀ			7 10 10 10 10 10 10 10 10 10 10 10 10 10	Exact stant (10x) associated protein hilase (10 kD)
969 ma	ma	0.1139767	0.3555978	0.303946	0.17418352 L05148	L05148_at	Protein tyrosine kinase related mRNA sequence
Me: 970 ma	Mesothelio ma	0.113762	0.113769 0.3555749	บ สกรหวย	0 47447956	0.47449356 \M96957	10 x 0 x v 17
	Mesothelio	75	1	0.00000	0.17 + 17.000	- 1	Nivervisa gene product
971 ma	ma	0.1136964	0.3554648	0.303822	0.17401099 U87460	U87460 at	Putative endothelin recentor type B-like protein mRNA
Me: 972 ma	Mesothelio ma	0.1135905	0.3553256	0.303599	0.17396036 M83738	M83738 at	PTPN9 Profein twosine phoenbates on procent mixers
	Mesothelio						FST vr36a04 r1 Home sanions cDNA clone 207342 5' similar to
973 ma	ma	0.1134531	0.355229	0.303591	0.17390057 H58818	at	contains Alu repetitive element: (from Genbank)
-	Mesothelio		i		×	30_f	EST: II6470.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
974 ma	ma	0.113278	0.3552262	0.303512	0.1738147	at	cDNA 5', mRNA sequence. (from Genbank)
Me: 975 ma	Mesothello ma	0.1132218	0.1132218 0.3550117	0.303492	0.173743551	D79052_s_a	EST: Human placenta cDNA 5'-end GEN-530B11, mRNA sequence. (from Genhank)
_	Mesothelio					VA480838 s	EST: zx87e06.r1 Soares overvitumor NhHOT Homo sapiens cDNA
976 ma	ma	0.1128792	0.3548782	0.303411	0.17369658		clone 810754 5', mRNA sequence, (from Genhank)
	Mesothelio						
977 ma	ma	0.1127837	0.3548776	0.303388	0.1736069 U10492	ä	MEOX1 Homeobox protein mox1
Me 978 ma	Mesothelio ma	0.1123052	0.3547699	0.303326	0 17352523 11/29077	+	EST: 56a9 Human retina cDNA randomly primed sublibrary Homo
-	Mesothelio		1		0.11.002.02.0	פֿ	sapieris curva, ilinna sequerice. (Irom Genbank)
979 ma	ma	0.1122921	0.3547059	0.303262	0.17349903 X02874 at	X02874 at	OIAS (2'-5') oligoadenvlate synthetase
	Mesothelio					M10277 s a	
980 ma	na	0.1122151	0.3545501	0.303166	0.17344719		ACTB Actin, beta
Mes 981 ma	Mesothelio ma	0.1121894 0.3542998	0.3542998	0.303102	0 17336857	D31628_s_a	4 HVDDOVVVDIETINA DVA TETANA DVA SANA D
	Mesothelio					AA247475 a	FILENCATE THE MILE TROVALE DIOANGENASE FST. csq2040 sea F Hilman fetal heart I ambda 240 Exercise Linear
982 ma	na	0.1121843	0.3542716	0.303055	0.17336363		sapiens cDNA 5', mRNA sequence, (from Genbank)
- 6	Mesothelio		1				
983 ma	na	0.1120/48	0.3542278	0.302891	0.17328395 T30341 s	T30341 s at	at Human Chromosome 16 BAC clone CIT987SK-A-211C6
984 ma	ma	0.1117274	0.3541208	0.30288	0.17320247	100231 f at	0.17320247 J00231 f at Immunodlobulin gamma 3 (Gm marker)
Mes 985 ma	Mesothelio	0 1117074	0.3540888	0 302844	RC_A	3C_AA4314	RC_AA4314 EST: zw70g01.s1 Soares testis NHT Homo sapiens cDNA clone
1	5		0.0010000	0.302044	0.17300922		/81584 3', mKNA sequence. (from Genbank)

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H. H. B., H. H., J. Han, Chan, S., J. et al., S., J. et al., S., J. et al., S., J. et al., S., J. et al., S., J. et al., S., J. et al., S., J. et al., S., S., S., S., S., S., S., S., S., S	1720.1.c.	Homo sapiens mRNA for p27, complete cds	AA4UU1// a EST; zu69e07.r1 Soares testis NHT Homo sapiens cDNA clone	FST: 202001 J Sequence. (from Genbank)	23 at Clone 784542 21 Coares total fetus Nb2HF8 9w Homo sapiens cDNA	EST: zv62f11.s1 Soares factic NLTT 11.	758253 3', mRNA sections (from Child Sapiens cDNA clone	Chimeric mRNA derived from AMI 4	partial sequence	EST: zr51f04.s1 Soares NhHMPu S1 Homo sapiens cDNA clara	obos43 3, mKNA sequence. (from Genbank)	CM/IO	FST: 7/71-06 rd ctt-	clone 510034 5' mana clon (#937204) Homo sapiens cDNA	Good 3, Illand Sequence. (from Genbank)	Clathrin light chain a sens	जाया व प्रवास	3'UTR of unknown protein	RC_AA1674 EST: zp08f09.s1 Stratagene overien constitution	cDNA clone 595817 3' mRNA comment (#93/219) Homo sapien	EST: ag03e04.s1 Soares testis NHT Homo sapiens CDNA clans	1036222 3, mRNA sequence. (from Genbank)	t sequence. (from Genbank)	EST: zw86c12.s1 Soares total fetus NhoHER o112	RC_AA4436 clone 783862 3' similar to WP:B0303.15 CE00004 RIBOSOMA	FRU IEIN L11; mRNA sequence. (from Genbank)	Genbank)
The state of the s	RC_AA4777	01 at	AA400177_8	RC AA4471	23 at	RC_AA4373	23_at			362			O	Í					3C_AA1674 E	6 i at	RC_AA6210 E	A364267 a E	S	Ш	A4436	7 17	
. sie Haalt miss	(0.1/30/152//01 at	0.17301151		0.17293644 23 at		U.17283714 23 at		0.172/591	0.1726766 49 c at		0.17258398 X56494 at		0.17256624		0.17250869 X81636 at	0 17241180 20002	20114	T	U.17232104 36 j at	0.1722512541 at	A	0.17221641		0.17214063 83 24		0.17197074 R51809 at
	4 0.302760		0.302728		0.302728	202606	3	0.303703	5	0.302617		0.302595		0.30251		0.302484	0.30247		0.302388	0.002,000	0.302281	207.000.0	0.302192		0.302169		0.302085
	8 0.353954	_	1 0.3539161		4 0.3537544	0.353748		0.3535135		0.1107583 0.3534746	0	0.3534361	0.9500474	- 1	0 3534724	- 1	0.3531734		0.3529702		0.3529194	0.3508404	0.0020121		0.3527307	0077016	0.332/138
C	0.1115528		0.1109471		0.1103444	0.1108445	 	0.110785		0.1107583	0.4400000	0.1100293	0.1105758	00100	0.1103812		0.1101894		0.1101144		0.1098023	0.10945			0.1089872	0.1088465	
Mesothelio	986 ma	Mesothelio	987 ma	Mesomello 988 ma	Mesothelio	989 ma	Mesothelio	·990 ma	Mesothelio	991 ma	992 ma	Mesotholio	993 ma	Mesothelio	ma	Mesothelio	та	Mesothelio		Mesothelio	o lo dio	nesourerio		othelio	11 410	Official	
	8		8			386)66·		991	992		993		994 ma		995 ma		996 ma		997 ma	998 ma			aaa ma	1000 ma	+

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0.8510338 0.7160559 0.620598 0.46732655[L02321 at GSTM5 Glutathione S-transferase M5	0.574083 0.43466276 M74093 at G1/S-SPECIFIC CYCLIN F	0.555416 0.4186588 M64936 at Retinoic acid-inducible endonemous retroviral DNA	0.541685 0.40732542[L00389 f at Cytochrome P-450 4 gene	RC AA4560 FST aan3f02 st Sparae NHHMPH St Homo sanions on NA Alana	ביין ביין ביין ביין ביין ביין ביין ביין	812187 3', mRNA sequence. (from Genbank)	DCC=deleted in colorectal cancer (alternatively spliced, exon 1A)	0.522472 0.5995995 0.526755 0.39146128 S81294 at Ihuman, brain tumor no 245 mRNA Partial 216 ntl
732655 L02321 at	466276 M74093 at	186588 M64936 at	732542 L00389 f at	RC AA4560	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0.3989954 55 at		146128 S81294 at
8 0.46	3 0.43	3 0.4	5 0.40					5 0.39
0.62059	0.57408;	0.555410	0.54168		0 500 407	0.33340		0.52675
0.7160559	0.7569259 0.6572545	0.6046355 0.6343286	0.5680414 0.6189399		0.5276704 0.6066090 0.623705	0.0000323		0.5995995
0.8510338	0.7569259	0.6046355	0.5680414		0 5276704	0.0210101		0.522472
1 Ovary	2 Ovary	3 Ovary	4 Ovary		5 Overv	o overy		6 Ovary
					_			

FIG. 10A

then after the part of the first tree for the first

RC_AA1648 EST: zp02c11.s1 Stratagene ovarian cancer (#937219) Homo sapiens 0.35224438 51_at cDNA clone 595220 3' mRNA seculation from Control of the control D87023_cds | J1 gene extracted from Human (lambda) DNA for immunoglobín light Cockayne syndrome complementation group A CSA protein (CSA) sapiens cDNA 3' end similar to EST containing Alu repeat, mRNA EST: EST17092 Aorta endothelial cells, TNF alpha-treated Homo EST: zp89g09.s1 Stratagene HeLa cell s3 937216 Homo sapiens 0.3566498 S74445_at | Cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt] EST: ye04h07.r1 Homo sapiens cDNA clone 116797 5' similar to cDNA clone 627424 3', mRNA sequence. (from Genbank) cDNA clone 595220 3', mRNA sequence. (from Genbank) ALPP Alkaline phosphatase, placental (Regan isozyme) 0.3765996|HT3413_f_at|Neurofibromatosis 2 Tumor Suppressor (Gb:L27065) Melanocorfin-4 receptor [human, Genomic, 1671 nt] RPE-retinal G protein-coupled receptor (rgr) mRNA THYROXINE-BINDING GLOBULIN PRECURSOR 0.34592605 T89571_f_at |contains Alu repetitive element; (from Genbank) Folate receptor alpha (hFR) mRNA, partial cds Gamma-B-crystallin gene (gamma 1-2) 0.3392305|Z49825_s_at|HEPATOCYTE NUCLEAR FACTOR 4 0.3499422|U10690_f_at|MAGE-5a antigen (MAGE5a) gene **40S RIBOSOMAL PROTEIN S17** Squalene epoxidase, partial cds CP Ceruloplasmin (ferroxidase) Cpg-Enriched Dna, Clone E06 sequence. (from Genbank) 0.34787157 M31667_f_at CYTOCHROME P450 IA2 mRNA 0.35952345 S72503 s_at HRK1 chain Pp52 RC_AA1906 M11973_cds RC AA3043 0.36822984 HT4257 at 0.3441474 S77415 at 0.3361613 M13699 at 0.3626741 U14910 at 0.34225956 M19159 at 0.33353886 D13644 at 0.33212996 M14091 at ₽ 0,3405618 D78129 at 0.33507967 U28413 at 0.3375607 S58733_at HG3236-HG3987-0.38639146 U78793 0.3810037 44_f_at 0.3651814 | 76 at 0.37242782 1 at 0.35449806|2_at 0.52132 0.515128 0.4869052 0.5789442 0.505045 0.501902 0.499049 0.488236 0.485709 0.479513 0.469214 0.468239 0.466516 0.510391 0.495929 0.493198 0.490725 0.4835830.481697 0.477994 0.470246 0.47624 0.473484 0.471184 0.474711 0.4831111 0.5726396 0.48102 0.5659592 0.4806888 0.5639328 0.4823868 0.5684215 0.4741597 0.5519682 0.4701093 0.5498317 0.4584377 0.5427226 0.584052 0.4853579 0.5760211 0.476544 0.5564995 0.4644734 0.545431 0.4605246 0.5448023 0.458623 0.5438333 0.4572116 0.5400738 0.4538827 0.5378203 0.4796256 0.5606981 0.4756043 0.5564252 0.4742535 0.5535537 0.5195484 0.5954214 0.5137958 0.5912506 0.4676537 0.5481562 0.535572 0.4525212 0.4945446 10 Ovary 7 Ovary 13 Ovary 18 Ovary 19 Ovary 20 Ovary 21 Ovary 22 Ovary 23 Ovary 8|Ovary 9 Ovary 11 Ovary 24 Ovary 25 Ovary 26 Ovary 27 Ovary 28 Ovary 12 Ovary 14 Ovary 15 Ovary 16 Ovary 17|Ovary 29 Ovary

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Docket No.:

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to 087 simono O montril manual (A montr)	WIT (antisense promoter, introli i) [intribut, world), denotine, roo in	veocomal hvaluronidase		COL18A1 Collagen, type XVIII, alpha 1	property of the team of the manager of the team of the	ווומו ווומול וומווסף סמטוס מפוויפווי, יסוויףוכיני סטויסטוסעם סטקעטוסט	LU gene for Lutheran blood group glycoprotein	Unknown protein expressed in macrophages	EST: zv26h12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	754823 5' similar to contains Alu repetitive element;, mRNA	sequence. (from Genbank)	CYP11A Cytochrome P450, subfamily XIA (cholesterol side chain	cleavage)	Putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds	K12 keratin	Metallothionein-If gene (hMT-If)			Estrogen Receptor (Gb:S67777)	Pax8 mRNA	Gag 2 protein from Human endogenous retrovirus HERV-	K10./ntype=DNA /annot=CDS		Calmitine Calcium-Binding Protein, Mitochondrial	Type 3 iodothyronine deiodinase	0.31364387 S79854 at-2 Deiodinase, iodothyronine, type III		BRAIN IVALKIUKE IIO PEPI IJE PRECUNOUN	Unknown protein mRNA, partial cds	0.341406051179301.at-2 Human clone 23842 mRNA sequence	Clone 23842 mRNA sequence		RPL32 Ribosomal protein L32	EXT1 Exostoses (multiple) 1	GDI-dissociation inhibitor RhoGDIgamma mRNA	DNA for cellular retinol binding protein (CRBP) exons 3 and 4
ļ .		AJ000099_s	201.00	.22548_at	10 3 N L 00 N	743314 I at		X89059_at		AA422123 i	at		M14565_at	L16782_at	D78367_at	M10943 at	HG3125-	HT3301 s a		X69699_at	M14123_xpt	3_at	HG4749-	HT5197_at	S79854_at	S79854 at-2	M31776_s_a		U82303_at	1179301 at-2	U79301 at	X04470 s a		S79639 at	U82532_at	X07438_s_a t
	0.3305585 579781	1 32038028	0.04000047	0.32837132 L22548_at	70707000	1.327 13124	0.32607558 X83425_at	0.32471213 X89059			0.32353207		0.32265148 M14565	0,32139966 L16782_at	0.32021856 D78367	0.31930768 M10943			0.3183145 t	0.3175664 X69699 at		0.3162978 3_at		0.31530195 HT5197	0.31457448 S79854 at	0.31364387		0.31302221	0.31221905 U82303 at	0.31140605	0.31059998 U79301 at		0.3095432	0.30862892 S79639	0.30785182 U82532	< 0.30696872 t
	0.465137	0 464586	0.404000	0.462596	, , , , , , , , , , , , , , , , , , ,	0.40,1329	0.46037	0.459307			0.458142		0.457301	0.45566	0.454693	0.453046			0.45159	0.451101		0.450069		0.448641	0.448021	0.446937		0.446596	0.445974	0.445373	0.443961		0.442638	0.442335	0.441541	0.441305
	0.5345969	0 5308317	0.0020017	0.5299715	1000	0.529/019	0.5288946	0.5282426			0.5270001		0.5255702	0.5253384	0.5235044	0.5229932		*****	0.522803	0.5218499		0.5191208		0.5190125	0.5188058	0.5174404		0.516957	0.5168963	0 5166276	1		0.5157086	0.4254899 0.5148147	0.4231078 0.5140933	0.4211866 0.5129408
1	0.4525142	0 454697	0.431021	0.4504809 0.5299715		- 1	0.4478474	0.4461511			0.4444712		0.4438221	0.4435201		0.4409986			0.4405581	0.4386855		0.4384039		0.4366822	0.4349622	0.4349622		0.4295164	0.4290302	0.4272335	0.4272335	222	0.4256684	0.4254899	0.4231078	0.4211866
	30 Ovary		o I Oval y	32 Ovary	(33 Ovary	34 Ovary	35 Ovary			36 Ovary		37 Ovary	38 Ovary	39 Ovary	40 Ovary			41 Ovary	42 Ovary	,	43 Ovary		44 Ovary	45 Ovary	46 Ovarv		47 Ovary	48 Ovary	VaevO 07	50 Ovary	(55)	51 Ovarv	52 Ovary	53 Ovary	54 Ovary
	30	ç	2	32	(3	34	35			36		37	38	39	40			41	42		43		44	45	46		47	48	40	2 2	3	5	52	53	54

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55 Ovary	0.4199884	0.5125253	0.440456	0.30648792 S82472 at	[human, Genomic, 124 nt, segment 1 of 2]
56 Ovary	0.4181991	0.510801	0.439134	0.3057578 Y10506_at	CD110 protein
57 Ovary	0.417632		0.438371	0.30515698 X77909_at	IKBL mRNA
58 Ovary	0.4154039	0.5097205		0.30438116 L15309_at	ZNF141 Zinc finger protein 141 (clone pHZ-44)
59 Ovary	0.4152832	0.5085704	0.437338	0.30353743 D49410 at	IL3RA Interleukin 3 receptor, alpha (low affinity)
60 Ovary	0.4146924	0.5076208	0.436682	0.30305088 D83767_at	Clone N9 Rep-8 mRNA
61 Ovary	0.4145735	0.5071911	0.436345	0.30218625 U12779_at	MAP KINASE-ACTIVATED PROTEIN KINASE 2
				HG3492-	
62 Ovary	0.4145672	$\mathbf{\mathcal{C}}$	0.434477	0.30170184 HT3686_at	Uncoupling Protein Ucp
63 Ovary	0.4142466	0.505419	0.434213	0.30103585 M32598_at	RPS11 Ribosomal protein S11
64 Ovary	0.4141421		0.433661	0.30053598 R11710_at	Transcobalamin I (vitamin B12 binding protein, R binder family)
65 Ovary	0.4131945	0.5046203	0.432994	0.29996446 L20815 at	S protein mRNA
(
66 Ovary	0.412573			0.2994829 Z74616_s	at COL1A2 Collagen, type I, alpha-2
67 Ovary	0.4112487	0.5035855	0.431944	0.29893354 Z74615_at	COL1A1 Collagen, type I, alpha 1
					UBE2H Ubiquitin-conjugating enzyme E2H (homologous to yeast
68 Ovary	0.4099566		0.431724	0.29830384 Z29331_at	(UBC8)
69 Ovary	0.4095814		0.431376	0.2978331 L01406 at	GHRHR Growth hormone-releasing hormone receptor
70 Ovary	0.4092659	0.5006956	0.430838	0.2971351 L35269_at	ZINC FINGER PROTEIN 35
71 Ovary	0.4084033	0.4988408	0.430237	0.29651558 U62437_at	Neuronal nicotinic acetylcholine receptor beta-2 subunit
					Facioscapulohumeral muscular dystrophy (FSHD) gene region, D4Z4
72 Ovary	0.4080739	0.4987781	0.429871	0.29609123 D38024_at	tandem repeat unit
				M55998_s_	a.
73 Ovary	0.4074743	0.4984912	0.429478	0.29559 t	Alpha-1 collagen type I gene, 3' end
74 Ovarv	0.4068982	0.4981076	0.428569	0.20540841141238 6	at GDS Glycoprotein V (Alatalat)
75 Ovary	0.4063406	0,4976544			Immunoalobulin lambda gene locus DNA, clone:92H4
				11	
76 Ovary	0.4057267	0.4976192	0.427583	0.29416174 S73840_at	mRNA Partial, 827 ntj
77 Ovary	0.4049314	0.497051	0.427454	0.293832 D31765 at	KIAA0061 gene, partial cds
78 Ovary	0.4046499	0.4965777	0.426667	0.29341102 M77836_at	
79 Ovary	0.403001	0.4959625	0.426381	HG3432- 0.29310068 HT3621 at	Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 4, K-Sam Iv
				AA434329	AA434329_a clone 770268 5' similar to contains element TAR1 repetitive element;
80 Ovary	0.401601	0.4956725	0.425764	0.29234478 t	mRNA sequence. (from Genbank)
81 Ovarv	0.4010463	0.4948143	0.425352	X96924_rna 0.2919402 1_at	Gene encoding mitochondrial citrate transport protein
, , , , ,		1	1		

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				X56411 rna	
82 Ovary	0.4007482	0.4940607	0.424348	0.29151362 1_at	ADH4 gene for class II alcohol dehydrogenase (pi subunit), exon 1
83 Ovary	0.4002867	0.4934896	0.424144	0.29114884 Z15005 at	CENPE Centromere protein E (312kD)
84 Ovary	0.3983925	0.492963	0.42353	0.29070893 M55420_at	IgE chain, last 2 exons
85 Ovary	0.3983288	0.4928631	0.423063	HG4058- 0.2903554 HT4328 at	Oncodene Aml1-Evi-1. Fusion Activated
	, ,		000		_
86 Ovary	0.39/3214	0.4915406	0.422256	0.2899093 51_at	795160 3', mRNA sequence. (from Genbank)
87 Ovarv	0.3964302	0.4915406	0.422067	RC_AA6091 0.2896022 3.1 at	EST: af11f03.s1 Soares testis NHT Homo sapiens cDNA clone
					Cancellous bone osteoblast mRNA for serin protease with IGF-binding
88 Ovary	0.3957653	0.3957653 0.4909155	0.421357	0.28913614 D87258 at	motif
89 Ovary	0.3951776	1 1	0.420984	0.2884789 X74764_at	Receptor protein tyrosine kinase
90 Ovary	0.3948695	0.4893472	0.420621	0.28808346 L06419 at	PLOD Lysyl hydroxylase
91 Ovary	0.3931691	0.48894	0.420116	0.28766322 L13197_at	PAPPA Pregnancy-associated plasma protein A
92 Ovary	0.3931588	f	0.419797	0.28737557 M55268 at	CSNK2A2 Casein kinase 2, alpha prime polypeptide
93 Ovary	0.392731	0.4872286	0.419466	0.2868552 U18018_at	ETV4 Ets variant gene 4 (E1A enhancer-binding protein, E1AF)
					(clone cD24-1) Huntington's disease candidate region mRNA
94 Ovary	0.3922851	0.486495	0.419272	0.2863664 L37199_at	fragment
70	0.2047770		0.4400	000000000000000000000000000000000000000	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DQ(2) ALPHA
33 Oval y	0.391779	- 1	0.418956	0.28598052 M17236 at	CHAIN PRECURSOR
96 Ovary	0.3917357	0.4859612	0.41828	0.28550702 L32164_at	Zinc finger protein mRNA, 3' end
97 Ovarv	0.3904399	0.4858529	0.417434	0.2850661 \$79219_\$ 8	at PCCA Pronionyl-coA carboxylase alpha chain
		l l		∄.	
98 Ovary	0.3877922	0.4853906	0.417191	0.28476134 HT4542 at	Hepatocyte Growth Factor Receptor
99 Ovary	0.3874707		0.416784	0.28440332 M94547 at	HUMMLC2At; Homo sapiens; ; 593 base-pairs
100 Ovary	0.3863349	0.4849725	0.41667	0.2840003 M68840_at	MAOA Monoamine oxidase A
101 Ovary	0 385558	0.4838240	0.418284	HG2480-	Emily Deleted December 1
(ma)	2000000		+0.201 F.0	M19309 c a	
102 Ovary	0.3843816	0.4836282	0.415891	0.283424 t	TNNT1 Troponin T1, skeletal, slow
103 Ovary	0.3839634	0.4833496	0.415752	0.28316036 L10377 s a	at (clone CTG-B37) mRNA sequence
104 Ovary	0.3837733	0.4828865	0.414906	0.2826997 U20428 at	SNC19 mRNA sequence
40E Ougan	0.2020442	7007007	0 444664		Transfer Transfer Contract Contract
100 Ovary	0.3830413		0.4 1400 1		Basic Itanscription Factor 2, 34 Kda Suburiit
106 Ovary	0.38256/1	0.38256/1 0.4823815	0.414504	0.28198874 D86425 at	Osteoblast mRNA for osteonidogen
108 Ovary	0.3806244	0.4021013	0.414039	0.28116593 D79995 at	I day nelper protein i
loc cvaly	12000010	00±010±0	2001 1.0	0.20110000 D10000 at	פווסף פיו טרעיוון

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. And the state of t

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	-				RC AA4304	
135 Ovary	0.3635305	0.4710352	0.404057	0.27211183 96_r	36_r_at	Ferritin, light polypeptide
136 0,000,	0.3690706	C370071 0	0 400500	1	AA401047_a	1) consistence of DMA for accordance and and and and and and and and and and
130 Oval y	0.3030700	- 1	0.403330	0.2777000		TOUR SAPIETS HINNA FOR HEALINDSHIP, COMPRETE CAS
137 Ovary	0.3014486	0.4699248	0.403429	0.2715823 M99063_at		KERATIN, TYPE II CYTOSKELETAL 2 OKAL
138 Ovary	0.3609935	0.4695281	0,402471	RC_AA2 0.27122495 33 s at	RC_AA2365 33 s at	Ecotropic viral integration site 1
		+			133	EST: zn70n06 s1 Stratagene Hel a cell s3 937216 Homo saniens
139 Ovary	0.3604792	0.4691197	0.402362	0.2708809 87 at	}	cDNA clone 563578 3', mRNA sequence. (from Genbank)
140 Ovary	0.3602834	0.4690814	0.402032	0.27066174 U78095 at	J78095_at	Placental bikunin mRNA
				7	Z80345_rna	
141 Ovary	0.3602108	0.4688845	0.401946	0.270291	1_s_at	SCAD gene, exon 1 and joining features
24.0	2000		9		373_xpt	ORF2: function unknown from Human Tigger1 transposable element,
142 Ovaly	0.3001318	_	0.401430	0.2/01456 2_at		complete consensus sequence.intype=DINA /annot=CDS
143 Ovary	0.3597421	0.4686669	0.400986	0.2697907 M64930_at		Protein phosphatase 2A beta subunit mRNA
144 Ovary	0.3590123	0.4685938	0.400711	0.26961127 M64497	at	APOLIPOPROTEIN AI REGULATORY PROTEIN-1
	•				M62628_s_a	
145 Ovary	0.3589212	0.4685489	0,400617	0.269178241		Alpha-1 lg germline C-region membrane-coding region, 3' end
146 Ovary	0.3589044	0.4681783	0.400056	0.26880133	.47125 s at	0.26880133 L47125 s at EEF1A1 Translation elongation factor 1-alpha-1
147 Ovary	0.3586063	0.4681377	0.399781	0.2685907 U07223	J07223 at	Beta2-chimaerin mRNA
148 Ovary	0.3584908	0.4678547	0.399623	0.26831234 M27826	M27826 at	Endogenous retroviral protease mRNA
149 Ovary	0.3577883	0.4677807	0.399517	0.268112 L77563	77563 at	DGS-F partial mRNA
150 Ovary	0.3572949	0.4673126	0.39897	0.26777637 D49490 at	749490 at	Protein disulfide isomerase-related protein (PDIR)
		1			RC_AA4046	EST: zt43h04.s1 Soares ovary turnor NbHOT Homo sapiens cDNA
151 Ovary	0.3572133	0.4671712	0.398723	0.26740307 09_s_at)9_s_at	clone 725143 3', mRNA sequence. (from Genbank)
152 Ovary	0.3571547		0.398685	0.26711863 D50495	D50495_at	Transcription elongation factor S-II, hS-II-T1
153 Ovary	0.3568475	0.4657049	0.398354	0.26689386 U05291	J05291_at	FMOD Fibromodulin
154 Ovary	0.3558626	0.465421	0.397805	0.26657844 M86546	M86546_at	PBX1 PBX1a and PBX1b
						Hepatic nuclear factor 1-alpha (TCF-1-alpha) gene, promoter region
155 Ovary	0.3556008	- 1	0.397473	0.2664457 U73499	J73499_at	and partial cds
156 Ovary	0.3554865	- 1	0.397251	0.26618755 X02956	X02956_at	IFINA5 Interferon, alpha 5
157 Ovary	0.3532516	0.4646909	0.396984	0.26594195 U17280	U17280_at	STAR Steroidogenic acute regulatory protein
158 Ovary	0.353161	0.4644649	0.396861	0.26553154	0.26553154 X78262 f at	H.sapiens mRNA for TRE5
					AA167824_a	
159 Ovary	0.3530989	0.4644649	0.396277	0.26535395 t		Cell division cycle 27
160 Ovarv	0.3529449	0.4641308	0.396244	X 0.26501605	X97675_rna 1_at	Plakophilin 2a gene extracted from H.sapiens mRNA for plakophilin 2a and b
161 Ovany	0.3510212	_!_	0 306074	0.0647671 00648	02648 at	TONO Transcobalamin II
101 Ovaly	0.3013212		0.33007 1	0.204101	ш	I UNA TIGHTSOUDAIGHHI II

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162	162 Ovary	0.3519083	0.4639741	0.395921	RC 0.26440114 01	AA6216 at	EST: af47g08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 1034846 3' similar to TR:G240986 G240986 LMW G-PROTEIN. ;; mRNA sequence, (from Genbank)
163	163 Over	0.2511/86	0.4632046	0.305162	0.2641507 032004	ħ	HuSAA10 nene for seriim amvloid A1 gamma exon 3 and intron 3
164	164 Ovary	0.3505362	- 1	0.395036	0.26341001 E92301 at	1	Clone 14 9B mRNA sequence
165	165 Ovarv	0.3499089	J	0.394608	0.26370892 X77307	क	5-HYDROXYTRYPTAMINE 2B RECEPTOR
166	166 Ovary	0.3490718		0.394232	0.2634417 M11433	at	RBP1 Cellular retinol-binding protein
167	167 Ovary	0.3475946	0.4619069	0.394048	0.26312995 M80482	80482_at	PACE4 Paired basic amino acid cleaving system 4
168	168 Ovary	0.3475035	0.4616751	0.393895	0.26288402 Z33642	33642_at	V7 mRNA for leukocyte surface protein
							Cytochrome P450 reductase [human, placenta, mRNA Partial, 2403
169	169 Ovary	0.3467984	0.4615618	0.393185	0.26259285 S90469	at	nt
170	170 Ovary	0.3458812	0.4612084	0.393098	0.26224127 D8	D83699_at	Brain 3'UTR of mRNA for neuronal death protein, partial sequence
					Ü	U20758_rna	
171	171 Ovary	0.3455918	0.4611816	0.39284	0.26195264 1_at	_at	Osteopontin gene
	AND DESCRIPTION OF THE PROPERTY AND PARTY AND				Œ.	RC_AA1557	EST: zo52g12.s1 Stratagene pancreas (#937208) Homo sapiens
172	172 Ovary	0.3453621	0.4607912	0.39259	0.26181865 63	3_at	cDNA clone 590566 3', mRNA sequence. (from Genbank)
173	173 Ovary	0.3453137	0.4607093	0.39249	0.26162684 U51127	51127_at	IRF5 Interferon regulatory factor 5
			i		<u>A</u>	RC_AA1583	EST: zo66c01.s1 Stratagene pancreas (#937208) Homo sapiens
174	174 Ovary	0.3438769		0.392429	0.26140743 86_at	5_at	cDNA clone 591840 3', mRNA sequence. (from Genbank)
175	175 Ovary	0.3438713	0.4605341	0.392272	0.26117808 U13220_at	13220_at	Forkhead protein FREAC-2 mRNA, partial cds
					王	HG3355-	
176	176 Ovary	0.3438034	0.4603596	0.392271	0.26105964 HT3532	T3532_at	Peroxisome Proliferator Activated Receptor (Gb:Z30972)
177	177 Ovary	0.3437833	0.4603063	0.391927	0.26081172 M20137	120137_at	Interleukin 3 (IL-3) mRNA
178	178 Ovary	0.3436563	0.460271	0.391749	0.26052493 U28281	28281_at	SCTR Secretin receptor
		A CALL DE LA CALLE		and the state of t			ORF1; MER37; putative transposase similar to pogo element from
					<u> </u>	U49973 xpt	Human Tigger1 transposable element, complete consensus
179	179 Ovary	0.343484	0.4591674	0.391135	0.26030207	1_at	sequence./ntype=DNA /annot=CDS
180	180 Ovary	0.3430626	0.4591604	0.390845	0.2601607 U51587	151587_at	Golgi complex autoantigen golgin-97 mRNA
181	181 Ovary	0.3429836	0.4589919	0.390492	0.2598922 X99920	.99920_at	S100 calcium-binding protein A13
		Approximate a particular and a particula			工	HG3570-	
182	182 Ovary	0.3426471	0.4583454	0.39033	0.2595495 HT3773_at	IT3773_at	Protein Phosphatase Inhibitor Homolog
							EST: zr29d01.s1 Stratagene NT2 neuronal precursor 937230 Homo
					<u>x</u>	RC_AA2522	sapiens cDNA clone 664801 3' similar to TR:G1060907 G1060907
183	183 Ovary	0.3422476		0.390084	0.25928584 89	9 at	QPRTASE ;, mRNA sequence. (from Genbank)
184	184 Ovary	0.3417338	0.4583368	0.389755	0.25912726 X59770	(59770_at	INTERLEUKIN-1 RECEPTOR, TYPE II PRECURSOR
							EST: H. sapiens partial cDNA sequence, mRNA sequence. (from
185	185 Ovary	0.3416281	0.4583199	0.389721	0.25896212 F15197	15197_at	(Genbank)
186	186 Ovary	0.3414222	0.458183	0.389451	HG3934 0 25852475 HT4204	HG3934- HT4204 at	G1 Phase-Specific Gene
3	Ovary	0.01			101120000000000000000000000000000000000		

The state of the s

					<u>cx</u>	RC AA0554	EST; zl74e11.s1 Stratagene colon (#93/204) Homo sapiens cDNA clone 510380 3' similar to contains Alu repetitive element;, mRNA
187	Ovarv	0.3413274	0.4580171	0,389399	0.25831652 04	fat	sequence. (from Genbank)
5			-				Interleukin-8 receptor type B (IL8RB) mRNA, splice variant IL8RB1,
188	188 Ovary	0.3409599	0.457955	0.388898	0.25806504 U11872	at,	partial cds
189(189 Ovary	0.3406475	0.457388	0.388815	0.25793046 U53442		P38Beta MAP kinase mRNA
190 (190 Ovary	0.340593	0.4573231	0.388576	0.25769994 M13903_at		Involucrin gene, exon 2
191 (191 Ovary	0.3402839	0.3402839 0.4570587	0.388246	0.25754994 X69910		P63 mRNA for transmembrane protein
192(192 Ovary	0.339761	0.4569697	0.388047	0.25725085 L18877	f_at	MELANOMA-ASSOCIATED ANTIGEN 12
193(193 Ovary	0.3396801		0.387903	0.2569487 U89606	J89606_at	Pyridoxal kinase mRNA
			1			000	SERINE/THREONINE-PROTEIN KINASE RECEPTOR R2
194	194 Ovary	0.3395448		0.387711	0.256/5/ /22536	22536 at	PRECURSOR " , ' , ' , ' , ' , ' , ' , ' , ' , ' ,
195 (195 Ovary	0.3384668		0.387684	0.2565639 U08049 at	108049_at	Peripheral myelin protein-22 (PMP22) gene, non-coding exon 1A
196 (196 Ovary	0.3383509	0.4548742	0.387421	0.25635135 D17525	017525_at	CRARF C4/C2 activating component of Ra-reactive factor
		6				1000	UDP-GLUCURONOSYLTRANSFERASE 2B10 PRECURSOR,
197 (197 Ovary	0.3381242		0.386991	0.25615/3 X63359	- 11	MICKUSUMAL
198 (198 Ovary	0.3380196		0.386978	0.25594023 S79267	379267_at	CD4 CD4 antigen (p55)
199	199 Ovary	0.3379935	0.4547222	0.386926	0.25571144 U90336	J90336_at	PEG3 mRNA, partial cds
200 (200 Ovary	0.3377791	0.4544876	0.386665	0.255556 Z17240	717240_at	HMG2 High-mobility group (nonhistone chromosomal) protein 2
201	201 Ovary	0.3376427	0.453914	0.386597	0.25532442 L11370_	.11370_at	Protocadherin 42 mRNA for abbreviated PC42
202	202 Ovary	0.3376159	0.453831	0.386409	0.2550344 U53786	J53786_at	EVPL Envoplakin
203	203 Ovary	0.337601	0.4536987	0.385996	0.25485766 U85658	J85658_at	Transcription factor ERF-1 mRNA
204	204 Ovary	0.3375918	0.4536511	0,385611	0.25462577 U28055	J28055_at	MST1 Macrophage stimulating 1 (hepatocyte growth factor-like)
205	205 Ovary	0.3374082	0.4536158	0.385451	0.25447085 U18914	J18914_at	19,8 kDa protein mRNA
						HG742-	
206	206 Ovary	0.3372495	0.4533797	0.385156	0.25425944 HT742	4T742_at	Latent Membrane Protein Lmp1
207	207 Ovary	0.3370855	0.4532545	0.384975	0.2540849 L36644	_36644_at	Receptor protein-tyrosine kinase (HEK7) mRNA, 3' end
						X78416_s_a	
208	208 Ovary	0.3370002	0.4531988	0.384794	0.25390726		CSN1 Casein, alpha S1
						4C000061_c	AC000061_c WUGSC:H_133K23.1c gene extracted from Human BAC clone
209	209 Ovary	0.3360256	0.4529272	0.384738	0.25370634 ds2_at	ds2_at	133K23 from 7q31.2
	NAME OF THE OWNER, WHICH SHAPE OF THE OWNER, WHICH SHAPE OF THE OWNER, WHITE OWNER,		!			RC_AA4958	EST: zw05c08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
210	210 Ovary	0.3356686		0.384636	0.25341874 11	11_at	768398 3', mRNA sequence. (from Genbank)
211	211 Ovary	0.3355818	0.4526873	0.384422	0.2531499 X97198	X97198_at	Receptor protein tyrosine phosphatase hPTP-J precursor, mKNA
						1158675 cds	OR17-40 gene extracted from Human offactory feception gene cusses on chromosome 17, OR17-228 and OR17-40, and OR17-24 and
212	212 Ovary	0.33531	0.4526272	0.384402	0.25298935 Z_at	2_at	
212	243 Overv	0 3359304	0.4523008	0.384103	0.2528791	HG1148- 0 2528791 HT1148 at	Linopolysaccharide-Binding Protein
21.2	Oval y	0.002000	•	_			

and the party plant, pl

0.3334721 0.4520645 0.3333991 0.4519715

> 215 Ovary 216 Ovary

0.3348942 | 0.4522636 |

214|Ovary

0.3331086 0.4513786

217 Ovary 218 Ovary 219 Ovary

0.3324413 0.4504939 0.3323246 0.4504926 0.3317945 0.4502795 0.3312594 0.4501259

220 Ovary 221 Ovary

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. TFAP4 Transcription factor AP-4 (activating enhancer-binding protein ATP6D ATPase, H+ transporting, lysosomal (vacuolar proton pump) Heterogeneous nuclear ribonucleoprotein D (hnRNP D), partial cds, WNT5A Wingless-type MMTV integration site 5A, human homolog EST: zr82h02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: 17c5 Human retina cDNA randomly primed sublibrary Homo Calcium-activated potassium channel mRNA, partial cds Skeletal muscle LIM-protein SLIM2 mRNA, partial cds COL4A5 Collagen, type IV, alpha 5 (Alport syndrome) T(3;5)(q25.1;p34) fusion gene NPM-MLF1 mRNA sapiens cDNA, mRNA sequence. (from Genbank) Putative zinc transporter ZnT-3 (ZnT-3) mRNA 682227 3', mRNA sequence. (from Genbank) NAGA N-acetylgalactosaminidase, alpha-BDNF Brain-derived neurotrophic factor HEPATOCYTE NUCLEAR FACTOR 4 Breast epithelial antigen BA46 mRNA MAGE-4a antigen (MAGE4a) gene 0.24989246 J05582_s_at MUC1 Mucin 1, transmembrane Kallistatin, Protease Inhibitor 4 PLGL Plasminogen-like protein XDH Xanthine dehydrogenase C7 Complement component 7 RPS3 Ribosomal protein S3 Zinc Finger Protein Znf155 XG mRNA (clone PEP11) Zinc Finger Protein 20 KIAA0149 gene Reticulocalbin clone cDx4 42kD 0.2508969 S73885_s_at[4]) RC_AA2566 U10687_s_a X87871_s_a 0.24812 HT4938 at 0.2504044 M93143 at 0.24880347 U02632 at 0.24842624 U39487 at 0.24777484 L20861_at 0.24744873 J04164 at 0.2503395 U04520_at 0.24938098 U02019 at 0.24912776 U76010 at 0.24830648 D42073 at 0.25257525 W25945 at 0.25137806 M62783_at 0.25016794 U58516 at 0.24907762 Z48511 at ₩, 0.25193855 HT4513 at 0.25163853 M61176 at 0.2523241 HT3647_at 0,25216863 U60116 at 0.25126776 D63483 at 0.25060543 L49054 at 0.25102973 J03507 at 0.24797988 J05682 HG4243-HG3454 0.24863297 68 at 0.24931112 t 0.24965535|t0.378191 0.378473 0.378508 0.38078 0.378525 0.380986 0.379314 0.379079 0.379028 0.3813 0.381188 0.380602 0.380353 0.379805 0.382089 0.381233 0.381519 0.381372 0.383329 0.3823 0.381631 0.382929 0.382833 0.383862 0.383773 0.382237 0.383731

0.3285583 0.4488469

228 Ovary

0.3285824 0.4492782

227 Ovary

0.3300763 0.4500448

0.3291991 0.4498737 0.3290296 0.4497706

225|Ovary

226 Ovary

0.3302882 0.450061 0.3302741 0.4500556

222 Ovary 223 Ovary 224 Ovary 0.3284228 0.4485688

229|Ovary

FIG. 10J

0.3263054 0.4461799 0.3255011 0.4460755

240 Ovary

239|Ovary

0.3263997 | 0.4461886

238|Ovary

0.446451

0.326834

237 Ovary

0.327109 0.4468249

234 Ovary 235 Ovary 236 Ovary

0.3282152 0.4485688 0.3277755 0.4478116

230|Ovary

231 Ovary

0.3276983 0.4470856 0.3275667 0.4470595

232 Ovary

233 Ovary

0.327092 0.4467199 0.3268701 0.4465624

241 Ovary 243 Ovary 244 Ovary 244 Ovary 245 Ovary 246 Ovary 249 Ovary 250 Ovary 255 Ovary 255 Ovary 255 Ovary 255 Ovary 256 Ovary 256 Ovary 256 Ovary 257 Ovary 258 Ovary 258 Ovary 259 Ovary 259 Ovary 259 Ovary 259 Ovary 259 Ovary 260 Ovary 261 Ovary 263 Ovary 263 Ovary 263 Ovary 264 Ovary 265 Ovary 266 Ovary 266 Ovary 267 Ovary 268 Ovary 269 Ovary 269 Ovary 269 Ovary 269 Ovary 269 Ovary 269 Ovary 269 Ovary 269 Ovary 269 Ovary 269 Ovary

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						to the transfer of the state of
266 Ovarv	0.315358	0.4408466	0.372938	X81836_s 0.24244083 t	σ.	Dents Disease candidate gene
					-	for colored actions (A Citiza)
267 Ovary	0.3152581		0.372877	0.24219371 2 at	+	Frataxin (FKDA) gene, promoter region and
268 Ovary	0.3143329	0.4405132	0.37271	0.2420173 M32053	ק	THE KINA GOID
					I 0 1	Human DNA from chromosome 19-specific cosmid F25965, genomic sequence::Human DNA from chromosome 19-specific cosmid
269 Ovary	0.3141116	0,4393335	0.37271	AC002; 0.24192733 ds4 at	398 c F	AC002398_c F25965, genomic sequence::rluman DNA Horn canonics 13- ds4_at specific cosmid F25965, genomic sequence
7	A LA LA CONTRACTOR DE L	1		D49487_s_a	_	
270 Ovary	0.313858	0.313858 0.4392479	0.372627	0.24169725 t		LEP Leptin (murine obesity homolog)
271 Ovary	0.3138369	0.4392319	0.372348	0.24149735 X59434	at	TST Thiosulfate sulfurtransferase (rhodanese)
				AD000	L 684 c fr	AD000684 c from Homo sapiens DNA from chromosome 19-cosmid R30879
272 Ovary	0.3138215	0.4391035	0.37204	0.24139927 ds1_at	ì	containing USF2, genomic sequence
		1			ш	EST: HUMGS0007866, Human Gene Signature, 3'-directed cDNA
273 Ovary	0.3136735	0.4388695	0.371979	0.24130292 C00476	at_	sequence, mRNA sequence. (from Genbank)
				RC_AA4602		EST: zx67d07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
274 Ovary	0.3136552	0.4386366	0.37193	0.24106702 57_at		clone 796525 3', mRNA sequence. (from Genbank)
275 Ovary	0.3134788	0.438628	0.371822	0.24082136 X52005	,क	MYL4 Myosin, light polypeptide 4, alkalı, atrıal, embryonic
						EST: yv29a08.r1 Homo sapiens cDNA clone 244118 5. (11011)
276 Ovary	0.3134194		0.371751	0.24064212 N75646_at		Genbank)
277 Ovary	0.3133209	0.4382579	0.371643	0.2405207 L13436_at	ज	Guanylate cyclase mRNA, complete mature peptide
278 Ovary	0.3131231	0.4378072	0.37128	0.24030808 D50911	at	KIAA0121 gene
279 Ovary	0.313045	0.4376422	0.371261	0.24015269 X89267	at	UROD Uroporphyrinogen decarboxylase
				HG2148-		
280 Ovary	0.3129973	0.4373537	0.371089	0.2398905 HT2218	4	at Mucin 3, Intestinal (Gb:M55406)
281 Ovary	0.3125866	1	0.3709	0.23970832 L02950	ät	CRYM Crystallin Mu
282 Ovary	0.3122273	ļ	0.370796	0.2394938 J03756_at		SOMATOTROPIN PRECURSOR
283 Ovary	0.3121966		0.370324	0.23923942 L34355_at		(clone p4) 50 kD dystrophin-associated glycoprotein mKNA
284 Ovary	0.3116051	0.4372887	0.370259	0.23916294 U00930	ä	Clone CE29 8.1 (CAC)n/(GTG)n repeat-containing mKINA
				HG759-	6	
285 Ovary	0.3109543		0.370071	0.23897909 H1755	s at	0.23897909 H1759 s at Adrenergic Receptor, Beta 1
286 Ovary	0.3109146	0.4370823	0.370071	0,23880526 D90276_at		CGM/ Carcinoembryonic antigen gene family member /
287 Ovary	0.3108355	0.3108355 0.4364497		0.23868537 L17330_at		Pre-T/NK cell associated protein (brisk) illikink
288 Ovary	0.310479	0.3104795 0.4364195	1	0.23850334 X80878	, m	K Kappa b mikiya
289 Ovary	0.3104476	0.3104476 0.4362122	0.369455	0.23842/09 X66436	aí	Ossible GIP-binding Fro Lein Horri

200						Clone K5685 5' similar to EST/VIO3403 P4) mpNA common control
7 700	zau Ovary	0.3100228	0.4361731	0.369239	0.23822524	Genbank)
291 (Ovary	0.3098479	0.4360671	0.369015	HG831- 0.23805574 HT831 at	Potassium Channel (Gh-1 02752)
292	292 Ovary	0.3097896	0 4359309	0 368708		
	Property and the second		1	5		at RPS11 Ribosomal protein S11
2	į				HG2987- HT3136 s a	
293 Cvary	wary	0.3093366	- 1	0	0.23770911	Vasoactive Intestinal Pentide
294 Ovary	wary	0.3089089	- 1		0.23762587 M60092 at	AMP DFAMINASE 1
295 Ovary	wary	0.308522	- 3	0.368597	0.2375019 M55153 at	PROTEIN-GILTAMINE CAMMA CHITANAM TEMBER: 22
296 Ovary	vary	0.3079246	0.4354538	0.368593	0.23741032 U25771 at	ARF4L ADP-ribosylation factor of the
297 Ovary	vary	0.3070011	0.4354359	0.368269	RC_AA4213 0.23732395.28 at	o sapiens cDNA
298 Ovary	vary	0.3065926	!	0.368121	RC_AA4577 0.2371692 18 at	EST: zx87d04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
2000		0000			M74587 ma	GOLD ST. 3, IIIKNA Sequence. (from Genbank)
230 Overy	wary	0.3059326		0.367913	0.23688458 1 s at	Insulin-like growth factor hinding profesio (h13ERB4)
oud Ovary	vary	0.3056498	0.4349167	0.367899	0.23680103 J03133 at	
301 Ovary	vary	0.3053604	0.4349098	0.367662	0.23667708 S81419 at	inje promoter, afternatively spliced}
302		100100			HG2320-	
206	vary	0.3053014	0.4348318	0.367598	0.2365616 HT2416 at	Integrin, Beta 3 Subunit
303 Ovary	Varv	0.3051694	0 49 46000	0000000		
304 Ovary	Varv	0.3051249	,	0.36/539	0.23636462 HT4504 at	ahydrofolate Reductase
305 Ovarv	varv	0.3050338		0.367262	0.2360//34 X05615 at	Thyroglobulin
306 Ovary	Vary	0.3047760		0.307203	0.23583615 L13720 at	las) mRNA
307 Ovary	Vary	0.3046756		0.367070	0.23563027 U79302 at	Clone 23855 mRNA, partial cds
308 Ovary	Vary	0.3040058	0.434 (423	0.36/0/2	0.23553297 L25119 at	OPRM1 Opiold receptor, mu 1
309 Ovary	Vary	0.3040667	0.4340047	0.300745	0.23539943 M59829 at	MHC class III HSP70-HOM gene (HLA)
		1000100:0	0.4338383	0.3000/6	0.23525032 Y14140 at	G protein gene encoding beta 3 subunit exon 1 and promoter
310 Ovary	/ary	0.3038235	0.4337996	0.366388	AA280228_a	EST: zt04c11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712148 5' mRNA semilance (from Conhant)
						delinaire codesinaire)
						FGFR2 Fibroblast growth factor receptor 2 (bacteria-expressed
311 Ovary	/ary	0.3037371	0.4337436	0.366339	0.23491555 M87770 at	Kinase, Keratinocyte growth factor receptor, craniofacial dysostosis 1, Critizon syndroma. Deliffor sundrame, Later 1997.
312 Ovary	/ary	0.3035098	0.4336832	0.366152		LAMC1 Laminin, gamma 1 (formerly 1 AMR2)
313 Ovary	/ary	0.3032565	0.4336724	0.366085		MYL4 Myosin, light polypeptide 4, alkali, atrial, embryonic

FIG. 10M

And the state of t

314	314 Ovary	0.3031955	0.4333319	0.366029	0.234441791108488 at	at INDD4 Inveitor relumbrembate 4 phoenhatens
315	315 Ovary	0.3031398		0	0.23430899 M93036 at	MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA733-2 PRECLIRSOR
316	316 Ovary	0.3029516	0.4329197	0.365475		Rhodanese
317	317 Ovary	0.3027791	0.4329096	0.365359	X14085_s_a 0.2340593 t	
318	318 Ovary	0.302771	0.4327172	0.36522	0.2338703 1 at	1
319	319 Ovary	0.302668	0.4326317	0.364835		MDS1B (MDS1) mRNA
320	320 Ovarv	0.3023225	0 432/4317	0.36/1823	RC_AA0589	
321	321 Ovary	0.3008312	0.4322963		0.23348193 X72790 at	Endocember 212485 3, mKNA sequence, (from Genbank)
322	322 Ovary	0.3006096	0.4321942	0.364214	0.23329866 X51954 at	IICP dene for uncompling protein even 5
323	323 Ovary	0.3005936	0.4321432	0.363897		PTH2 parathyroid hormone receptor mRNA
324	324 Ovary	0.2996019	0.4319474	0.363784	0.23300894 S69189 at	Peroxisoma 200/ 1000 March 2001
325	325 Ovary	0.2993978	0.4319191	0.363499	0.23281892 U88063 at	Adolti (molise) related profess
326	326 Ovary		0.4317655	0.363417	0.23270716 X01630 at	ASS Argininosuccinate synthetase
327	327 Ovary		0.4316864	0.363316	0.2326083 U67934 at	44.9 kDa protein C18B11 homolog gene partial cds
328	328 Ovary	0.2982498	0.4316292	0.363211	0.23249696 Y11897 at	Brx gene 3'UTR
329	329 Ovary	0.2980638	0.4312482	0.363091	0.23240772 L40157 at	P162 mRNA
330	330 Ovary	0.2977973	0.4312281	0.362982	0.23223758 L33404 at	Stratum corneum chymotryptic enzyme mRNA
23.	331 Ovary	0.2977416	0.4311388	0.362896	0.23200443 D16350_at	SA mRNA for SA gene product
332	332 Ovary	0.2976578	0.4310868	0.362844	0.23183209 X06268 at	COL2A1 Collagen, type II, alpha 1 (primary osteoarthritis, spondyloeniphyseal dysplasia concentral)
333	333 Ovary	0.2973583	0.4308829	0.362724	0.23157568 10 r at	civity, 14F1, Livity, 14F2, DOB, DQB2 and KiNG8, 9, 13 and 14 genes
334	334 Ovary	0.2973435 0.4301039	0.4301039	0.362447	0.23145604 M59979 at	PTGS1 Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H
335	335 Ovary	+	0.4298395	0.362432		Integrin alpha 6
336	336 Ovary	1	0.4291033	0.362424		Unknown profein mRNA partial cds
337	337 Ovary		0.4290307	0.362398		CCAAT BOX-BINDING TRANSCRIPTION FACTOR 1
338	338 Ovary	0.2962611	0.4290212	0.362163		POLA DNA polymerase alpha subunit
339	339 Ovary	0.2959635	0.4289011	0.361954	0.23082802 237987 s a	at FFF1A1 Translation alongation factor 4 Julys 4
340	340 Ovary	0.2958476	0.42873	0.361728	B	Cystatin SN
341	341 Ovary	0.2957599	0.4286155	0.361652	AA092261_a 0.2305297 t	+

The grant grant grant grant data grant gra

3.40 Over		0.2056087	0.4283784	0.364548	U88	88902_cds 1	U88902_cds Integrase gene extracted from Human endogenous retrovirus H clone of f at at all all all all all all all all a
Z OVE	ary	0.2930907	- 1	0.301310	0.23040030	T	910.04 minglings and parameters of the parameter
343 Ovary	Ju	0.2955886	0.4281563	0.361164	0.2304 1008 A30078 at	1	o lou alpha protein
		0.0054047	0.4070570	0.964499	A. 0.22010546	AA393104_S	Maramanlohin 2
344 Ovary	2 2	0.2954217	- 1	0.360758		ta	IFNA8 Interferon alnha 8
5	aı y	0.4143		0.000.0	7. 1.2000002.0	5.	Insulin-like growth factor binding protein-2 Ihuman, placenta,
346 Ovary	эгу	0.2946013	0.4276598	0.360738	0.22971661 S37730_s	ä	at Genomic, 1342 nt, segment 4 of 4]
347 Ovary	ary	0.293713	0.4275924	0.360667	0.22961067 303915	s at	at CHGA Chromogranin A
348 Ovary	arv	0.2936141	1 .	0.360601	0 22947325 W67675	i te	EST: zd37c12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342838 5', mRNA sequence, (from Genbank)
2	Ś	200	1				EST; yv46a09,r1 Homo sapiens cDNA clone 245752 5'. (from
349 Ovary	ary	0.2933178	0.4273311	0.360455	0.22929354 N73185_at		Genbank)
350 Ovary	ary	0.2933112	0.4273259	0.360337	0.22920062 U59228_at	159228_at	EDA Ectodermal dysplasia protein
351 Ovary	ary	0.2921804	0.2921804 0.4272642	0.360107	0.22906823 Z73677	73677_at	Gene encoding plakophilin 1b
352 Ovary	ary	0.2918409	0.4271641	0.360081	0.22898206 U32659	J32659_at	CTLA8 Cytotoxic T lymphocyte-associated serine esterase 8
353 Ovary	ary	0.2914525	0.4271562	0.359842	0.22881638 X99140_at	(99140_at	Hair keratin, hHb5
354 Ovary	ary	0.2914246	0.4269381	0.359765	0.2286694 L	25286_s_at	0.2286694 L25286_s_at COL15A1 Collagen, type XV, alpha 1
-			1		4	AA4539	
355 Ovary	ary	0.291405	- 1	0.359653	0.2285167788	ਰ	795244 3', mRNA sequence. (from Genbank)
356 Ovary	ary	0.2913615	0.4268948	0.359592	0.2283418 U70981	J70981_at	IL13 receptor
357 Ov	Ovary	0.291014	0.4268904	0.359579	0.22822042	\A479835_s at	AA479835_s clone 740786 5' similar to TR:G1001232 G1001232 HYPOTHETICAL at 21.5 KD PROTEIN.;, mRNA sequence. (from Genbank)
			1			AA410617_s	
358 Ovary	ary	0.2908981	0.4265733	0.359224	0.22809975	at	clone 723799 5', mRNA sequence. (from Genbank)
		10.00000	0.4265744	0.25006	HG3517	HG3517- HT3711 at	Alpha-1 Antitrunein 5' Find
oos Ovary	al y	0.2301044	- 1	0.0000	1.26210122.0	11	
360 Ovary	ary	0.2907384	0.4265699	0.358976	0.22776932	1_s_at	Ly-6-related protein (9804) gene
361 Ovary	ary	0.2906261	0.4264962	0.358718	0.22767004 D49394)49394_at	HTR3 5-hydroxylryptamine (serotonin) receptor 3
362 Ovary	Zić.	0.2897787	0.4263888	0.358709	0.22759067 H42262	H42262 at	EST: yo63a04.r1 Homo sapiens cDNA clone 182574 5. (from Genbank)
363 Ovary	ary	0.289736	1	0.358487	0.2274408	X63187_at	
364 Ovary	, Ale	0.2895342	0.2895342 0.4261453	0.358302	0.22731112	RC_AA4865 79_at	EST: ab16f05.s1 Stratagene lung (#937210) Homo sapiens cUNA clone 840993 3', mRNA sequence. (from Genbank)
· > [00	Z Z	>>>>>>					

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365 0 van	9080800	0.2880828 0.4250440		100 C	3
oco Cvary	0.4003040	0.4233140	0.328075	0.22714211 D14520 at	it GC-Box binding protein BTEB2
366 Ovary	0.2888683	0.4256082	0.358058	X54667_s_a 0.22701569 t	GST4 Cystatin S
367 Ovary	0.2886474	0.4253817	0.358006	0.22686821 X67325	
368 Ovary	0.2886202	0.2886202 0.4253469	0.357974	0.22672059 U26424 at	T
369 Ovary	0.2883739		0.357898	0.22655448 X52022	
370 Ovary	0.2883459		0.357682	0.22650886 M28983	Τ
371 Ovary	0.2882215	0.4251061	0.357628	0.22635423 D25248 at	
372 Ovarv	0.2880524	0 4248702	0 357552	0.0000000000000000000000000000000000000	
	10000000				at lactor/vascular permeability factor receptor)
373 Ovary	0.2877684	- 1	0.357377	0.22598389 U09609 at	NFKB2 Nuclear factor of kappa light polypeptide gene enhancer in B- it cells 2 (p49/p100)
374 Ovary	0.2876712	0.4240072	0.357257	0.22579683 M91083 at	
375 Ovary	0.2873843	0.4239157	0.357165	RC_AA4125 0.22561815 05_at	
376 Ovary	0.287114	0.4238419	0.356904	0.22547539 Y08134 g	0.22547539 Y08134 at-2 H caniene mBNA for ASM like phombodiodome ob
377 Ovary	0.287114	L	0.356564	0.2253858 Y08134 at	t ASM-like phosphodiesterase 3h
378 Ovary	0.2866591	0.423739	0.356299	0 22525188 s at	-
379 Ovary	0.2865467	0.4235776	0.356221	3	KIAA0072 dene nartial cds
(i		M57506 rna	a
380 Ovary	0.2864013	0.4235012	0.356174	0.22501242 1_at	
381 Ovary	0.2860443	0.2860443 0.4233095	0.356154	RC_AA4266 0.22491688 40 at	,
382 Ovary	0.2860022	0.2860022 0.4233008	0.355837	0.22474885 X68994 at	\top
383 0 0 2 2 2	0.0003475		1000	 	
384 Ovany	0.7857202	0.2033173 0.4231295	0.355/0/		
385 Ovary	0.2032303	0.2032303 0.4227376	0.355449	0.22454898 M60828 a	
		0.722101	0.000500	U.2243032 D26137 at HG3998-	RPS11 Ribosomal protein S11
386 Ovary	0.2846023	0.4227178	0.35523	0.22414948 HT4268 at	t - L-Glycerol-3-Phosphate: Nad+ Oxidored ictase
387 Ovary	0.2845584 0.4226161	0.4226161	0.355099	0.22407779 X13930 f	
388 Ovary	0.2845058	0.4223986	0.354692	0.22399472 00 at	RC_AA4613 EST: zx65a08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 00 at clone 796310 3', mRNA sequence. (from Genbank)
389 Ovary	0.2842396 0.4219515	0.4219515	0.354627	X57351_s	ന
390 Ovary	0.283926	0.4219432	0.354536		
391 Ovary	0.2837994	0.4219196	0.354363	Y09912_rna 0.22355713 1_at	(2)
				With the second	The state of the s

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											A clone							<u> </u>					er), member 2					And the state of t) Illon d	J)-IIKG I	partial cds		
DTD Diastrophic dysplasia (sulfate transporter)	G6PD Glucose-6-phosphate dehydrogenase	Hair keratin, hHb6	Human clone 23564 mRNA sequence	Clone 2358/ mBNA sequence	Cione 20004 III and 3chacalco	Glial Growth Factor 2		AFFX-BioDn-5_st (endogenous control)		AFFX-BioDn-5 st (miscellaneous control - 11k chips)	EST; zt93e07.s1 Soares testis NHT Homo sapiens cUNA clone 729924 3', mRNA sequence. (from Genbank)		Spermidine synthase gene	Putative OSP like protein mRNA, partial cds		FOLLITROPIN BETA CHAIN PRECURSOR	PK-120	Alternatively spliced variant C7f (C3f) mRNA, partial 3'UTR	LAMB1 Laminin B1 chain	Arylacetamide deacetylase mRNA	CDA Cytidine deaminase	Bradykinin Receptor	St. C15A2 Solute carrier family 15 (H+/peptide transporter), member 2	Protease Receptor-1, Effector Cell		C-erbA-1 mRNA for thyroid hormone receptor alpha	Purinergic receptor P2Y9 mRNA	69/71 KD	SPERM ANTIGEN HEZ PRECURSOR	SNF2L1 SNF2 (sucrose nontermenting, yeast, nomolog)-like	NMDA receptor subtype 2B subunit (GRIN2B) mRNA, partial cds	Spectrin, alpha, erythrocylic 1 (elliptocytosis 2)	HTK Hepatoma transmembrane kinase
at	at	at,	at-2	+6	ä	at	- L C	i st	BioDn-		43996	M64231_ma	1_at	J89916_at	M54914 s.a				M61916_at	L32179_at	L27943_at	HG2668- HT2764_at	U67674_at	HG3231- HT3408 at	X55005 ma	1_at	U66578_at	M87284_at	X67697 at	M88163_at	U28758_s_a t	H52378_at	U07695_at
0.22333421 014528	0.22326332 M24470	0.22313873 X99142	0.223030751190910	0.2220015	0.62223000	0.2227879 HT5146	1	0.22263035 5_st		0.22252668 5_st-2	RC 0.22237244 33		0.22226556 1_at	0.2220912 U89916		0.22199528	0.22189172 D38535	0.22175573 U72517 at	0.22154498 M61916 at	0.22145319 L32179	0.22126916 L27943	HG2668 0.22116962 HT2764	0.2210543 U67674	HG3231-00216 HT3408	2000	0.2208674 1_at	0.2207376 U66578	0.22054425 M87284	0.22046967	0.2202613 M88163	0.22012547	0.21995997 H52378	0.21987474 U07695
0.354064	0.354032	0.353982	0.3538	0.0000	01000000	0.353524		0.35319		0.352988	0.352858		0.352814	0.352545		0.352474	0.352473	0.352153	0.352058	0.351965	0.351854	0.351516	0.351427	0.354294	0.00	0.35129	0.35129	0.351271	0.351197	0.350903	0.350744	0.350728	0.350681
0.4218976	0.4218059	0.4217534	0.4246939	0.4210000	0.4213317	0.4215039		0.4214258		0.4213758	0.4213321		0.4212547	0.4210324		0.4209334	0.4209192	0.4207298	0.4207082	0.4205895	0.4199428	0.4198133	0.4196879	0.4406585	0.410	0.4193187	0.4192111	0.419054	0.4189279	0.4187685	0.4187465	1	0.418268
0.2837583		0.2834689	0.7834870		0.2831879	0.2830176		0.2829984		0.2829984	0.2829951	The state of the s	0.282854	0.2826962		0.2825628	0.2820657	0.282002	0.2812738	0.2811636	0.2809862	0.2801471	0.2799327	0.9709408	0.51.05.100	0.2788408	0.2784462	0.2783903	0.2772172	0.2767097	7099976 0	0.2753914	0.2751567
392 Ovary	393 Ovary		306	ogo Ovaly	396 Ovary	397 Ovarv		398 Ovary		399 Ovary	400 Ovary		401 Ovary	402 Ovary		403 Ovary	404 Ovary	405 Ovary	406 Ovary	407 Ovary	408 Ovary	409 Ovary	410 Ovary	144 0,000,	411 Ovaly	412 Ovary	413 Ovary	414 Ovary	415 Ovary	416 Ovary	A47 Overv	418 Ovary	419 Ovary

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

FIG. 10Q

and play the permitted with the property of the permitted with the per

EDN3 Endothelin 3	Gdf5 gene	CA6 Carbonic anhydrase VI		CREB-RP (creb-rp) mRNA	P55pik	SHBG Sex hormone-binding globulin	EST: za55e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens	cDNA clone 296488 5', mRNA sequence. (from Genbank)		CCKAR Cholecystokinin A receptor	Quiescin (Q6) mRNA, partial cds	ZNF183 gene	Olfactory receptor-like gene	Preferentially expressed antigen of melanoma (PRAME) mRNA	RARG Retinoic acid receptor, gamma 1	GLUL Glutamate-ammonia ligase (glutamine synthase)	PRKCI Protein kinase C, lota	5 EST: zt73b05.s1 Soares testis NI+T Homo sapiens cDNA clone	727953 3', mRNA sequence. (from Genbank)	a Metabotropic glutamate receptor 8 mRNA		Claudin 3	EST: zb92a04.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320238 5', mRNA sequence. (from Genbank)	Cyclophilin C [human, kidney, mRNA, 883 mt]	at-2 Peptidylprolyl isomerase C (cyclophilin C)	Angiotensin II type 2 receptor mRNA		Phenylethanolamine n-methyltransferase gene extracted from Human gene for phenylethanolamine N-methylase (PNMT) (EC 2.1.1.28)	EST: zr22c03.s1 Stratagene NT2 neuronal precursor 937230 Homo	
X52001_at	X80915_ma 1_at	M57892 at	U31903_s_a		D88532_at	M31651_at		W01059_at	U23430_s_a		L42379_at	X98253 at	L35475_at	U65011_at	M38258 at	X72475 at	L33881_at	RC_AA3985	33_at	AC000099_a t	AA292466_a	1	W31287_at	S71018_at	S71018 at-	U20860		X52730_ma 1_at	RC_AA2271	46_at U51586_at
0.21978685 X52001	0.21967626	0.2195222 M57892 at		0.21937796	0.21914612 D88532	0.21911949 M31651		0.21893924 W01059_at			0.21882677	0.21867739 X98253_at	0.21854211 L35475 at	0.21845086 U65011	0.21834032 M38258	0.21828201 X72475	0.21812978 L33881		0.2180722 33_at	0.2178827		0.217822051	0.21763584 W31287	0.2175184 S71018	0.21740979 S71018	0.21732847	0.21723093 M97815	X52 0.21712686 1_at		0.21703608 46_at 0.21695489 U51586_
0.350208	0.350177	0.350161		0.349742	0.349615	0.349531		0.349496		0.349296	0.34927	0.349171	0.349166	0.349072	0.349072	0.349056	0.348809		0.348564	0.348491		0.348257	0.34823	0.348108	0.347962	0.347832	0.347574	0.347446		0.347136
0.4181652	0.4181488	0.4181164		0.4181044	0.4180789	0.4178208	MANAGE AND AND AND AND AND AND AND AND AND AND	0.4177589		0.4176905	0.4176888	0.4176083	0.4174984	0.4172265	0.4168316	0.4167488	0.4162361		0.4160873	0,4160379		0.4158911	0.4155899	0.4154755	0.4153767	0.41521	0.4151868	0.4151128		0.4149669
0.2750188	0.2748964	1			0.2743574	0.2742131	1	0.2741422				0.2733313	0.273136	0.2729535	0.2727675	1	0.272344		0.272289	0.2721697		0.2718494	0.2715959	0.2713278	0.2713278	0.271245	0.2709535	0.2705047		0.2703179
420 Ovary	421 Ovarv	422 Ovary		423 Ovary	424 Ovary	425 Ovary		426 Ovary		427 Ovary	428 Ovary	429 Ovary	430 Ovary	431 Ovary	432 Ovary	433 Ovary	434 Ovary		435 Ovary	436 Ovary	The state of the s	437 Ovary	438 Ovary	439 Ovary	440 Ovarv	441 Ovary	442 Ovary	443 Ovary		444 Ovary 445 Ovary

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446 Ovany		0 2600740 0 4440500	ľ		
		13 0.4 14853	9 0.347037	0.21679743	NSCL-1 mRNA sequence
447 Ovary		39 0.4147767	7 0.346839	AA292809_a	
448 Ovary	y 0.2690276	76 0.4147117	0.	C	
449 Ovary	у 0.2689862	52 0.4145296		L	NGER Narva growth factor recognition
(M74509 s	α
450 Ovary		1	-	0.21638729	Endodemon S retrovirus time C oncomirus occurrente
451 Ovary	y 0.2686271	1 0.4144711	0.346482	0.21618497 U43177 at	
452 Ovary	y 0.2685032	12 0.4144135	0.346429	0.21612753 \$85963 at	Deally cooperate and the second control of t
453 Ovary	y 0.2682308	18 0.4143538	L	0.91508009 033093	T
454 Ovary				0.21583405 X96969 at	
455 Ovary		0.2679211 0.4141609	0348369	27.00114 627.07310	EST: yw81e10.r1 Homo sapiens cDNA clone 258666 5' (from
456 Ovary		0.2678742 0.4140211		0.215703651.25084	Genbank)
457 Ovary		8 0.4139188		0.215586351101102 at	AKTS Aplysia ras-related homolog 9
				OMEGOGGAA	EST: zt52e09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
458 Ovary		5 0.4138277	0.346122	0.21541144 †	AASSECT COME (725992.5' similar to contains element PTR5 repetitive element.,
459 Ovary				0.21521002 D63481 at	KIAAAAA7 gana martial ada
460 Ovary		9 0.4136404	0.345712		CKM Crasting kinger musels
461 Ovary	0.2672732	2 0.4135974	0.345535		VIP Vasoactive intestinal pentide
462 Ovary	0.2672488	8 0413538	0 345372	0.04400444	
463 Ovary		10		0.21490474 U93553 at-	0.21430474 U93553 at-2 Fetoprotein-alpha 1 (AFP) transcription factor
		200001111		0.2 147 4050 U93553 at	Alpha1-fetoprotein transcription factor (hFTF) mRNA
464 Ovary		1 0.4132712	0.345161	0.214700481	AASU4629 a ES11/6060 Colon carcinoma (Caco-2) cell line II Homo sapiens
465 Ovary	0.2667795	5 0.4132262		0.21462113 M57609 at	CI 13 DEOTEIN
466 Ovary	0.2666887	0.4131307	0.344933	0.21443458 D80011 at	KIAA0189 gene
467 Ovary	-		0.344926	0.21433756 D80011 at-	at-2) KIAA0189 cene product
468 Ovary	0.2665639	0.4127077	0.34488	0.21412256 U82310 at	Unknown protein mRNA partial cds
469 Ovary	0.2665055	0.4125737	0.344428	0.21412256 H78886 at	EST: yu11a03.r1 Homo sapiens cDNA clone 233452 5'. (from Genhank)
				HG2175-	-
470 Ovary	0.2663021	0.4124796	0.344228	HT2245_s_a	
471 Ovary	0.2659546	0.2659546 0.4123149	0.344219	0.21367392 U66406 at	EPLG8 Enh-related recentor tyrocine discount of
472 Ovary	0.2659378	0.4122962	0.344192	0.21355115 1 at	
			-		

FIG. 10s

The principal pr

473 Ovary	0.2657849	t 1	0.344092	0.21327704 L77730	1 11	ADORA3 Adenosine receptor A3
474 Ovary	0.265/564	0.4120143	0.343891	0.213158 D38145	3145_at	Prostacyclin synthase
475 Ovary	0.2657276	0.4120076	0.343813	HG908- 0.21310914 HT908	HG908- HT908_at	Mg61 Protein (Gb:L08239)
VaevO 476	0.265711	0.444082	0.949755	HG3884-	HG3884-	I I was a still Death at 1 Law 40
410 Oval y	0.203711	0.411300	0.343733	U.Z13UZ/30 H14	4154 at	Homeotic Protein Hpx-42
477 Ovary	0.2656896	0.41183	0.343676	HG; HT2 0.2129512 at	HG371- HT26388_s_ at	Mucin 1. Epithelial. Alt. Splice 9
			-	X57	X57348 s a	
478 Ovary	0.2655256	0.4118093	0.343528	0.21284524 t	 	SFN Stratifin
479 Ovary	0.2652213	0.4117406	0.343528	0.2127327 X82634_at	.634_at	Partial mRNA for hair keratin acidic 3-II
480 Ovary	0.2651835	0.4117106	0.343505	0.21265955 X96698	3698_at	D1075-like gene
481 Ovary	0.264683	0.4116855	0.343401	0.21251659 Y08564	3564 at	GalNAc-T4 gene
482 Ovary	0.2646747	0.4115379	0.343283	0.21232747 M59911	9911 at	ITGA3 Integrin alpha-3 subunit
483 Ovary	0.2645927	0.2645927 0.4114965	0.343152	0.21222517 U54804	1804_at	Has2 mRNA
484 Ovary	0.2644429	0.2644429 0.4112892	0.34296	0.21219595 Y10209)209_at	CD30L protein
						BMP-5=bone morphogenic protein-5 (promoter) [human, Genomic,
485 Ovary	0.264427	0.4110016	0.342949	0.21210513 S81957_at	957_at	1116 nt]
486	0.0644950	7007077	0.0000	RC_	RC_AA3720	EST: EST83940 Parathyroid gland tumor I Homo sapiens cDNA 3'
400 Ovaly	0.2044236	0.4107987	0.342839	0.21205978 18 at	77704	end, mKNA sequence, (from Genbank)
107 0 101	7007		200	KC RC	A211/	ES1: zn57d02.s1 Stratagene muscle 937209 Homo sapiens cDNA
487 Ovary	0.204282	0.4107699	0.342835	0.21204166 77_at	at	clone 562275 3', mRNA sequence. (from Genbank)
1				<u>ත</u>	RC_AA1612	
488 Ovary	0.2639894	0.4107074	0.342768	0.21178684 92_s_at	s_at	Interferon, alpha-inducible protein 27
489 Ovary	0.2638342		0.342618	0.21167074 M86849	3849_at	Connexin 26 (GJB2) mRNA
490 Ovary	0.2637067	0.4102355	0.34243	0.21147881 X54667	1667_at	CST4 Cystatin S
				X65	X65962_s_a	CYP2C17 Cytochrome P450, subfamily IIC (mephenytoin 4-
491 Ovary	0.2635544	0.4100462	0.342324	0.2113911 t		hydroxylase), polypeptide 17
700	0000	1	0			Bone marrow serine protease gene (medullasin) (leukocyte neutrophil
492 Ovary	0.2034786	⊃	0.342284	0.21120098 Y00477	0477_at	elastase gene)
493 Ovary	0.263438	0.409926	0.342233	0.21114148 X60483 at	1483_at	H4/d gene for H4 histone
						Growth hormone-releasing hormone receptor form b gene extracted
0.00	00000		0		579_rna	from Human growth hormone-releasing hormone receptor gene,
494 Ovary	0.2629789	0.4098917	0.342184	0.21098363 1 at		alternatively spliced forms a, b, and c, partial cds
()	0000000		0000		U16720_ma	
495 Ovary	0.2628802	0.409/485	0.342069	0.210848231 s	s at	Interleukin 10 (IL.10) gene
496 Ovary	0.2627642	0.4097359	0.341919	X173 0.21071276 1 at	X17360_ma 1 at	HOX 5.1 gene for HOX 5.1 protein
497 Ovary	0.2621831	0.4096476	0.341842	0.21056288 Z38026_at	026_at	CAP-18 protein

							Ti	ocke itle: vent	G	enet	ic N		ers	for '	Tu	mor: y, et d									
Somatostatin receptor isoform 2 (SSTR2) gene		Gene encoding E-cadherin, exon 3 and joined CDS		SDC4 Syndecan 4 (amphightean partocen)	A1 chain of type XIX collagen, exon +3'	EST: H. sapiens partial cDNA sequence, mRNA sequence. (from	GGCX Gamma-qlutamyl carboxylase	EST: zc54a05.r1 Soares senescent fibroblasts NbHSF Homo sapiens	CDNA Gone 32b09b 5' similar to contains element MER6 repetitive element :: mRNA secuence (from Genhank)	EST: zr69b08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	SPRRTB Small proline-rich protein 18 (comiffin)	Chorinais Samotomorphism Harris Process 1	CD86 CD86 antigen (CD28 antigen ligand 2. B7-2 antigen)		Carnitine palmitoyltransferase I (CPTI) mRNA	Claudin 3	Phosphoglucomutase 1, Alt. Splice	D-BETA-HYDROXYBUTYRATE DEHYDROGENASF PRECLIRSOR	D3 donamine recentor mRNA	SLC17A2 Solute carrier family 17 (sodium phosphate), member 2	Homo sapiens (clone ch13lambda7) alpha-tubulin mRNA, complete	hum alu at (miscellaneous control)	No description for gene: hum alu at	ELK4 SRF accessory protein 1B (SAP-1)	Flg-2 gene for fibroblast growth factor receptor
0.21051963 M81830 at	RC_AA0013 0.21044078 99 at	735402 ma 0.21028979 1 s_at	HG25930- 0.21018983 HT26386 at	D79206_s_a	0.21005002 D38462 at	0.20982467 E15201 at	R 1		0.20958297 W52493 at	RC_AA2331	0.20944946 M19888 at	"			0.20915589f	0.20901753 26_at	HG3893- 0.20893502 HT4163 at	0.20877808 M93107 at	U32499_s_a	0.2085401 L13258 at	RC_AA4357 0.20844713 20 i at	0.20836873 hum alu at	0.20830174 2	0.20807372 M85164 at	0.20799507 X58255_at
0.34175	0.341669	0.341611	0.341594	0.341536	0.34151	0.341487	0.341324		0.341269	0 344202	0.341108	0.341084	0.34103	0.940064		0.340949	0.340887	0.34044	0.340212	0.339996	0.33993	0.339912	0.339657		0.339552
0.2615432 0.4094477	0.4093441	0.4092804	0.409172	0.4091594	0.409025	0.4089933	0.408914		0.4087319	0.4086904	0.4086684	0.4083718	0.4081817	0.4081304	0.4001394	0.4079959	0.4079853	0.4079454	0.4078276	0.407768	0.4075463	0.4074981	0.4074932	0.4074622	0.4073862
0.2615432	0.2614543	0.2613242	0.261281	0.2610615	0.26083	0.260621	0.2600528		0.2598971	0.2598472	0.2596304	0.2592468		0.2580365	0.2300303	0.2578356	0.2575471	0.2573818	0.2573291	0.2573051	0.2566785	0.2563115	0.2563115		0.2560056
498 Ovary	499 Ovary	500 Ovary	501 Ovary	502 Ovary	503 Ovary	504 Ovary	505 Ovary		506 Ovary	507 Ovary	508 Ovary	509 Ovary	510 Ovary	511) Ovany	S C C C C C C C C C C C C C C C C C C C	512 Ovary	513 Ovary	514 Ovary	515 Ovany	516 Ovary	517 Ovary	518 Ovary	519 Ovary	520 Ovary	521 Ovary

If H. H. H. M. M. M. M. M. M. M. M. M. M. M. M. M.	0.339329 0.20789853 76 at	0.4072704 0.339237 0.20779629 HT1098 at Costatin D	æ.	AB002293_a	0	0.338742	0.338646 0.20710474 U62432 at	0.338603	0.338562 0.20700388 ₁ t	0.338454 0.20605395110000	0.338421 0.20833891 L19493 s at	AF012270_a	0.336317 0.20677233	.4058106 0.338288 0.20669466 t-2 complete cds	0.338262 0.20655999 H50398 at	0.338179 0.2065201 M37245 at	0.338094 0.20643477 t	Jordania Hollidie Leceptor	AD001527_c	0.337847 0.20629868	0.201011 0.20020194 L10123 at	.404902 0.337765 0.20609696 U39905 at SLC18A1 Solute carrier family 18 (vesicular monoamine), member 1
				0 33887	0.338761	0.338742	0.338646	0.338603	0.338562	0.338454	0.338421	1,70000	0.338317					_				- [
	0.2559532 0.4073812					0.4066447	0.4066334	0.4063708	0.4061648	0.4061568	1		- 1	0.4058106	0.4054902	0.4054203	0.4052288		0.4050864	0.405033		0.404902
	0.255953;	0.2558202	0.2557321	0.2555668	0.2553219	0.2551437	0.2551437	0.2550468	0.2550132	0.2549136	0.2548626	0.2548583		0.2548583	0.2548117	0.2545832	0.2543919		0.2535895	0.2535449		0.2534203
	522 Ovary	523 Ovary	524 Ovary	525 Ovary	526 Ovary	527 Ovary	528 Ovary	529 Ovary	530 Ovary	531 Ovary	532 Ovary	533 Ovary		534 Ovary	535 Ovary	536 Ovary	537 Ovary		538 Ovary	539 Ovary		540 Ovary

	<u>u</u>	er al.	
EST: ze14b12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358943 5' similar to PIR:A49128 A49128 cell-fate determining gene Notch2 product;, mRNA sequence. (from Genbank)	Human DNA sequence from PAC 127820 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat COL4A6 Collagen, type IV, alpha 6 GABA-A receptor epsilon subunit mRNA Homo sapiens secretory mucin MUC6 (MUC6) mRNA, partial cds Phospholipid Transfer Protein	Unnamed protein product gene extracted from Human gene encoding preproglucagon. Glucagon is a 29-amino acid pancreatic hormone stimulating hepatic glycogenolysis and gluconeogenesis. Also included in the proglucagon sequence are two regions (GLP-1 and GLP-2) which are homologous to glucagon itself but not identical Ceruloplasmin (ferroxidase) EST: zt62a05.s1 Soares testis NHT Homo sapiens cDNA clone Z-19 gene (2-19 protein) extracted from H.sapiens G6PD gene for CFTR Cystic fibrosis conductance regulator CETTR Cystic fibrosis conductance regulator clone 503759 3', mRNA sequence. (from Genbank) Description: orf3 gene extracted from region centromeric to t(12,17) amino acid transcript [human, testis, acampomelic campomelic dysplasia and sex reversal patient, Genomic, 3 genes, 3414 nt] Kidney epithelial sodium channel gamma subunit (gamma hENaC)	Hypothetical protein downstream of DMPK and DMAHP
W92242_s_3at	0.20591557 Z83838 at 0.2057685 D21337 at 0.20571235 U66661 at 0.20555034 U97698 at HG3945-	5 cds	
W 0.20595223 at		0.20532483 1 at 0.20524211 47 at 0.20519333 2.3 at 0.20507078 M55131 at 0.20507078 M55131 at 0.20507078 M55131 at 0.20507078 M55131 at 0.20507078 M55131 at 0.20507078 M55131 at 0.20507078 M55131 at 0.20503685 89 at 0.20476466 X87160 at 0.20476466 X87160 at 0.20449251 X76059 at 0.20449257 231357 at	0.2044589 Y10936 at
 1 0.337599	5 0.337578 9 0.337528 0.337442 0.337292	01 -1 3 @ 21 88	0.336514
 6 0.4043981	0.2532885 0.4043856 0.2531765 0.4043479 0.2527888 0.4039888 0.2527282 0.4039433		0.4027182
 0.2533096	0.2532885 0.2531765 0.2529089 0.2527888	0 0 0	0.2308315 0.
 541 Ovary	542 Ovary 543 Ovary 544 Ovary 545 Ovary 546 Ovary	547 Ovary 548 Ovary 550 Ovary 551 Ovary 552 Ovary 553 Ovary 554 Ovary 555 Ovary 655 Ovary	

FIG. 10W

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0	0.0508087	0.4026777	0336329	0.20436396 1.s. at	Pmel 17 mRNA
330 Oval y	0.200001		2 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0 20425408 D55640 at	Monocyte PABL (pseudoautosomal boundary-like sequence) mKNA, right Mo2
559 Ovary	0.2506595	0.4026501	0.330178		EST. H. sapiens putatively transcribed partial sequence; UK-HGMP
					sequence ID AAAAGNB; single read, mRNA sequence. (from
560 Ovary	0.2505702	0.4026042	0.336157	0.20419258 Z19675_at	Genbank)
					NADP dependent leukotriene b4 12-nydroxydenydrogeriase, paruar
561 Ovary	0.2503649	0.4024495	0.33606	0.20410079 D49387 at	cds
562 Ovary	0.2500466	0.2500466 0.4023899	0.335987	0.20396836 U26914 at	Ras-responsive element unitually protein (INNED-1) minutes
0	0.000000	0.4023804	0 335878	0.20386107 X17622 at	MCNAb Polassium vollage-galed origins, stand construction member 6
564 Ovary	0.2499203		0.335661	0.20374103 M60614_at	WT1 Wilms tumor 1
	0.2400082	0 4021704	0.335404	0.20361574 X13255 at	DBH Doparnine beta-hydroxylase (doparnine beta-monooxygenase)
505 Oval y	0.2433008		2000	RC AA4593	
566 Ovary	0.2497903	0.4020307	0.335277	0.20359892 89_at	Tyrosylprotein sulfotransferase 2
	7100017	0.4040073	0 3352/5	M24351_cds	PTHLH gene (parathyroid hormone-like protein A) extracted from Human parathyroid hormone-like protein (PLP) gene
567 Ovary	0.2490047	- }	0.335243	0.2033138 15702 at	BF B-factor, properdin
568 Ovary	0.249279		0.333212	11	CSE2 Colony-stimulating factor 2 (GM-CSF)
569 Ovary	0.2492415	0.4018194	0.335155	0.20323310 MI13201 at	Clone 350/2 melanoma ubiquitous mutated protein (MUM-1) gene,
570 Ovarv	0.2492151	0.4018015	0.335105	0.20316797 U20908_at	partial cds
		_		AF009368_2	
571 Ovary	0.24917)	0.20292385 t	Luman mRNA
572 Ovary	0.24912	Ì		0.20289564 L13977 at	LYSOSOMAL PRO-X CARBOX PEP IIDASE PRECONSON
573 Ovary	0.2489907	1	l i	- 14	GGTB2 Glycoprotein-4-beta-galactosylli at islet ase z
574 Ovary	0.2489894			0.20267986 U55258 at	HBRAVO/Nr-CAM precursor (IIBRAVO/Nr-CAM) gene
575 Ovary	0.2480893	0.4013435	0.334376	0.20258774 U10362_at	GP36b glycoprotein mklvA
•	0		2767660	HGZ/15-	Tyrosine Kinase (Gh:725437)
5/6 Ovary	0.24/94/1	0.4013455		0.20245755 D86966 at	KIAA0211 gene
or r Oval y	0.01		5		1
578 Ovary	0.2478948			0.20241871 6 at	Folate receptor (FOLK1) gene
579 Ovary	0.2478382			- 13	I KANSCKIP HON INH PATION PACTON IT IN 250 NO COCCUR.
580 Ovary	0.2477879	9 0.4009556	0.333938	0.20223966 X81637 at	CLIB Clathin, light polypepulae (LCD)
				RC AA4910	
581 Ovary	0.247733	0.2477336 0.4009417	0.333898		mRNA sequence. (from Genbank)
582 Ovarv	0.247437	0.2474372 0.4007636	0.33389	0.20211579 U38276 at	Semaphorin III family homolog mKINA
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583 Ovary	0.2471709	0.400761	0.333736	0.20197856 J03474 at	SERUM AMYLOID A PROTEIN PRECURSOR
584 Ovary	0.2471177	0.400758	0.333728	0.20187068 X78706_at	CRAT Carnitine acetyltransferase
585 Ovary	0.247063	0.4005463	0.333717	0.20176512 D45906_at	LIMK-2
586 Ovary	0.2470482	0.4005349	0.333695	0.20169307 X83127_at	K+ channel beta 1a subunit mRNA, alternatively spliced
587 Ovary	0.2470227	0.4004628	0.333615	0.20166042 X80923_at	Nov gene
588 Ovary	0.246805		0.33339	0.20148031 D38305_at	Tob
589 Ovary	0.2467307		0.333314	0.2014147 L17328_at	Pre-T/NK cell associated protein (3CI) mRNA
590 Ovary	0.2466294		0.333281	0.2012465 Z21966_at	POU6F1 POU homeobox protein
591 Ovary	0.2464729	0.4001063	0.333254	0.20116653 U03270_at	Centrin mRNA
					EST: yy75e09.r1 Homo sapiens cDNA clone 279400 5'. (from
592 Ovary	0.2462271	0.4000655	0	0.20110865 N48927 at	Genbank)
593 Ovary	0.2460588		0.33297	0.20103784 U46569_at	Aquaporin-5 (AQP5) gene
594 Ovary	0.2459124	0.3999254	0.332862	RC_AA2358 0.20091069[34_s_at	EST: 2s41a10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687738 3' mRNA segrence (from Genhank)
595 Ovary	0.2456928	0.3998796	0.332828	0.20062262 U89942 at	Lysyl oxidase-related protein (WS9-14) mRNA
596 Ovary	0.245507	0.399838	0.332657	0.20060207 L38500 at	Na+/myo-inositol cotransporter (SLC5A3) gene
			And the second s	RC AA4314	EST: zw72f05.s1 Soares testis NHT Homo sapiens cDNA clone
597 Ovary	0.2454886	0.3996636	0.332516	0.20050538 79_at	781761 3', mRNA sequence. (from Genbank)
				2 AA202600	AA202600 2 MAGE-701616 F similar to contains 11 to 11 ropetitive element
598 Ovary	0.2452701	0.3995775	0.332393	0.20043796 t	mrdcc., orong a similar to contains critical repetitive element, mrRNA sequence. (from Genbank)
599 Ovary	0.2451796	0.3992013	0.332368	0.20032588 X51441_at	SERUM AMYLOID A PROTEIN PRECURSOR
				HG2280-	
600 Ovary	0.2451349	0.3991809	0.332226	0.2002477 HT2376_at	D-Amino-Acid Oxidase
9				RC_AA4889	
601 Ovary	0.2450647	0.3991486	0.332219	0.20016891 79_at	Homo sapiens cell cycle-regulated factor p78 mRNA, complete cds
602 Ovary	0.2449481		0.332093	HG172- 0.2000227 HT3924_at	Spermidine/Spermine N1-Acetyltransferase, Alt. Splice 2.
603 Ovary	0.2447337	0.3990979	0.332067	0.19998762 X59892_at	TRYPTOPHANYL-TRNA SYNTHETASE
				HG919-	
604 Ovary	0.2446139	0.3990898	0.332053	0.19980809 HT919_at	Dna Polymerase, Epsilon, Catalytic Subunit
605 Ovary	0.2445739	0.3990673	0.331969	RC_AA4007 0.19976458 68 at	EST: zt71c01.s1 Soares testis NHT Homo sapiens cDNA clone 727776 3', mRNA sequence. (from Genbank)
606 Ovary	0.2445341	0.3989032	0.331947	0.19964974 L10615 s at	at CSN2 Beta-casein
607 Ovarv	0.2441043	0.3988426	0.331898	0.19958155 74 at	RC_AA0312 EST: zk15a10.s1 Soares pregnant uterus NbHPU Homo sapiens 74 at cDNA clone 470586 3' mRNA sequence. (from Genbank)
608 Ovary	0.2440666		0.331799	0.19954087 X52479 at	PRKCA Protein kinase C, alpha
609 Ovarv	0.2438923	0.3987324	0.331619	HG363- 0.19948214 HT363 at	Fordermal Growth Factor Receptor-Related Protein
6.000	>	- 1	2122		Forder Hall Closus Cover Covered Covered Covered

and plant, plant, given given year, near,

610 Ovary	0.2438448	0.3986809	0.331495	0.19938543 L24203_at	24203_at	Ataxia-telangiectasia group D-associated protein mRNA
2.7	000000000000000000000000000000000000000	1	007.700.0	A	RC_AA3981	
611 Ovary	0.2435269	- 1	0.331429	0.19933096 24	4_s_at	Growth factor receptor-bound protein 14
612 Ovary	0.2435159	į.	0.331299	0.1990926 X98176_at	.98176_at	MACH-alpha-2 protein
613 Ovary	0.2430712	0.3982059	0.331242	0.19904166 U69263_at	169263_at	Matrilin-2 precursor mRNA, partial cds
614 Ovary	0.2428666	0.398203	0.331239	0.1988269	HG3107- HT3283_s_a	Plasma Memhrane Calcium Pump Homca2a
615 Ovary	0.2428224	0	0.331192		125182 at	Antioxidant enzyme AOE37-2 mRNA
					U28749 s a	
616 Ovary	0.2426744	0.398058	0.331106	0.19867557 t	1	High-mobility group phosphoprotein isoform I-C (HMGIC) mRNA
617 Ovary	0.2426077	0,3980478	0.33103	HG3288 0.19867557 HT3465	HG3288- HT3465 at	Xanthine Dehydrogenase (Gb:U06117)
618 Ovary	0.2422744	0.3978426	0.330952	HG2290 0.19864419 HT2386	HG2290- HT2386_at	Calcitonin
619 Ovary	0.2422255	0.3978349	0.330876	0.19851272 D43642	043642_at	YL-1 mRNA for YL-1 protein (nuctear protein with DNA-binding ability)
620 Ovary	0.2421735	0.3978189	0.330752	D. 19849677	D86096_cds	EP3-IV gene extracted from Human DNA for prostaglandin E receptor FP3 subtyne
621 Ovary	0.2421258	1	0.330716	0.1983327 M85085	185085 at	CSTF2 Cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kD
622 Ovary	0.2418219	0.3977831	0.330456	0.19824454 X02544 at	02544 at	ORM1 Orosomucoid 1
623 Ovary	0.2416403	8602708 0	0 330376	0.40824772 MERED3	455502 at	MMP2 Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase,
624 Ovary	0.2414672	-	0.330341	0.19814219119711	13 **	Distroctive (DAG1) mRNA
		1				
625 Ovary	0.2411349	0.3975974	0.330334	0.19798787 HT2556	IT2556_at	Integrin Beta 1 (Gb:M34189)
626 Ovary	0.2409652		0.330293	0.19784574 X04325	.04325 at	GJB1 Gap junction protein, beta 1, 32kD (connexin 32, Charcof-Marie-Tooth neuropathy, X-linked)
627 Ovary	0.2408217	0.397472	0.330215	0.19776194 U65932	165932_at	Extracellular matrix protein 1 (ECM1) mRNA
628 Ovary	0.2408072	0,3974669	0.330197	0.197711691114269 at	14269 at	SI C18A2 Solute carrier family 18 (vesicular monoamine) member 2
629 Ovary	0.240689	0.3974335	0.330111	0.19754815 U79251 at	179251 at	OPCML Opioid-binding cell adhesion molecule
630 Ovary	0.2404317	0.3970117	0.330029	0.19750503 U47931 at	147931 at	G-protein beta-3 subunit alternatively spliced form mRNA sequence
631 Ovary	0.2403633	0.3969821	0.329919	0.1974592 M86808	/86808 at	Pyruvate dehydrogenase complex (PDHA2) gene
632 Ovary	0.2401766	0.3969784	0.3299	0.1972791 U82467	J82467_at	Tub homolog (TUB) mRNA
633 Ovary	0.2400923	0.3965403	0.3299	0.1971084 L22524		s_at MATRILYSIN PRECURSOR
634 Ovary	0.2400444	0.3964808	0.329758	R 0.19710705	RC_D58185 at	EST: Human aorta cDNA 3'-end GEN-354C01, mRNA sequence. (from Genbank)
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Acetylcholinesterase (14-E5 doman) [human, tumor cell lines,		90	ase kinase, isoenzyme 4		ated factor mRNA		3	de galactosyl transferase	de o, regulatory	RC_A44778 EST: zu39g07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	lence. (from Genbank)	Human line-1 reverse transcriptase gene, partial cds. and granulocyte	2) gene	L43579 Soares fetal liver splean 1NETS 11	call IIVI LO HOIHO Sapiens CUNA clone	mRNA	1 peptide-1			o di		EST: zx89d12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	ence. (from Genbank)	EST: yw29e12.r1 Homo sapiens cDNA clone 253678 5'. (from Genhank)	EST: ym50f03.r1 Homo sapiens cDNA clone 51827 5'. (from	CDKN2A Cyclin-dependent kinase inhibitor 2A (melanoma. p16.		JL	
		T		\top	Endometrial bleeding associated factor mRNA	Refinoblactomo	T	MYL5 Myosin light polymentide E rocal Attensferase	dadyind men construction	0.19618486.26 at Collagen, type I, alpha 2	GCP-2 nene (granufont a chome)	Human line-1 reverse transo	S' mRNA of PECAM 4 2001-2) gene	L43579 Soares fetal liver sp	110298, mRNA sequence	Eyes absent homolog (Eab1) mRNA	Reg-related sequence derived peptide-1	HTS1	XMP mRNA	Estrogen Sulfotransferase	Amplaxin (EMS1) mRNA	1	ANX4 Appexin IV (alacada)		EST: ym50f03.r1 Homo sapie	CDKN2A Cyclin-dependent k	(inhibits CDK4)	CC chemokine LARC precursor	(clone 35 3) DRAI mPNA
0.19703965 671100	0.196940881190905 at		0.19664232 1103272 at	f1	HG4036-	0.19644605 HT4306 at		0.19628023 L03785 at	19623984 103464 2	0.1961848626 at	מני מני	U83303_cds	0.19579662 X96849 at		0.1957729 L43579 at			0.19332177 U15131 at	HG4185-	0.1953924 HT4455 at	0.19535156 M98343 at	0.1952818 at	11 ===	H89896_s_a	0.19490215 H24127 at		0.19404132 UZ012/ at	0.19462222 D80008 at	
0.329738	0.329653	0.329652	0.329584	0.329419		0.329395	0.329368	0.329354	0.329278 0		1.	0.329059			0.328813						0.328375 0.	0.328192 0		0.328116 0.1	0.328112 0.1	0.32792	3276	7544	0.327505 0.1
8 0.3964537	l í	5 0.3963174	0.3962031	3 0.3960701		0.3960078		0.3957806	0.3956446	0.3955021		0.2375645 0.3954524	0.2371658 0.3953841		0.3933473		0.3951756	0.3951675		ー し	0.394908	0.3947818	0.3946359	0.3945908	0.3945717	0.3945151	0.3943844	0.3943701	0.3943402
0.2399658	0.2399486	0.2397565	0.2395354	0.2394803	6	0.2388746	0.2381230	0.23/8548	0.2377848	0.2377693		0.2375645	0.2371658	0.9374944	0.2370138	0.2369099	0.2366379	0.2363132	200000	0.2360780	601007.0		0.2358091	0.2356793	0.2356619	0.2354938 0.3945151	0.2352029 0.3943844	0.234788	0.2346284
635 Ovary	636 Ovary	637 Ovary	638 Ovary	639 Ovary	640	644 Ovary	647 Ovary	042 Ovaly	643 Ovary	644 Ovary		645 Ovary	646 Ovary	647 Ovary	648 Ovary	649 Ovary	650 Ovary	651 Ovary	659 000	653 Ovary		654 Ovary	app Ovary	656 Ovary	657 Ovary	658 Ovary	659 Ovary	660 Ovary	661 Ovary

FIG. 10A2

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nd, mRNA	scle		apíens gene		emative		oliced form 2,		apiens cDNA		con 9. (from	clone	lements.
AA358888_a EST: EST67818 Fetal lung II Homo sapiens cDNA 5' end, mRNA	Tropomyosin, Alpha, Muscle, Alt. Splice 2, Skeletal Muscle (Fibroblast) Cadherin, partial cds	DAKA Cuktamili li an a	Cone transducin alpha subunit gene extracted from H.sapiens gene for cone transducin alpha subunit	Sop2p-like protein CNTN1 Confactin 1 ATP1AI 1 ATD drives in	PTGER3 Prostaglandin E receptor 3 (subtype EP3) (alternative products)	Instruction of the IA CHAIN PRECURSOR Insulin-like growth factor binding protein 2 (36kD) Pre-pro-megakaryocyte potentiating factor	Type I keratin, hHa5 Death domain receptor 3 (DDR3) mRNA, alternatively spliced form 2, partial cds	Mucin 6, Gastric (Gb-1 07547)	EST: zx02a09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785272 3', mRNA sequence. (from Genbank) ADENOSINE A2A RECEPTOD	KIAA0009 gene APEH N-acylaminoacyl-peptide hydrolaca	Homo sapiens cytochrome P4502C9 (CYP2C9) gene, exon 9. (from Genbank)	STRESS-ACTIVATED PROTEIN KINASE JNK1 EST: zt70a07.s1 Soares testis NHT Homo sapiens cDNA clone 727668 3', mRNA sequence (from Carbon)	EST: Human mRNA sequence containing Alu repetitive elements. (from Genbank) ADRA1C Adrenergic, alpha-1C-, receptor Homo sapiens TACC1 (TACC1) mRNA, complete cds
8_a EST: EST6	Tropomyosin, Alpha, at (Fibroblast) at Cadherin, partial cds	CT.	a		të,	w a		Mucin 6, Gas	1	KIAA0009 gene APEH N-acylam			EST: Human m (from Genbank) ADRA1C Adren Homo sapiens T
	HG2442- 6 HT2538 4 1 D88797 8	HG1827- HT1856 s	Z18859_rna 1_at	0.1940/21 Y08999 at 19404262 Z21488 at 19401522 L42563 at	S68874 s M25164 at	11 1) ;;	X90763_at U83600_at	HG880- HT880_at	RC_AA4764 15_at X68486_at	D13634 at J03068 at	တုိ တုံ	t RC_AA3985 98_at	J51704 at J32202 at 09468 at
0.19453587	HG2442- 0.19446646 HT2538 0.19442731 D88797	0.1942794			0.19392665 S68874 s 0.1938264 M25164 at	0.193794 t 0.1937344 U40434	0.19348839 U83600	HG880- 0.19337085 HT880	RC_AA 0.19333906 15 at 0.19320577 X68486	0.19311209 D13634 0.1930455 J03068		0.19278567 t RC 0.19267742 98	0.192559 U51704 at 0.192559 D32202 at 0.19250238 T09468 at
0.327322	0.327253	0.327167	0.327152		0.326899	0.326816	0.326579	0.326579	0.326553	0.326234	0.326201	0.326109	0.325983 0.325716 0.325702
0.3942555	0.394174	0.3940532	0.3940191	0.3938775	0.3936808	0.3934652 0.3932697 0.3931069	0.3929695	0.3928176	0.3927828 0.39275	0.3925849	0.3924752	0.3923096	0.3922575 0.3922218 0.3921641
0.234362	0.2343044	0.2332717	0.2330434 0.3940191 0.2330377 0.3939594	0.2329765	0.2327498	0.2324094 0.2322222 0.2316186	1 1	0.2314241	0.2313847 (0.2307315	1 1	0.2304064 0		0.2300397 0 0.2297734 0 0.2296775 0
662 Ovary	663 Ovary 664 Ovary	665 Ovary	666 Ovary 667 Ovary	668 Ovary 669 Ovary	670 Ovary 671 Ovary	672 Ovary 673 Ovary 674 Ovary	675 Ovary	676 Ovary	677 Ovary 678 Ovary 679 Ovary	680 Ovary	681 Ovary 682 Ovary	683 Ovary	684 Ovary 685 Ovary 686 Ovary

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FIG. 10B2

the state of the control of the cont	M19720_ma L-myc gene (L-myc protein) extracted from Human 1	gene gene 6 s a	HMGI-C					ä	7	a.	KIAA0384 gene	DNA sequence from clone RP1-151B14 on chromosome 22 Contains	Tibosomal protein 130 p. 23, gene, pseudogene similar to		1		Neuropilin 2	T		(0	812971 3', mRNA sequence. (from Genbank)			2 a				Guanine nucleotide regulatory protein (tim1) mRNA	0.19074714 U82169 at-2 Frizzled (Procentile) L.	t Frizzled homolog (FZD3) mRNA		mRNA from TYL gene
The trade duck in the first ind	0.40000440	0.13239140	0.19232488		0.13210312JU5158 at	0.19206144 J03161 at	HG4332.	0		AB002382 0 10178550	18000116176			0.000	0.1917211 Z86000 at	0.1916235 98 at	O		0.19145368 M13666 at	RC_AA4646	U.19137146 03_at	0.19129649 M59941 at	0.19110961 Z37976 at	AB006190_a	0.19106191t	0.19103483 U/8/22 at	0.19056073 1102082	2:12010013 002082 81	0.19074714 U82169 at	0.1906824 U82169 at	0.19064657 L41351 at 0.19058192 Voneso	STANDARD BE
	1 0.32559A		0.325402 R 0.325969	1	_	0.325249	0.325153			0.325069			-	0.325002	7000700	0.324888	0.324843	0.324605	0.32456	0.324478	0.024410	0.324425	0.324384	0 304000	0.324283	0.323969	0.323937		0.32392	0.323812	_	1
	5 0.392119		- 1	1 1		0.3918904		0	0.39145	0.3911955				0.3911682		0.3911057	0.3911035	0.3906581	0.3905812	0.3902359		0.390088	0.3899641	0.3899183	0.3898705	0.3897544	0.3895951		0.3895175	3893352	0.3893337	
	0.2293986	0.2290153	0.2290026	0.2289286	0	0.2286594	0.2281737	0.227524	0.2270346	0.2268547				0.2267593			0.2264652	- 1	0.2259493	0.2256623	1	0.2254506	0.1110.42.0	0.2250925 0	_ f	1	0.2247052 0	0000000		10	0.2239232 0.	
	687 Ovary	688 Ovary	689 Ovary	690 Ovary	694 0000	oo l Ovaly	692 Ovary	694 Overy	oct Cvaly	695 Ovary				696 Ovary	607	698 Overy	699 Overy	700 Ovany	(IDA)	701 Ovary	7002	703 Ovary		704 Ovary		1	/u/ Ovary	708 Ovary	1		/11 Ovary (

FIG. 10C

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762 Overv	0.2157192	0.3854658	0.319782	0.1862895 20 at	2514 EST: ZSU9911.ST NOT COAT GOD! HOLLO SAPERS COLVE CONC. (MAGE: 684740 3', mRNA sequence. (from Genbank)
763 Ovarv	0.2156471		0.319677	0.18625464 t	Ø,
Zev Over	0.0458437		0 340667	0 48642033 747956	0.48642033 T47256 e at Crowth arract-enacific 6
104 Ovaly	12.1.20.1.20	_1	0.0	0.1001.001.0	ס מו כו כאינו מווכפו סרכיווס פ
765 Ovary	0.2153332	0.385348	0.319662	0.1860313 J02871 s at	s_at CYP4B1 Cytochrome P450 IVB1
766 Ovary	0.2150727	0.3852523	0.319635	RC_AA1214 0.18600565 33_s_at	214
767 Ovary	0.2148703	0.3850054	0.319493	0.18587162 68 at	2570 EST: zr82b05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682161 3', mRNA sequence. (from Genbank)
				AA476704_a	J
768 Ovary	0.2148693	0.3849889	0.319487	0.18574493 t	clone 783987 5', mRNA sequence. (from Genbank)
769 Ovarv	0.2147891	0.3849504	0.319358	0.18564777 D60964 at	EST: Human fetal brain cDNA 5'-end GEN-143D03, mRNA sequence. at (from Genbank)
770 Ovary	0.2146678		0.31931	0.18553908 D10995 at	
				M22348_s	σ,
771 Ovary	0.2144604	0.3846716	0.319198	0.18547864 t	UQCRB Ubiquinol-cytochrome c reductase binding protein
772 Ovary	0.2143412	0.3846225	0.319198	0.18534003 S77576	ERV9 reverse transcriptase homolog {clone RT18} [human, multiple state sclerosis, brain plaques, mRNA Partial, 84 nt]
				U65533_s	a
773 Ovary	0.2142831	0.3844945	0.319196	0.1852607 t	KIAA0221 gene
774 Ovarv	0.2142806	0.3844911	0.319024	0 18523401 M6493	0.18523401 M64936 f at Homo sapiens retingic acid-inducible endogenous retroviral DNA
775 Ovary	T	1	0.319018	0.1851715 X85786	s at BINDING REGULATORY FACTOR
776 Ovary		0.3843627	0.318913	0.18511751 M35128 at	8 at Muscarinic acetylcholine receptor gene
777 Ovary		3 0.3842661	0.318863	0.18503377 X64994_at	1_at HGMP07I gene for olfactory receptor
120	200		207070	X79683_s	1. S. a I AMBO I aminin hata 2 flaminin C)
779 Ovary	0.213033	0.304203	0.316795	0.184738871144754	7
780 Ovary	0.2129948			0.18471654 D87449	; to
781 Ovary	0.2125735	E	1	0.18468161 M11119	ਰ
782 Ovary	0.2125442	1 1	0.318523	0.18458816 U02310	at
					AA004333_a EST: zh91a01.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
783 Ovary				0.18458341 t	
784 Ovary	0.2119414	4 0.383513 5 0.3835011	0.318199	0.18448752 U77604 0.18438028 U22816	4 at Microsomal glutathione S-transferase (GST-tl) Illinux 6 at LAR-interacting protein 1b mRNA
100 Cvaly	1101110		_		

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786 Ovary	0.2114469	0.3833741	0.318097	0.184320361	M96738_s_a	Somatostatin recentor subtano 9 (COTD9) and
787 Ovary	0.2112345	0,3833125	0		D79997_at	KIAA0175 gene
788 Ovary	0.2110709	0.3832769	0.31794	HG2566 0.18417068 HT4867	HG2566- HT4867_at	Microtubule-Associated Protein Tau, Alt. Splice 5, Exon 4a
789 Ovary	0.2108621	0.3832431	0.317908	0.18412977 M90299	M90299 at	GCK Glucokinase (hexokinase 4, maturity onset diabetes of the young 2)
790 Ovary	0.2101338	0.3831612	0.317908	HG2239- 0.18412505 HT2324	HG2239- HT2324_at	Potassium Channel Protein (Gb:Z11585)
791 Ovary	0.2100628	0.383081	0.317834	0.18400887 778289 at	778289 at	Z78289 Homo sapiens brain fetus Homo sapiens cDNA clone 1D2,
792 Ovary	0.2099933	0	0.317827	0.18397938 U59914	U59914_at	Chromosome 15 Mad homelog Smode menta
793 Ovary	0.2099743		0.317726	l	D37965 at	PDGF recentor heta-like fumor sunarassor (DDI TC)
/94 Ovary	0.2099292	0,3828823	0.317663	0.18383309	D42123_at	ESP1/CRP2
795 Ovary	0.2098618	0.382842	0.317647	0.18378854t	U40152_s_a t	Origin recognition complex 1 (HsORC1) mRNA
796 Ovary	0.2097012	0.3828374	0.317639	0.18370338 t	D49372_s_a t	SCYA11 Small inducible entoking A14 (cotoxin)
797 Ovary	0.2093392	0.3827462	0.317623	0.183674131	C00038_s_a	EST: HUMGS0003443, Human Gene Signature, 3'-directed cDNA
798 Ovary	0.2092109	1	0.317613	0.18362753 (156418 at	U56418 at	Asonhoenhafida ad a female
799 Ovary	0.2091021	0.3826528	0.317601	HG1078- 0 18353024 HT1079 et	HG1078-	Propriocipation and abylitid Islet ase-Deta MikinA
800 Ovary	0.2089959		0.317572	0 18335396 S3/380 at	C3/1380 at	LAMOV3 1
801 Ovary	0.2089027	1	0.317476	0.18327694 M28439	W28439 at	KERATIN TYPF I CYTOSKFI FTAI 17
802 Ovary	0.2088515	0.3824928	0.317368	0.18321551 H55437	-155437_at	EST: CHR220376 Homo sapiens genomic clone C22_491 5'. (from Genbank)
803 Ovary	0.2087314	0.3824579	0.317308	0.18319185 S72493	S	at KERATIN, TYPE I CYTOSKELETAL 17
804 Ovary	0.2084796	0.382425	0.317109	0.18310583 HT4206	्रं च	Interleukin 9 Receptor (Gb:S71404)
805 Ovary	0.2081756	0.2081756 0.3824143	0.317	RC_A 0.183064875 at	A4494	EST: zx08f10.s1 Soares total fetus Nb2I-IF8 9w Homo sapiens cDNA clone 785899 3' similar to contains Alu repetitive element; contains element MER22 repetitive element; mRNA sequence. (from Genhank)
806 Ovary	0.2081726 0.3824058	0.3824058	0.316918	0.1829516 X00129	(00129 at	PLASMA RETINOL-BINDING PROTEIN PRECIIRSOR
807 Ovary	0.2078704	0.3823701	0.316911	0.18283588 t-2	9377_s_a	Msh (Drosophila) homeo box homolog 2
808 Ovary	0.2078704	0.382341	0.316714	0.1828001 t	089377_s_a	Adult tooth pulp of third molar fibroblast mRNA for MSX-2
						The state of the s

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800 Overv	0.2078187	0.2078487 0.3823499	0.346624	M18391_s_a	TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR
out of the state o	0.2077808	0.3894343	0.316527	0 182637411 40992 at	(clone PEBP2aA1) core-binding factor, runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds
o to Ovary	0.201			1	EST: zk68a03.s1 Soares pregnant uterus NbHPU Homo sapiens
811 Ovarv	0.2077745	0.3821238	0.316493	RC_AA0547 0.18259025 15 at	CDNA clone 48/948 3 similar to WP:R04E5.0 CE04/30 ,, inrNA sequence. (from Genbank)
7.5.5		- [RC_AA1490	EST: zl46b12.s1 Soares pregnant uterus NbHPU Homo sapiens
812 Ovary	0.2077466	- 1	0.316348		cDNA clone 504959 3', mRNA sequence. (from Genbank)
813 Ovary	0.2075722		0.316244	0.1824599 U76189 at	EXTL2 (EXTL2) mRNA, partial cds
814 Ovary	0.2073383	0.3817716	0.316209	0.1823877 L38517_at	Indian hedgehog protein (IHH) mRNA, 5' end
				HG1496- HT1496 s a	
815 Ovary	0.2071717	0.3817098	0.316178		Adrenal-Specific Protein Pg2
816 Ovary	0.2069506	1	0.316122	0.18214336 S78569 at	LAMA4 Laminin, alpha 4
817 Ovary	0.2064033	0.3813432	0.316109	0.1820708 U45880_at	X-linked inhibitor of apotosis protein XIAP mRNA
818 Ovary	0.2058696		0.316064	0.18204506 M74525_at	UBE2B Ubiquitin-conjugating enzyme E2B (RAD6 homolog)
810 Ovary	. 0.2055314	0.3812586	0.34605	X95238_s_a	H saniens mRNA for cysteine-rich secretory protein-1 delta
(in a					
820 Ovary	0.2053392	0.3812457	0.31604	0.18189794 HT4603_at	Zlnc Finger Protein Znfpt7
200	00000000		0.945003	HG4194-	Codium (Hydrogen Evoluner 5
02 I Oval y	0.4032498			- 11	Condition lyalogor Eveninger of
822 Ovary	0.2051002	-	0.31		IREBT Iron-responsive element binding protein 1
823 Ovary	0.2050945	0.3812057	0.315859	0.18166459 D63485_at	KIAA0151 gene
					Putative envelope protein; orf similar to env of 1ype A and 1ype B retroviruses and to class II HERVs gene extracted from Human
			,	1	U60269_cds endogenous retrovirus HERV-K(HML6) proviral clone HML6.17
824 Ovary	0.2049917	0.3811966	0,315/85	0.18159531	putative polymerase and envelope genes, partial cus, and our n
825 Ovary	0.2049604	0.3810985	0.315769	HG2264- 0.1815839 HT2360_at	Atpase, Ca2+ Transporting, Plasma Membrane 1, Alt. Splice 6
775/O 878	N 2042084	0 3840538	0.31573	0 18115345	AA191072_a EST: zq43c11.r1 Stratagene hNT neuron (#937233) Homo sapiens
OZO CYCII)	0.50	1			Hydroxyindole-O-methyltransferase promoter B-derived (HIOMT)
827 Ovary	0.2041318		0.31		mRNA
828 Ovary	0.2035693	3 0.3810171	0.315693	0.18136963	KIAA0134 gene
829 Ovary	0.2034448	3 0.3808361	0.315683	HG982- 0.18131539 HT982_s	at Pre-T/Nk-Cell-Associated Protein 1f6

FIG. 10H2

gens, den, gens, pass pass gens, seen, gens, den, gens, den, gens, den, gens, den, gens, g

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- 111	Olfactory Receptor Or17-209 XG mRNA (clone PEPS)	EST: zr49c02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666722 3' similar to TR:G469478 G469478 SM-20.;; mRNA	EST: zk54h07.s1 Soares pregnant uterus NbHPU Homo saniens	cDNA clone 486685 3', mRNA sequence. (from Genbank)	MHC class I molecule (MICB) gene	CALCR Calcitonin receptor	High-mobility group phosphoprotein (HMGI-C) gene, exons 1-3	at ADCYAP1 Adenylate cyclase activating polypeptide 1 (pituitary)	Orto-binding factor and design the state of	RTP	Integrin, alpha subunit	I D Colorest	EST: zw37a04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	udne 772206 3', mRNA sequence. (from Genbank)	Orphan receptor GPR9 (GPR9) gene, partial cds	HNL=neutrophil lipocalin [human, ovarian cancer cell line OC6, mRNA Partial. 534 ntl	RD Radin blood group		EST: zl29e12.s1 Soares pregnant uterus NbHPU Homo saniens	CDNA clone 503374 3', mRNA sequence. (from Genbank)	Cadherin FIB1, partial cds	Acidic hair keratin 1	MVK Mevalonate kinase	Transcription factor SUPT4H mRNA	Kynurenine 3-monooxygenase	LAWITZ Lysosome-associated membrane protein 2 {alternative products}
7777011	0.18124525 HT4384 at 0.18114795 Z48512 at	RC_AA2338	RC_AA0442	U65416 ma	X69920_s_a	3.1	1.46353 at	S83513 s	je d	at	X68742_at	0.18038128 M25322 at	1043	Sa		at		w.	_AA1258	B000895 a		at	्व	ं ज	[a]	at
***************************************	1 1			0 40000734	0.1000973	0.18077508	0.100173081.46353	0.18073854	0.1806245	0.18054736 D87953	U.1804437 X68742	0.18038128	0.18030246 R1 f at	0 400004704	0.100247041	0.18014386	0.18005228 X16105 at	0.17996652	RC 0.17986195.08	201000111	0.17985153 [0.1/9/6114 X86570	0.17971715 M88468	0.1795772 U43923	0	0.17947468 1.09717
	0.31563	0.315522			1	0.315187		0.3150/7	0.314984	0.314983	0.014942	0.314823	0.314676	0.3146	0.0140	0.314587	0.314529	0.314423	0.314416		0.314414	0.314404	0.314369	0.314302		0.314245
	0.3807914	0.3803895	0.3803838			1	0.300000	0.000083	0.2016619 0.3798647	0.3797779		0.3797258	0.3796482	0.379615		0.3795275	0.3794918	0.3794338	0.3791668	0.000000	0.3790240	0.3789289	0.3788907	0.3788375		0.3788328
	0.2030279	0.2025874	0.2024833	0.2022828	0.2024611	0.2018699		100	0.2016619	0.2015148		0.2010873	0.2010492	0.2010197		0.2009825	- 1	0.2008977	0.2007899	0.2007868						0.1998798 0.3788328
	830 Ovary 831 Ovary	832 Ovary	833 Ovary	834 Ovary	835 Ovary	836 Ovary	837 Ovarv	0000	839 Ovany	840 Ovary		841 Ovary	842 Ovary	843 Ovary		844 Ovary 845 Ovary		846 Ovary	847 Ovary	848 Ovarv	849 Ovany	850 Ovary		852 Ovary		853 Ovary

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FIG. 10IZ

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854 Ovary	0 199725	0 1997251 0 3789036	0001700	L		en fand tank Uraji dinji linji
	7	0.01.000	- 1	0.17938206 U43148 at	13148 at	PTCH Patched (Drosophila) homolog
855 Ovary	0.1989991	0.3787949	9 0.314199		1- 3026	ELAV-like neuronal protein 1 isoform Hel-N2 (Hel-N1) mRNA, partial
856 Ovary	0.1988059	1	1	0.17933122 U 13/10 al	Sruo at	SDO
857 Ovary	0.1987526				4303 at	PEKIPHERIN
			丄	0.11 303311 043030 at	รบรบ at	Cardiotrophin-1 (CTF1) mRNA
858 Ovary	0.1987522		2 0.313982		1036 : 01	
859 Ovary	0.1985444		1		1893 at	.178956791 21893 at Floring Sapiens retinoic acid-inducible endogenous retroviral DNA
860 Ovary	0.4000007				RC AA4546	EST: x76a07 s1 Society Cottansporting polypeptide
861 Ovany	0.130230		0	0.17885178	<u></u>	
862 Ovary	0.1962101				3629 at	CDH3 Cadharin 3 (D codh)
SOE CVAILY	0.1960929	9 0.3785956	0.31376		5610 at	COL4A2 Colladen Ivne IV aleks 2
863 Ovary	0.1979989	9 0.3785528	0.313759	0.17862225	HG862- HT862 c at	T
864 Ovarv	0.4070040				A28	EST: 202006 st NCI COAP CORT II.
o company	0.137.0046	0.3785414	0.313739	0.17861186	at	IMAGE:711994 3: mRNA seritore (from Contact)
865 Ovary	0.1977714	4 0.3784512	0.31369	0.17850742 X13444	444 21	T-CELL SURFACE GLYCOPROTEIN CD8 BETA.3 CHAIN
866 Ovary	0.1974371	0.378/33		1		Fragile X locus M2C containing an unidentified once reading an
867 Ovary	0.197321			0.17848812 M16282	at	end
				U.11643/ M/3489	ja,	Heat-stable enterotoxin receptor mRNA
868 Ovary	0.1972371	0.3782725	0.313624	AA2	06625_a	AA206625_a EST: zq56d06.r1 Stratagene neuroepithelium (#937231) Homo
86al Ovani		1			HG3994-	sapiens cDNA clone 645611 5', mRNA sequence. (from Genbank)
oos Oval y	0.19/1943	0.3782334	0.313624	0.17825852 HT4264	,ਰਜ	Cpg-Enriched Dna, Clone S16
870 Ovary	0.1971036	0.3781698	0.313624	0.17821059 H79230	te	EST: yu27e05.r1 Homo sapiens cDNA clone 235040 5'. (from Genhank)
871 Ovary	0.1969368	0.3780294	0.313487	0.17808999 T83397	ta	Homo sapiens peroxisomal phytanoyl-CoA alpha-hydroxylase (PAHX)
872 Ovary	0.1966432	0.3779567	0.313437	0.17807466[446740	1	LGALS3 Lectin, galactoside-binding, soluble, 3 (galectin 3) (NOTF
				HG2197-	\neg	redefinition of symbol)
873 Ovary	0.1965922	0.3779428	0.313348	0.17794518II	S	Allowed Township Att 1
or 4 Ovary	0.1965641	0.3777723	0.313284	0.17785382 J00146 at		DHFRP1 Dihydrofolale reductase neguidance 4
875 Ovary	0.1964848	0.3777543	0.31328	0.17782108 t	C16161_s_a E	EST: Human aorta cDNA 5'-end GEN-234B03, mRNA sequence.
876 Ovary	0.1963598	0.3776805	0.313262	0.17770942 HT174 at		
				11 111	7	Desiriopiakin i

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FIG. 10J2

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877 Ovarv	0.1962343	0.3776398	0.313242	X 0.17761466	X99393_s_a t	CMKBR5 gene, non-functional mutant
878 Ovarv	0.1961761	1	0.313099	0.17759982 t	A076003_a	AA076003_a Zm89c09.r1 Stratagene ovarian cancer (#937219) Homo sapiens t
879 Ovary	0.1961386	1	0.313096	0.17754743 Z28339_at		Delta 4-3-oxosteroid 5 beta-reductase
880 Ovary	0.1956929	0.3774835	0.312813	X52150 0.1773755 1 s at	X52150_rna 1 s_at	Arylsulfatase A
				X	s a	
881 Ovary	0.1956315		0.312769	0.177321021		ANK1 Ankyrin 1, erythrocyfic
882 Ovary	0.1955971	0.3772588	0.31268	0.1772554 D83779 at		KIAA0195 gene
883 Ovary	0.1955952	0.3770583	0.312657	RC_A 0.17720369 75 at	A5989	EST: ae40c09.s1 Gessler Wilms tumor Homo sapiens cDNA clone 898288 3', mRNA sequence. (from Genbank)
884 Ovary	0.1952489	0.3769278	0.312598	0.17714316 D83778	383778 at	KIAA0194 gene, partial cds
885 Ovarv	0.195103	0.3769049	0.312571	HG4167 0.1770328 HT4437	HG4167- HT4437 at	Nuclear Factor 1, A Type
886 Ovarv	0.1947902		0.312467	0.17698736 33_at	A4062	EST: zv10e07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753252 3. mRNA sequence. (from Genbank)
887 Ovarv	0.1947533		0.312342	0.17690822 U07151	J07151 at	GTP binding protein (ARL3) mRNA
888 Ovary	0 1946614	0.1946614 0.3765677	0.312274	1 1 1 1 1 1 1 1	HG3412- HT3593_s_a t .	Blue Cone Photoreceptor Pigment
889 Ovary	0.1946374	0.1946374 0.3765479	0.312182	0.17677781 M31932 at	M31932 at	FCGR2A Fc fragment of IgG, low affinity Ila, receptor for (CD32)
	_				4A262132 a	EST: zs23b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686011 5' similar to SW:YIHI6_YEAST P32793 AA262132 a HYPOTHETICAL 41.8 KD PROTEIN IN SPO13-ARG4 INTERGENIC
890 Ovary	0.1945941	0.3764178	0.312151	0.1767181 t	1	REGION:;, mRNA sequence. (from Genbank)
891 Ovary	0.1943887	0.376358	0.312022	0.17657585 \\ Y00815_	Y00815_at	PTPRF Protein tyrosine phosphatase, receptor type, f polypeptide
892 Ovary	0.1943494	0.3763244	0.311752	0.17652713 X81892	X81892_at	HE6 Tm7 receptor
893 Ovary	0.1941002	0.376241	0.311736	0.17650083	AA252752_a t	EST: zs26b10.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:686299 5', mRNA sequence. (from Genbank)
894 Ovary	0.1940012	0.3762325	0.311662	0.17634219 J03258 at	J03258 at	VDR Vitamin D (1,25- dihydroxyvitamin D3) receptor
895 Ovary	0.1939615	0.3762209	0.311659	V0053E 0.17627579 2 s at	V00535_ma 2 s at	Interferon beta 1 gene extracted from Gene for human fibroblast interferon beta 1
896 Ovary	0.1935352	2 0.3761881	0.311643	0.17620535 X85106_at	X85106_at	Ribosomal S6 kinase
897 Ovary	0.1932634	4 0.3757755	0.311151	0.17616215 U62325_al	U62325 at	FE65-like protein (hFE65L) mRNA, partial cds
898 Ovary	0.193139	9 0.3754952	0.311083	0.17610224 L41607	L41607_at	GCNT2 Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
899 Ovary	0.1930834	4 0.3754535		0.17605074 U46023	U46023_at	Xq28 mRNA
900 Ovary	0.1929601	1 0.3753222	0.310989	0.17593881 Y13620	Y13620 at	BCL9 gene

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							her that their takes that the takes that
901 Ovary	ary	0.1926704	0.1926704 0.3753078	0.310983	0.17590858 U09303 at		Placenta LERK-2 (EPLG2) mRNA
					M68	516_ma	PCI gene (plasminogen activator inhibitor 3) extracted from Human
902 Ovary	ary	0.1925829	0.3752275	0.310757	0.17588069 1_at		protein C inhibitor gene
						-	EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1
903 Ovary	ary	0.1923133	0.3752243	0.310733	0.17572318 M57730	at	PRECURSOR
904 Ovary	ary	0.1923027	0.3751989	0.310709	0.17563832 X03635_at		ESR Estrogen receptor
905 Ovary	ary	0.1921478	0.3751304	0.310638	0.17561139 038548	,at	KIAA0076 gene
906 Ovary	ary	0.1921162	0.3749445	0.310588	0.17551304 X72964	at	CALT Caltractin (20kD calcium-binding protein)
907 Ovary	ary	0.1920067	0.3749433	0.310403	0.17545338 L05188	fat	Small proline-rich protein 2 (SPRR2B) gene
					X82	X82279_s_a	
908 Ovary	ary	0.1917377	0.3749367	0.310385	0.17530051 t		Fas, Apo-1 gene (promoter and exon I)
909 Ovary	ary	0.1917295	0.3748834	0,310373	0.1752377 L11369 at		Protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8
					RC	A0132	EST; ze28h05.s1 Soares retina N2b4HR Homo sapiens cDNA clone
910 Ovary	ary	0.1914227		0.310298	0.17521891 31_at	भ	360345 3', mRNA sequence. (from Genbank)
911 Ovary	ary	0.1913304	- 1	0.310269	0.17518118 X69878	878_at	FLT4 Fms-related tyrosine kinase 4
912 Ovary	ary	0.1913173	0.3746395	0.310087	0.17513362 M21305	305_at	Alpha satellite and satellite 3 junction DNA sequence
913 Ovary	ary	0.1910931	0.3745894	0.31002	0.1750784 U66083	ਬ	MAGE-9 antigen (MAGE9) gene
914 Ovary	ary	0.1907415	0.3745084	0.309991	0.17494902 M37190	7190_at	Ras inhibitor mRNA, 3' end
					015	U15642_s_a	
915 Ovary	ary	0.1907338	0.3743423	0.309921	0.174903271		E2F5 E2F transcription factor 5, p130-binding
25	2	0.4000044		707000	HG	1	
910 Ovary	ary	0.1900041		0.309797	0.17484218 1114001	T	Immunogiobulin Heavy Chain, Vojrc Regions (GD:L23566)
917 Ovary	ary	0.1906285	0.3741354	0.309763	0.17475237 D31766_at	766_at	PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE
							EST: zt22h02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
					0	200644 70	COTEDANICACIONES DEL ATED DECATEMINA COMICACO (From
918 Ovarv	arv	0.190567	0.3740816	0.309617	0 17469741 45 at	10874	GOT RAIVOT ON LER-RELATED TROTEIN, HINNY Sequence. (1911)
919 Ovary	ary	0.190565	1	0.309561	0.17465876 D26129	1729 at	RNS1 Ribonuclease A (pancreatic)
920 Ovary	ary	0.1904499	0.3738669	0.309505	0.17461519 M17754 at	754 at	BN51T BN51 (BHK21) temperature sensitivity complementing
200		7004400		00000			
32100	Ovaly	0.1304400	0.3/3/41	0.309338	0.17453624 KUC	629 r at	0.17453624 K00529 T at Human kpni repeat mma (cdna cione pcd-kpni-4), 3 end
000	į	0 4004666		100000	HG.	HG3566-	
Sec Ovaly	aly	0.1301000	1	0.303334	U.1744245 H13769	sroy at	Zinc Finger Protein (50:M88339)
923 Ovary	ary	0.190132	0.3735214	0.309205	0.17437154 X95191	191 at	Delta-sarcoglycan
924 Ovary	ary	0.1901048	0.3734771		0.17433326 U06088_at	3088_at	N-ACETYLGALACTOSAMINE-6-SULFATASE PRECURSOR
925 Ovary	ary	0.1900652		ļ	0.17425455 U79242)242_at	Clone 23560 mRNA sequence
926 Ovary	ary	0.1896956	0.3734359	0.309031	0.17418864 X90568_at	1568 at	TTN Titin

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				THE TANK IN THE MICE. II	The state of the s
	,				3-beta-hydroxysteroid dehydrogenase gene extracted from Human
•	1			M77144_ma	M77144 _ma type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta
927 Ovary	0.1896563	0.373349	0.309003	0.17410888 1_at	isomerase gene
				X14008_ma	
928 Ovary	0.1896153	0.3733118	0.308968	0.17403305 1 f_at =	Lysozyme gene (EC 3.2.1.17)
929 Ovary	0.1895359	0.3731683	0.308892	0.17398849 L27080_at	Melanocortin 5 receptor (MC5R) gene
				RC_AA4300	EST: zw65e11.s1 Soares testis NHT Homo sapiens cDNA clone
930 Ovary	0.1895244	0.3731147	0.308891	0.17391339 26_at	781100 3', mRNA sequence. (from Genbank)
931 Ovary	0.189448	0.3730601	0.308862	0.17384143 M85165 at	ELK4 ELK4, ETS-domain protein (SRF accessory protein 1) NOTE: Symbol and name provisional
				M95585 s a	The contract of the contract o
932 Ovary	0.1893279	0.3729532	0.308752	0.17381038 t	HI.F Hepatic leukemia factor
933 Ovary	0.1893212	0.1893212 0.3729438	0.308701	0.17378779 U41515_at	Deleted in split hand/split foot 1 (DSS1) mRNA
Č	7.4.000 G F O		10000	U31120_rna	Vot 10 of 1.1
934 Ovary	0.1889277	- 1	0.308527	0.173687 1 at	Interleukin-13 (IL-13) precursor gene
935 Ovary	0.1887721	0.3729209	0.308491	0.17358208 U72209_at	YY1-associated factor 2 (YAF2) mRNA
				X06700_s_a	
936 Ovary	0.1884949	0.3728914	0.308382	0.173521131	COL3A1 Alpha-1 type 3 collagen
937 Ovary	0.1884324		0.308356	0.17340389 U21049 at	DD96 mRNA
938 Ovary	0.1883637	0.3727579	0.308327	0.17334872 L13210_at	Mac-2 binding protein mRNA
939 Ovarv	0.1883624	0.3727554	0.308248	RC_AA2905 0.17326896 99_at	EST: zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE-700416.3* mRNA sequence (from Genhank)
	and the second s			HG1140-	
				HT4817_s_a	
940 Ovary	0.188347	0.372631	0.308168	0.17321515	Collagen, Type Vi, Alpha 2, Alt. Splice 2
				AA402971_s	
941 Ovary	0.1883355	0.3726174	0.308155	0.1731141 at	Homo sapiens mRNA for serine protease (TLSP), complete cds
				D13720_s_a	
942 Ovary	0.1882888	- 1		0.17308483 t	TYROSINE-PROTEIN KINASE ITK/TSK
943 Ovary	0.1882583		0.307962	0.17305243 U30313_at	Diadenosine tetraphosphatase mRNA
944 Ovary	0.1882418	0.3720534	0.30796	0.17299137 U17894_at	Alpha(1,2)fucosyltransferase
				AF004709_a	
945 Ovary	0.1880472	0.3720158	-	0.172919631	Protein kinase mitogen- activated 13
946 Ovary	0.1879802			0.1728786 U34976 at	Gamma-sarcoglycan mRNA
947 Ovary	0.1876881	0.3719514	0.307498	0.17278095 U46461_at	Dishevelled homolog (DVL) mRNA

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969 Ovary 0.1857371 970 Ovary 0.1856695 972 Ovary 0.18566064 973 Ovary 0.1853963 974 Ovary 0.1853963 975 Ovary 0.1853963 976 Ovary 0.1853019 977 Ovary 0.1853019 978 Ovary 0.1853019 979 Ovary 0.1853085 980 Ovary 0.1850845 981 Ovary 0.1848842 982 Ovary 0.1848842 984 Ovary 0.1848841 985 Ovary 0.1848841 986 Ovary 0.1848841 987 Ovary 0.1848841 986 Ovary 0.1848842 987 Ovary 0.1846284 988 Ovary 0.1846284 989 Ovary 0.1846284 989 Ovary 0.1845043 989 Ovary 0.184469 980 Ovary 0.1845043	371 0.3706249 223 0.370395 695 0.3703745 064 0.3703034 401 0.3702684 401 0.370245 302 0.3701245 302 0.3701243 119 0.3699404	49 0.306371 45 0.30618 445 0.305967 84 0.305967 45 0.305493 43 0.305478 72 0.305441	RC_AA243 0.17139001 58 at 0.17137764 W26652 at RC_AA135 0.1712809 85 at 0.17122948 U11701 at 0.17122948 U11701 at	AA2430 at 6652 at	AA2430 EST: zr24h08.s1 Stratagene NT2 neuronal precursor 937230 Homo at sapiens cDNA clone 664383 3', mRNA sequence. (from Genbank)
	000 000	0 0 0 0	0.17137764 W26 0.1712809 85 0.17122948 U11 0.1712527 U75	at	(MIDOLINO)
		0 0 0 0	0.1712809 85 c 0.17122948 U11 0.17115727 U75		EST: 34c6 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genhank)
		0 0 0 0	0.17122948 U11	A1351	EST: zo27a05.s1 Stratagene colon (#937204) Homo sapiens cDNA
			0.17115727 U75	1	I'M homodex domain and the first Service (If On Genbank)
		0 0 0		at	Isopeptidase T-3 (ISOT-3) mRNA
		0 0 0	HG4	1.	
			HT4:	HT4333_s_a	Transacintion Fraction 1165 0
			0.17100959 D16469 at		ORF. Xa terminal nortion
			AF0(10.	
	1 1 1		0.17096443 t		Estrogen receptor-binding fragment-associated gene 9
			HG2850-		Civile 23346 HIRINA Sequence
		٥	HT48	s l	7. C. C. C. C. C. C. C. C. C. C. C. C. C.
		0.	0.17083211 X12453	₩	blidly diycoprotein, Ait. Splice 5, A S-ARRESTIN
	85 0.3698041	11 0.305344	0.1707683 (210770)	1	EST: yf36a08.r1 Homo sapiens cDNA clone 128918 5'. (from
	1 1		0.1706713 M74297	Ť	GGIDBIIN) HOXA4 Homeo hox A4
			X514	sa	the Von Coulon in the Coulon i
	0.369603	0.305179	0.17061892 t		SERUM AMYLOID A PROTEIN PRECURSOR
	42 0.3696023	3 0 305136	0 47054044 045404		Human fetal brain cDNA 5'-end GEN-140D09, mRNA sequence.
			0.17051065.103634	7 T	(nom Genbank) INHBA Inhibit hata A (califor A califor And 11)
			RC_	A6090	EST: af10f08.s1 Soares testis NHT Homo saniens cDNA clone
	91 0.3694773		0.17043974 53 at		1031271 3', mRNA sequence, (from Genbank)
			0.17036076 U25750	ä,	Chromosome 17q21 mRNA clone 1046;1-1
	1		0.17033893 X64643	äţ,	C6.1A PROTEIN
	43 0.3093574 69 0 3602077	7 0.304959	0.17028628 X06825	at	Skeletal beta-tropornyosin
_			0.170168361.14817338	कं क	RFC2 Replication factor C (activator 1) 2, 40kD subunit
	_	1.	X544	Tha	ייטיר ואינוויטעומאנטוומאווא ו (ף ועו)
			0.17003818 1_at	1	Melanoma growth stimulatory activity (MGSA)
1	0	j	0.16992377 D10656 at		CRK V-crk avian sarcoma virus CT10 oncodene homolog
993 Ovary 0.1841096	96 0.368921	1 0.304749	0.16984268 D28364_at		Annexin II, 5'UTR (sequence from the 5'can to the start codon)

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					EST: aa59c02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
				AA504384_a	AA504384_a IMAGE:825218 5' similar to contains element MIR repetitive element;,
994 Ovarv	0.1840693	0.3688842	0.304749	3,1840693 0.3688842 0.304749 0.169748161	mRNA sequence. (from Genbank)
995 Ovarv	0.1839207	1.1839207 0.3688733 0.304582	0.304582	0.16971926 U45982 at	0.16971926 U45982_at G protein-coupled receptor GPR-9-6 gene
996 Ovary	0.1838374	0.3687535	0.304525	0.16964038 X70811_at	0.1838374 0.3687535 0.304525 0.16964038 X70811 at ADRB3 Adrenergic, beta-3-, receptor
997 Ovary	0.1837558	0.1837558 0.3687232 0.304496	0.304496	0.1696318 M58583 at	0.1696318 M58583_at CEREBELLIN 1 PRECURSOR
998 Ovary	0.1837549	0.1837549 0.3686511 0.304458	0.304458	1	0.16958816 X72841_at Retinoblastoma-binding protein (RbAp46) mRNA
999 Ovary	0.1836975	0.1836975 0.3686487 0.304438	0.304438	0.1695004 S82592_at Evi-1	Evi-1
				U64315_s_a	•
000 Ovary	0.1834772	0.3686337	0.304397	0.1834772 0.3686337 0.304397 0.16941014	XPF Xeroderma pigmentosum, complementation group F

FIG 10P2

0.9278966 0.7129607	<u> </u>	0.625972	0.46574747	X51698_s_a	
0.1 12,0001 0.02,0312	0.020912		1 /1 /1 /60		SPASMOLY HC POLYPEPTIDE PRECURSOR
0.7787252 0.6661443 0.579693 0	0.579693		.4348104 J	0.4348104 J00268 s at INS Insulin	INS Insulin
0.6587432 0.6388133 0.556793 0.4	0.556793	0.4	0.41948733 J05412_at	05412_at	REG1A Regenerating islet-derived 1 alpha (pancreatic stone protein, pancreatic thread protein)
0.6290712 0.6197183 0.543397 0.	0.543397	0	0.40783224 X52003_at	52003 <u>a</u> t	TFF1 Trefoil factor 1 (breast cancer, estrogen-inducible sequence expressed in)
0.6119224 0.534312	0.534312	0	.39945528 Z	48314 s at	0.39945528 Z48314 s at MUC5B Mucin 5, subtype B. tracheohronchial
0.5983197 0.6003079 0.528163	0.528163		0.3925389 U31449 at	31449 at	Intestinal and liver tetraspan membrane protein (il-TMP) mRNA
0.5949147 0.521431	0.521431		0.3871077	05036_s_at	0.3871077 J05036_s_at CTSE Cathepsin E
0.5958913 0.5919794 0.514464 0	0.514464 0	0	0.38182062 M84424_at	184424 at	CATHEPSIN E PRECURSOR
0.5700184 0.5832725 0.509603 0.5	0.509603	0	0.37752536	AA372630_s _at	Homo sapiens GW112 protein (GW112) mRNA, complete cds
0.5565532 0.5786274 0.505425 0.3	0.505425	0,3	37383676 JC	04813_s_at	0.37383676 J04813_s_at Cytochrome P450, subfamily IIIA (niphedipine oxidase), polypeptide 5
0.5406267 0.5773224 0.501868 0	0.501868	0	RC_AA. 0.3697819 51_f_at	C_AA2623 1_f_at	RC_AA2623 EST: zr44g03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 51 f_at 666292 3', mRNA sequence. (from Genbank)
				AB006781_s	
0.5728496 0.50052	0.50052	0	0.36606857	at	Galectin-4
0.5711106			0.363105 L08010 at		Regenerating protein I beta
0.5348939 0.5670255 0.492834 0.	0.492834	0	0.36071837 M24400	Ħ,	CTRB1 Chymotrypsinogen B1
0.5152407 0.5668822 0.49035			U3120 0.3580921 2_s_at	spo_l	Laminin gamma2 chain gene (LAMC2)
0.5134798 0.5623378 0.487834 0.	0.487834	0.	35570014 D	83847_f_at	0.35570014 D83847_f_at ELASTASE IIIB PRECURSOR
0.5104177 0.5595179 0.485651 0	0.485651	0	.35347328 M	22612 f at	0.35347328 M22612 f at PRSS1 Protease, serine, 1 (trypsin 1)

FIG. 11,

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The state of the s	0.35122478 K01396_at PI Protease inhibitor 1 (anti-elastase), alpha-1-antitrypsin	0.34885228 M27602 f at Protease serine 2 (frynsin 2)	0.3466433 M16653 at Pancreatic elastase IIB mRNA	TO THE WEATON A STATE OF THE ST	 	0.3431327 L32137_at COMP Cartilage oligomeric matrix protein	at		1T2906_s_a		0.33800283 JUS 125 at PNLIP Pancreatic lipase	a	0.33502817 U21128 at LUM Lumican	a	0.33354896 t Phospholipase A2, group IB (pancreas)	0.3323119 at Pancreatits_associated protein (DAD) and	X67318 at	te	a t		σ,	0.32453454 L22524 s at MATRILYSIN PRECURSOR	X90579_s_a	0.32330972lt H.sapiens DNA for cyp related pseudogene	at	 HT3616_s_a	02883 at	1357		0.318234 Z71389_at Skin-antimicrobial-peptide 1 (SAP1)	0.31721777 J05068_at TCN1 Transcobalamin I	0.3164184 S75256_s at Partial, 534 nt]
	481914 0.35	0.480139 0.34	0.478336 0.3	0.47639			0.473367 0.3	duo•		0.47 1479 0.33			0.465752 0.33		0.465018 0.333	0.463772 0.33		0.461915 0.328		59889 0.3	.45902 0.328	.45802 0.324			0.455625 0.322	0.453677 0.32			0.452509 0.31		0.450535 0.317	
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	0.559412	0.5581134	0.5550363	0.5535024	i i	- 1	0.5494857		0 5476469		- 1		0.5427789		0.5414159	0.5404347	0.5398616	0.5381253	0.5380885	0.5371567	0.5359932	0.5328612	0	0.5319334	0.531292	0.5302596	0.5292271		0.5274373	0.5254321	0.5250532	0.5236372
	0.5086832 0.5594127	0.5085123	0.5063022	0 5047094	00000000	0.5045138	0.5037171		0 5036004	0.5050034	CtCtCCC's	0.497818	0.4964372		0.4941935	0.4880559	0.485838	0.4848106	0.4799522	0.4793133	0.4768606	0.4708147	0,000,000	0.4000343	0.4678389	0.4635845	0.4605548		0.4553431	- 1	0.451321	0.4501483
	18 Pancreas	19 Pancreas	20 Pancreas	21 Pancreas	22 Dangrage	railcieas	23 Pancreas		24 Pancreae	25 Pancreas	200	26 Pancreas	27 Pancreas		28 Pancreas	29 Pancreas	30 Pancreas	31 Pancreas	32 Pancreas	33 Pancreas	Pancreas	35 Pancreas	26 Donouge	a ICI eas	3/ Fancreas	38 Pancreas	39 Pancreas		40 Pancreas	41 Pancreas	42 Pancreas	43 Pancreas
	18	19	20	2	00	777	23		176	25.1	1	261	27		28	29 [301	311	321	33 }	34 F	35 F	200	200	3/1	38 F	39 F		40 F	415	42 F	43 P

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The state of the s	C7 Complement company 7	ĺ	t l De co Brita l'ansforming growth factor beta binding protein 1	=	FEST: zx07e10.s1 Soares Intal fetus Nh2HE8 Out Long	clone 785802 3', mRNA sequence, (from Genhank)	FST: zx77c10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	-	IGFBP4 Insulin-like growth factor-binding profein 4	Ataxia-telangiectasia group D-associated protein mRNA		CYP3A7 Cytochrome P450 IIIA7 (PA50 LIE)		EST: zb26f06 r1 Sparse fatal ling NEU1 4000 11	clone 303203 5', mRNA sequence (from Ganhank)	AA314779 a EST: EST186601 Colon carcinoma (HCC) cell line II Homo sapiens	CONTROL OF THE NAME OF THE SECTION O	Laminin S B3 chain (1 AMB3) cons	Somatostatin I dene and flanks	SPINK1 Serine professe inhibitor 1/214.		Glone 588057 3', mRNA sequence. (from Genbank)	DEINE HIKNA, partial cds	Mucin 5, subtype B, tracheobronchia	PI5 Protease inhibitor 5 (maspin)	Pancreatic lipase related protein 2 (PLRP2) mRNA EST: 7/18h/n6 < 1 Society Protein 1 (PLRP2) mRNA	cDNA clone 502331 3', mRNA sequence. (from Genbank)
The state of the s	0.31540367 J03507 at	0.31452382 M34057 at	11 X71345 F	0.31310672 Y00757 at	RC_AA4497	0.31222358 49 at	RC_AA4547 0.31143254 33 s at	S	1 4	0.3097.360 L24203 at	D00408 s a		M16652_s_a		0.30695662 W20514 at		U17760 ma	11_at	0.30490136 J00306 at	0.30435598 Y00705 at	RC_AA1349	117077 at	U06711_s_a	1	0.30104077 U04313 at	A1567	
				0						0.3097.30	1100000	0.30840552	0.3075618		0.3069566	0.3063722	The second secon	0.30575418 1 at	0.30490136	0.30435598	RC A	0.3030284 [117077		0.3023557	0.30104077	0.00004004	0.30048516 92 at
		0.447189	0.446309	0.445197		0.444231	0.443862	0.443330	0 44			0.44059	0.439691		0.438925	0.438508		0.438022	0.437687	0.437068	0.436298	0.435287	0.494000	0.434372	0.433536		0.432771
	0.4495522 0.5234609		0.5185894			0.5168417	0.5161458	0.5160719		0.5150696	í	0.0140320	0.5124851	0.421436 0.5424607	0.0121027	0.5115693	1	0.5108511	0.510508/	0.0101459	0.5096456	0.5091632	0.5087509	0.5084084	0.507421	1000	75/2000:0
0 440 1100	0.449552	0.448858	0.4431819	0.4355238	0.4347070	0.10.140.10	0.4306283	0.4301526	0.4244237	0.4240417	0.4239698	0.1200030	0.4231774	0.421436	21.20	0.4210104	0.4469404		0.407.9030			0.3999345	0.3993665	0.3954412	1	3803445	0.5055445 0.5065/3/
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Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. each arm pens gam seen pens pens men, arm a term trong and a term to a term of the second and th

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66 Pancreas	0.3875845	0.3875845 0.5065606	0.431797	U66061_cds	TRY8 gene (trypsinogen E) extracted from Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV29S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY6, TRY6, TRY7, TRY8, TCRBD1, TCRBV1S1, TCRBJ1S3, TCRBJ1S4, TCRBJ1S5, TCRBJ1S1, TCRBJ1S5, TCRBJ1S6, TCRBJ2S1, TCRBJ2S2, TCRBJ2S3, TCRBJ2S4, TCRBJ2S5, TCRBJ2S6, TCRBJ2S7, TCRBC2, TCRBV20S1A1N2 genes from bases 452324 to 684973 (section 3 of 3)
67 Pancreas	0.3849158		0.431333	1708	HSD17B2 17 beta hydroxysteroid dehydrogenase, type 2
00 rainteas	0.3840338	0.5055683	0.430483	0.2988619 M16652 at	ELA1 Elastase 1, pancreatic (elastase IIA)
69 Pancreas	0.3835028	0.5052698	0.43013	HG371- HT26388_s_ 0.29827955 at	Mucin 1, Epithelial, Alt. Splice 9
70 Pancreas	0.3828116	1	0.429693	0.29767913 19 s at	Non-specific cross reacting antigen
71 Pancreas	0.3811176	0.5033779	0.428787	0.29708844 D90097_at	ALPHA-AMYLASE 2B PRECURSOR
72 Pancreas	0.380816	0.5026341	0.428532	S71043_rna 0.29656819 1_s_at	lg alpha 2=immunoglobulin A heavy chain allotype 2 {constant region, germ line} fhuman, peripheral blood neutrophils. Genomic, 1799 nt
/3 Pancreas	0.3807718	0.5024124	0.427945	0.29608276 M11718 at	COL5A2 Collagen, type V, alpha
/4 Pancreas	0.3780765	0.5023708	0.427088	0.2956553 M14949 at	RAS-RELATED PROTEIN R-RAS
/b Pancreas	0.3758304	0.5020343	0.426697	0.29510015 M11321 at	GC Group-specific component (vitamin D binding protein)
76 Pancreas	0.3743256	0.5015573	0.426078	U27333_s_a 0.2946248 t	Alpha-1,3 fucosyltransferase 6 (FCT3A) mRNA
77 Pancreas	0.3729319	0.5015123	0.42574	0.29379228 68 at	EST: zw51f07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773605 3', mRNA sequence, (from Genhank)
78 Pancreas	0.3725418	0 5000542	0.474760	X06700_s_a	(unperior mark) househouse
79 Pancreas	0.3715697	- 1	0.424700	0.29330301	COL3A1 Apha-1 type 3 collagen
80 Pancreas	0.3690722		0.424136	0.2550001 ZZ4660 at	Galp gene mKNA
81 Pancreas	0.3669019		0.4241	0.2921337 L27560 at	Ends Endogrin (Osler-Rendu-Weber syndrome 1) Insulin-like growth factor binding protein 5 (ICEBDS) = DNA
82 Pancreas	0.3668293	0.4991988	0.423788	0.29161403 M35252 at	TUMOR-ASSOCIATED ANTIGEN CO-029
83 Pancreas	0.3665817	0.497894	0.42304	X60382_rna 0.29106683.1_at	COI 10A1 gene for collagen (alpha_1 tyme X)
84 Pancreas	0.3663838	0.4977385	0.422691	0.29063255 J02611 at	APOD Apolipoprotein D
85 Pancreas	0.3642896	0.4976251	0.422397	M55998_s_a 0.29017088 t	Alpha-1 collagen type I gene, 3' end
86 Pancreas	0.3641634	0.4971929	0.422094	0.2898828 X82153_at	CATHEPSIN K PRECURSOR
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as 0.353644 0.4971874 0.421636 ass 0.3590803 0.4970192 0.420811 ass 0.3562413 0.495301 0.420813 ass 0.3562413 0.495301 0.419768 as 0.3562031 0.4957914 0.419768 as 0.3528661 0.4926478 0.418744 as 0.3528661 0.4922782 0.418744 as 0.3520236 0.4923139 0.418702 as 0.3528661 0.4926478 0.417717 as 0.3528684 0.4910463 0.4177777 as 0.342884 0.4910463 0.415035 as 0.342987 0.4906896 0.415035 as 0.342989 0.4893701 0.415035 a 0.340963 0.4893701 0.412655 a 0.3387594 0.4888622 0.414265 a 0.3388856 0.4885137 0.412887 a 0.3288856 0.48879515 0.412556 a 0.3278747 0.4877526 0.412794 a 0.3278788 0.4877526 0.412794 a 0.3278188 0.4877563 0.41774	W. Tank Same of Control of Control	RC_A	0.28880373 K0302	0.28827852 X68314 at	0.28785974 U78556	AD000 0.28751352 ds1_at	0.2870863 142464	0.28664374 X5492F	0.28630418 U19977	0.28595534 M8105, 0.28537646 0.1406	M15517	U.284984 5_at	0.28457248 X04412	RC AA4518	0.2030/0/8 // at	***	AA4650) 283444EE 1000-0	7.28275925 M85290	0.2823444 [166674	353	2.40195548 at	.28170332 J05582 s	0.2811877 X53331	.2008/282 582198	.28060302 M61853	0.280084 2	27966347 \00565 <
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28			0.359080	0.356241	0.356203	0.3551772	0.3548342	0.3528661	0.3520485	0.3520236	0.3478723	0.3429684	0.3424987	0.3411254					, ,	ı		l	- 1	- 1	1		ł	
		87 Pancreas	88 Pancreas	S - C - C - C - C - C - C - C - C - C -	90 Pancreas	91 Pancreas	92 Pancreas	94 Pancreas	95 Pancreas	96 Pancreas	97 Pancreas	98 Pancreas	99 Pancreas	100 Pancreas			_	1	\dashv	+	105 Pancreas		+-	1-1			110 Pancreas 0	111 Pancreas 0

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0.2729665 M34516_r_at Omega light chain protein 14.1 (Ig lambda chain related) gene, exon 3 EST: zf65e11.r1 Soares retina N2b4HR Homo sapiens cDNA clone EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence. C01409_s_a EST: HUMGS0008391, Human Gene Signature, 3'-directed cDNA Homo sapiens secretory mucin MUC6 (MUC6) mRNA, partial cds 0.27870932 U78551_at-2 Homo sapiens gallbladder mucin MUC5B mRNA, partial cds ADH1 Alcohol dehydrogenase 1 (class I), alpha polypeptide PRELP Proline arginine-rich end leucine-rich repeat protein PTGIR Prostaglandin 12 (prostacyclin) receptor (IP) 0.27198407 L27559_s_at IGFBP5 Insulin-like growth factor binding protein 5 C1S Complement component 1, s subcomponent Gallbladder mucin MUC5B mRNA, partial cds 381836 5', mRNA sequence. (from Genbank) Low-Mr GTP-binding protein (RAB31) mRNA sequence, mRNA sequence. (from Genbank) Putative OSP like protein mRNA, partial cds Tryptophan oxygenase (TDO) mRNA Na,K-ATPase beta-1 subunit mRNA C1R Complement component C1r 0.2757695|Z74616_s_at|COL1A2 Collagen, type I, alpha-2 ITGB4 Integrin beta-4 subunit SERUM PROTEIN MSE55 THBS4 Thrombospondin 4 THBS2 Thrombospondin 2 F5 Coagulation factor V (from Genbank) IPL (IPL) mRNA FBLN2 Fibulin 2 Tg737 mRNA RGP3 mRNA Lrp mRNA 0.2782639 U78551 at 0.2780548 M88338 at AF001294_a U59877 s a 0.27374786 X82494 at F AA059327_i 0.27659935 M14058 at 0.27942872|X79882 at 0.27907494 D31294_at U16799_s_a 0.27550986 M16967_at M12963_s_a 0.27523875|X53587_at 0.27504593 Z19585_at 0.27472496 U20362_at 0.27424577|U27655_at 0.27444765|L12350_at 0.27250776 J04080_at 0.27167347 U41344 at 0.2713921 U89916_at 0.27114147 U32989 at 0.27083558 U97698 at ä 0.27699953|t0.27633497|t 0.27776566 0.27745736 0.27397862 0.27216664 0.3274485 | 0.4861364 | 0.410985 0.410523 0.410112 0.409909 0.4086350.409570.409530.409257 0.407868 0.407673 0.408297 0.407351 0.406636 0.405915 0.406177 0.405457 0.406607 0.40554 0.40506 0.404705 0.404395 0.403966 0.403486 0.402715 0.403724 0.402063 0.402501 0.40165 0.3261286 | 0.4857553 0.322083 0.4849784 0.322083 0.4853031 0.48354 0.3215038 0.4839324 0.3203934 | 0.4838944 0.3198348 | 0.4838789 0.482961 0.3193275 | 0.4826955 | 0.316809 | 0.4823362 0.3118338 0.4794049 0.314764 0.4809273 0.3121455 0.4805009 0.3120098 0.4799707 0.311305 0.4789395 0.3101831 | 0.4781972 0.3067206 | 0.4776905 0.3112249 0.4785829 0.3084479 0.4776994 0.477582 0.3053519 | 0.4769051 0.3050191 | 0.4764769 0.3087581 0.4779261 0.2989849 0.4763989 0.2967506 0.4755846 0.2928493 0.4748476 0.2932977 0.4755001 0.3197726 0.3194833 0.3059252112 Pancreas 113 Pancreas 114|Pancreas 115 Pancreas 116 Pancreas 117|Pancreas 118|Pancreas 120 Pancreas 119|Pancreas 121|Pancreas 124 Pancreas 122|Pancreas 123 Pancreas 125 Pancreas 133 Pancreas 126 Pancreas 128 Pancreas 132/Pancreas 127 Pancreas 129|Pancreas 130 Pancreas 131 Pancreas 134 Pancreas 135|Pancreas 136 Pancreas 137 Pancreas 138 Pancreas 139 Pancreas

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. RC_AA4914 | EST: ab04a05.s1 Stratagene fetal retina 937202 Homo sapiens cDNA ABP1 Amiloride binding protein 1 (amine oxidase (copper-containing)) AA452428_a EST: zx15g01.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA O.27024934 32 at clone 740189 3', mRNA sequence. (from Genbank) ITGA2 Integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) Thyroid receptor interactor (TRIP10) mRNA, 3' end of cds VTN Vitronectin (serum spreading factor, somatomedin B, GLUL Glutamate-ammonia ligase (glutamine synthase) done 740189 3', mRNA sequence. (from Genbank) clone 839792 3', mRNA sequence. (from Genbank) clone 786576 5', mRNA sequence. (from Genbank) 0.26950166 HT1034_f_at Atpase, Na+/K+ Transporting, Alpha 1 Polypeptide 0.26635092|J03934_s_at |NMOR1 NAD(P)H:menadione oxidoreductase Two P-domain K+ channel TWIK-1 mRNA Mucin 5b, Tracheobronchial (Gb:X74955) Osteoblast specific factor 2 (OSF-2os) FBN1 Fibrillin 1 (Marfan syndrome) CHDR Chlordecone reductase 0.2685563 HT880_s_at | Mucin 6, Gastric (Gb:L07517) PPY Pancreatic polypeptide 0.26430032 X97261 r at Metallothionein isoform 1R Sulfotransferase mRNA complement S-protein) CST6 Cystatin M KIAA0057 gene KRT8 Keratin 8 MIA gene Mac25 D13666_s_a U11862_s_a M63438_s_a X74929_s_a X84707 ma 0.26922756 M11726 at 0.26816157 U62800_at 0.2679188 S68287_at 0.26479402|HT2785_at 0.26873595 D31762 at 0.26494673 M28249 at 0.26582745 U66036 at 0.26531574 U33632 at 0.26561254 X03168 at 0.26449436 L13923 at 0.2671547 L40379 at 0.2706232|HT987 at HG1034-HG880-HG987. 0.2674058 65_at 0.2670215/1 at 0.26979876|t0.2675533t 0.2689106 0.26654932 0.26615363 0.396443 0.401411 0.401142 0.400938 0.397065 0.397045 0.396816 0.395874 0.395492 0.39496 0.401627 0.3999998 0.399564 0.398909 0.398898 0.396795 0.395207 0.394631 0.400722 0.400221 0.399341 0.398177 0.398047 0.397251 0.474475 0.4677942 0.4739853 0.472558 0.2878242 0.4721525 0.2831808 | 0.4710011 0.2820395 0.4705439 0.2773519 0.4690745 0.2924698 0.4747597 0.2848009 0.4717545 0.2842883 0.4717306 0.2823113 0.4707929 0.468315 0.4737241 0.4728 0.4724881 0.2884169 0.472351 0.2817896 0.4700401 0.2807249 0.4699358 0.2788769 0.4695598 0.277946 0.4691865 0.2771673 0.4689885 0.468899 0,4680592 0.2911396 0.2915885 0.2916048 0.2905367 0.274682 0.2894171 0.275548 0.2747399 0.2906164 0.2753103

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						TGFBR3 Transforming growth factor, beta receptor III (betaglycan,
164 Pancreas	0.2743028	· · · · · · · · · · · · · · · · · · ·	0.394423		L07594_at	300KD))
165 Pancreas	0.2730731	I	0.394142		X13916_at	LDL-receptor related protein
166 Pancreas	0.2728557		0.394016	0.26332533 D38583	D38583 at	Calgizzarin
167 Pancreas	0.2720528		0.393935	0.26314235 X57766	X57766_at	PSG11 Pregnancy-specific beta-1 glycoprotein 11
168 Pancreas	0.2719561	0.4661515	0.393646	0.26282045 D87012	D87012_at	Immunoglobulin lambda gene locus DNA, clone:61D6
169 Pancreas	0.2707795		0.393127	0.26253322 L.29433_at	L29433_at	COAGULATION FACTOR X PRECURSOR
170 Pancreas	0.2693385		0.392992	0.26223975 L42176 at	L42176 at	(clone 35.3) DRAL mRNA
171 Pancreas	0.2689302	0.4650724	0.392674	0.26197657 M82809 at	M82809 at	ANX4 Annexin IV (placental anticoaculant protein II)
172 Pancreas	0.2683395	0.4650724	0.392517	0.26173648 L13720 at	L13720 at	Growth-arrest-specific protein (gas) mRNA
173 Pancreas	0.2674237	0.464959	0.392372	0.26142424 L34155_at	L34155_at	Laminin-related protein (LamA3) mRNA
174 Pancreas	0.2674237	0.4648172	0.392069	0.26105756	0.26105756 L34155 at-2	Laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD), epilegrin)
					HG2788-	
175 Pancreas	0.2674176	0.464741	0.391972	0.26080438 HT2896	HT2896 at	Calcyclin
176 Pancreas	0.2671013	0.4644892	0.391845	0.26062673 L20591 at	L20591 at	ANX3 Annexin III (lipocorfin III)
177 Pancreas	0.2660541	$^{\circ}$	0.391238	0.26037118 U01062	U01062 at	ITPR3 Inositol 1.4.5-triphosphate receptor. type 3
178 Pancreas	0.2654402		0.391109	0.26004875	U36221 at	Pancreatic zymoden granule membrane protein GP-2 mRNA
179 Pancreas	0.2652055	0.4641528	0.391001	0.25991356 U42408	U42408 at	Ladinin (LAD) mRNA
					HG2743-	
180 Pancreas	0.265055	0.463705	797005 0	OPEDEFAED	HT2846_s_a	
	0:400000	0.1001.0	0.030101	0.7.0300100		Caldesmon 1, Alt. Splice 4, Non-Muscle
181 Pancreas	0.2646077	0.463795	0.390317	0 259351	U51010_s_a	Nicotinamida M. mothyltransforma agon a gone 1 and 11 and 12
182 Pancreas	0.2645448	0.4637207	0.390182		U79293 at	Clone 23948 mRNA seguence
					C	DAE Doors proporation forther for some 1
183 Pancreas	0.2635272	0.4624023	0.389677	0.25895628	14515101510141 t	DAF Decay accelerating factor for complement (CD55, Cromer blood) group system)
184 Pancreas	0.2631126	0.4623061	0.389545	0.2586853 D11428_at	D11428_at	PMP22 Peripheral myelin protein 22
r C	0				U75272_s_a	
165 Fancreas	0.2629194	0.462205	0.389476	0.25830814	+	PGC Gastricsin (pepsinogen C)
			***		HG1067-	
186 Pancreas	0.262751	0.4620446	0.389285	0.2581156	HT1067 r at	0.2581156 HT1067 r at Mucin (Gb:M22406)
187 Pancreas	0.2625998	0.4616099	0.389171	0.25783736 M14338	M14338 at	PROS1 Plasma protein \$
188 Pancreas	0.260711	0.4613836	0.388803	0.25762293 X68742 at	X68742 at	Integrin, alpha subunit
189 Pancreas	0.2606377	0.4613482	0.388368	0.25740916 K02765 at	K02765_at	COMPLEMENT C3 PRECURSOR
190 Pancreas	0.259076	0,4612887	0.388247	0.25710133	X66357_s_a	Ovciin-dependent kipase 3
191 Pancreas	0.258786	0.4610257	0.388037	0.25685441 X03350	äţ	ADH2 Alcohol dehydrogenase 2 (class I), beta polyneptide
		-		·		

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192 Pancreas	0.2587/32	0.4608453	780886 0	RC RC	_AA0374	EST: zc03h03.s1 Soares parathyroid tumor NbHPA Homo sapiens
193 Pancreae	3	0.25742 0.4000433		0.23073719 at	٩	CUNA Cione 321269 3', mRNA sequence. (from Genbank)
404 Deportoge		0.4001220		0.2304930 011		Gem G Pase (gem) mKINA
134 FallCleas	0.200030	0.4588281	0.387413	0.25624022 X66839	6839_at	MaTu MN mRNA for p54/58N protein
195 Pancreas	0.2562678	0.4596589	0.387269	X1400 0.25608438 1_f_at	X14008_rna 1_f_at	Lysozyme gene (EC 3.2.1.17)
196 Pancreas	0.2557063	0.4594903	0.387189	X57 0.25586015 t	X57348_s_a t	SFN Stratifin
407 00000	0.0			X5	X53002_s_a	
197 Pancreas	0.2556424		0.387067	0.25564355 t		ITGB5 Integrin beta-5 subunit
190 Fancieas	0.254/33/		0.386753	0.25527582 L08488_at	3488_at	INPP1 Inositol polyphosphate-1-phosphatase
199 Pancreas	0.2519156	i	0.386604	0.2550488 L00352 at)352_at	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR
Z00 Pancreas	0.2513616	0.4577566	0.386122	0.25489885 105633	633 at	ITGB5 Integrin beta-5 subunit
201 Pancreas	0.2504257	0.457121	0.386102	AA(AA009826_a	EST: ze82b02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
202 Pancreas	0.2493664	0	0.38599	0.2545078 Y00503	3503 at	KRT19 Keratin 19
203 0222	0.0400464		11			PDE4C Phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-
200 I allulas	0.2403434	0.4371134	60/085.0	0.25408345 246632	3632 at	homolog phosphodiesterase E1)
204 Pancreas	0.2480411		0.385664	0.25396025 HT4580	HG4310- HT4580 at	Cellular Retinol Binding Protein Ii
205 Pancreas	0.2469718		0.385538	0.25373492 D50683 at)683 at	TGFBR2 Transforming growth factor, heta recentor II (70-80kD)
206 Pancreas	0.2463778		0.385377	0.25356093 M25756	5756 at	SECRETOGRANIN II PRECURSOR
207 Pancreas	0.2452414	0.4551576	0.385324	0.2533396 X67325	7325_at	INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN
208 Pancreas	0.2451037	0.4550618	0.385152	AA7	AA147510_s	EST: zl50c12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA
			7010000	_ !!		GIOTIE 303306 3, MKNA sequence. (from Genbank)
209 Pancreas	0.2445737	1	0.384839	0.25282523 J05481	481_s_at	Endoglin (Osler-Rendu-Weber syndrome 1)
210 Pancreas	0.2435489	0.4549896	0.384735	0.25253943 M31994 at	1994_at	ALDH1 Aldehyde dehydrogenase 1, soluble
211 Pancreas	0.2431813	0.454711	0.384353	0.25235546 M21574 at	1574 at	PDGFRA Platelet-derived growth factor recentor alpha polynantide
212 Pancreas	0.240173	0.4545118	0.384215	0.2520813 M59371	9371 at	TYROSINE-PROTFIN KINASE RECEPTOR FOR PRECIESOR
213 Pancreas	0.2399713		0.383889	0.25183654 D00017	Đ.	ANX2 Annexin II (libocortin II)
214 Pancreas	0.2394403	0.4543074	0.383456	0.25164106 M37721		PAM Peptidylalycine alpha-amidating monocycrenase
215 Pancreas	0.238449		0.383426	0.2514285 Z74615	D - 1	COL1A1 Collagen, type I, alpha 1
216 Pancreas	0.2384211	0.4541328	0.383383	0.25118315 M20530 at	3530 at	SPINK1 Serine protease inhibitor, Kazal type 1
	0.237254	0.237254 0.4541205	0.383042	0.25094923 U66077	3077 at	DAZ Deleted in azoospermia
218 Pancreas	0.2365542	0.4540057	0.383009	0.2506271 D14520	1520_at	GC-Box binding protein BTEB2
219 Pancreas	0.2359637	0.4539793	0.382752	X01038 0.2504809 1 s at	X01038_ma 1 s at	Fetal gene for apolipoprotein Al precursor

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

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250 Pancreas	0.2160575	0.449934	0.375965	X02761_s_a 0.24437046 t	FN1 Fibronectin 1
251 Pancreas	0.2150459	0.449934	0.375694	D79206_s_a	SDC4 Syndecan 4 (amphictycan ryddocan)
				RC_AA4479	EST: zw82g03.s1 Soares testis NHT Homo sapiens cDNA clone
252 Pancreas	0.2139522	0.4497347	0.375545	0.24386409 94_at	782740 3', mRNA sequence. (from Genbank)
253 Pancreas	0.2136497	0.4496954	0.375449	RC_AA2279 0.24364659 06_at	EST: zr57d06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667499 31 mRNA sequence (from Genhank)
		,			
254 Pancreas	0.2134282	0.4494686	0.375202	0.24348773 J03464_s_at	Collagen, type I, alpha 2
255 Pancreas	0.2116019	0.4494176	0.374616	AB002354_a	KIAA0356 gene product
256 Pancreas	0.210531	0.4493226	0.374585	0.24314104 M38591_at	S100A10 S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light polypeptide (p11))
257 Pancreas	0.2100283	0.4485026	0.374204	M13690_s_a 0.24288653 t	C1NH Complement component 1 inhibitor (angioedema, hereditary)
258 Pancreas	0.2099217	0.4483339	0.373941	0.24273656 D86479_at	Non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds
259 Pancreas	0.2098654	0.4475095	0.373782	0.24257857 L03840 s at	FGFR4 Fibroblast growth factor receptor 4
260 Pancreas	0.2094783	0.4474704	0.373604	0.24238108 L36983 at	Dynamin (DNM) mRNA
261 Pancreas	0.2089765	0.447446	0.373414		TÚMOR-ÁSSOCIATED ANTIGEN L6
262 Pancreas	0.2082431	0.4472224	0.373285	0.24192399 M57710 at	LGALS3 Lectin, galactoside-binding, soluble, 3 (galectin 3) (NOTE: redefinition of symbol)
200	0000000		- 0	RC_AA2554	EST: zr85f08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
264 Pancreas	0.2076829	0.44/086	0.373057		682503 3', mRNA sequence. (from Genbank)
265 Pancreas	0.2068356		0.37281	0.24139366 U66075 at	Cysteine-rich fibroblast growth factor receptor (CFR-1) mKNA Transcrintion factor hGATA-6 mRNA
266 Pancreas	0.2067316		0.372722	0.2412918 W27099 at	EST: 20c4 Human retina cDNA randomly primed sublibrary Homo
267 Pancreas	0.2066826		0.372488	0.24121895 D28124 at	Unknown product
268 Pancreas	0.20614	0.4467433	0.372304		ERK6 mRNA for extracellular signal regulated kinase
269 Pancreas	0.2054201	0.446303	0.372189	0.2407174 L25286_s_at	0.2407174 L25286_s_at COL15A1 Collagen, type XV, alpha 1
0.70			1	RC_AA1478	RC_AA1478 EST: zl50b04.s1 Soares pregnant uterus NbHPU Homo sapiens
Z/U Pancreas	0.204237	0.4462716	0.371703	0.24058916 84_at	cDNA clone 505327 3', mRNA sequence. (from Genbank)
271 Pancreas	0.2028583	0.4460846	0.371602	0.24028708 U14394_at	
272 Pancreas	0.2027239	0.4457809	0.371431	0.24007523 04_at	EST: zw90h07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784285 3', mRNA sequence. (from Genbank)
273 Pancreas	0.2026614	0.4455964	0.371253	0.23986627 M95787 at	22kDa smooth muscle protein (SM22) mRNA

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274 Dancrass	0.2028	253 O 1155061	64 0 3712E3	0.230744041145389 of 10 DDOTEIN C	A WILLIAM WITH THE BEACH TO THE CONTROL OF THE CONT
414	-		3		UDP-GLUCIJRONOSYLTRANSFERASE 287 PRECURSOR
275 Pancreas	-	0.2023137 0.4455882	82 0.370798	0.2395318 J05428 at	MICROSOMAL
276 Pancreas	-	0.2020412 0.4455882		0.2392989 D42045 at	KIAA0086 gene
277 Pancreas		0.2017758 0.4451509	09 0.370685	0.23918618 M15656 at	ALDOB Aldolase B, fructose-bisphosphate
278 Pancreas	eas 0.2013191	191 0,4450379	79 0.370592	0.23898017 D21255_at	CDH11 Cadherin 11 (OB-cadherin)
					EST: aa43a01.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
					AA489716_a 823656 5' similar to contains element MER22 repetitive element ;,
279 Pancreas	eas 0.2012664	564 0.445013	13 0.370514	0.23876333 t	mRNA sequence. (from Genbank)
				Y11306_ma	
280 Pancreas	\dashv	9		0.23868455 1_at	HTcf-4 gene extracted from H.sapiens mRNA for beta catenin/TCF-4
281 Pancreas	71	424 0.444548		0.23854801 X86163 at	BDKRB2 Bradykinin receptor B2
282 Pancreas	77	0.2004194 0.4444534	34 0.369925	0.23831032 X71877_at	CTRL Chymotrypsin-like
				M27436_s_a	
283 Pancreas	eas 0.1985597	597 0.444445	45 0.369925	0.23805958 t	F3 Coagulation factor III (thromboplastin, tissue factor)
					EST: HUMGS0003714, Human Gene Signature, 3'-directed cDNA
284 Pancreas		9		0.23789924 C01766_r_at	at sequence, mRNA sequence. (from Genbank)
285 Pancreas		832 0.444424		0.23781882 Z24727 at	TPM1 Tropomyosin alpha chain (skeletal muscle)
286 Pancreas	-	961 0.4443879		0.2375083 M76180_at	DDC Dopa decarboxylase (aromatic L-amino acid decarboxylase)
287 Pancreas		0.1965919 0.4442333	33 0.369292	0.23730977 J04177 at	COL11A1 Collagen, type XI, alpha 1
288 Pancreas		0.1964797 0.4441634	L	0.23720081 U09278 at	Fibroblast activation protein mRNA
289 Pancreas		0.1964206 0.4439878	78 0,369187	0.23699033 Y09267 at	Flavin-containing monooxygenase 2
290 Pancreas	_	0.1960992 0.4439692	92 0.368869	0.23684187 J03801 f at	LYZ Lysozyme
	_			RC_AA0019	EST: zh83a05.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
291 Pancreas	\dashv	0.1960305 0.4438405		0.23672394 08_at	cDNA clone 427856 3', mRNA sequence. (from Genbank)
292 Pancreas	\neg	9		0.23660825 U40223_at	Uridine nucleotide receptor (UNR) gene
293 Pancreas		396 0.443327		0.23645079 X05409 at	ALDH2 Aldehyde dehydrogenase 2, mitochondrial
294 Pancreas		0.1943116 0.4432485		0.23626012 Z37976 at	LTBP2 Latent transforming growth factor beta binding protein 2
295 Pancreas		0.1939876 0.4428038		0.23617645 X56677_at	MYOD1 Myogenic factor 3
296 Pancreas		- 1		0.2360612 U08021_at	Nicotinamide N-methyltransferase (NNMT) mRNA
297 Pancreas	eas 0.1908299	299 0.4424619	19 0.367897	0.2358742 M92934 at	CTGF Connective tissue growth factor
(M65292_s_a	
298 Pancreas	eas 0.190257	257 0.4422684	84 0.367837	0.23571731 t	HFL1 H factor (complement)-like 1
				RC_AA4282	EST: zw51d04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
299 Pancreas		515 0.4419518		0.2355775 40_at	clone 773575 3', mRNA sequence. (from Genbank)
300 Pancreas	0	472 0.4418405		0.23537093 D87292_at	Rhodanese
301 Pancreas	eas 0.188899	899 0.4417597	97 0.367744	0.23517503 TNFa_at	No description for gene: TNFa_at
20.2 Dange	0.400	074470	אטאבשה ט	hum_alu_at-	Mis describition from a british of
SUZIFAIIG	302 FallCreds 0.1003300 0.4417 033	000 0.44170		0.23503512/2	INO DESCRIPTION FOR GENETING AIL

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hum alu at (miscellaneous control)	Plasma cell membrane glycoprotein (PC-1) mRNA	Matrix metalloproteinase 21	CST4 Cystatin S	EST: zx99f06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	811907 3, MKINA sequence. (from Genbank)	ris Frotease finibitor 3, skin-derived (SKALP)	Potassium Channel Protein (Gb:Z11585)		Lysyl oxidase-like protein gene	SDC1 Syndecan 1	EST: zu36d09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone / 40081 3', mRNA sequence. (from Genbank)	CYPZC9 Cytochrome P450, subfamily IIC (mephenytoin 4- hydroxylase), polypeptide 9	EST: zl71a06.r1 Stratagene colon (#937204) Homo sapiens cDNA contents 510034 Ft mRNA contents (from Conhant)	orico cross of mineral sequence, (non delibativ)	Desmin gene	ITGB1 Integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	0.23256098 M19045 f at LYZ Lysozyme		KIAA0331 gene product	PML Probable transcription factor PMI (alternative products)	RIG mRNA, complete sequence	Protein Kinase Hf31 Cama Donandont	Lysophospholipase homolog (HU-K5) mRNA		Jyrosiite Kiriase, Receptor Axi, Alt. Splice 2 (clone Hi lambda-17) Jambda-like gene	KIAA0202 gene, partial cds	Fc Receptor lib3 For log 1 ow Affinity
0.2348528 hum alu at	1	σ,	X54667 at	9	1	100000	at .	U24389_s_a			790		at	AA053052_a	M63391 rna		at	M19045 f at	RC_AA4969		(63131_s_a	at	, 70	जं :			D86957 at	
0,2348528	0.23466507	0.23456301	0.23436244 X54667 at	RC 0 93499958 E4	0.23423230 34 at	0.204 12003	HGZZ39- 0.2338312 HT2324		0.23369552	0.23360941 Z48199 at	0.700000000	0.2333031244 s at	0.23330152 M61855	0.23315011		0.2329875 1_at	0.23279957 X07979	0.23256098		0.23248978 80_at	0.232387381	0.23225546 U32331	HG2167 0 23197828 HT2237	0.2318316 U67963	0.2246842	0,23155992	0.23138705 D86957	HG491- 0.23120856 HT491 at
0.367066	0.366863	0.366586	0.366447	0 366353	0.366287	0.000201	0.366114	000000	0.306029	0.36581	0.365634	0.000004	0.365446	0.36543		0.365283	0.365079	0.36483		0.364581	0.364421	0.364351	0.364295	0.363996	863638	0.363792	0.363628	0.363449
0.1885506 0.4415661	0.1879477 0.4413022	0.44122	0.4412107	0.440699	0	- 1	0.4404019	1400100		0.4402908	0.4409803	- 1	0.4402766	0.4399118		0.4397945	0.4395127	0.4395041		0.4394699	0.4393834	0.4392951	0.4391857	0.4388098	0.4384459	0.4384019	0.4383445	0.4381441
0.1885506	0.1879477	0.1877398	0.1874823	0.186752	0.1863556		0.1861374	0.4055044	0.1000041	0.1849923	0 1847203	0.1041200	0.1841381	0.1829358		0.18191	0.1810602	0.1806336		0.180214	0.1797838	0.1786759	0.1784829	0.1784077	0 1783882	0.1782384	0.1781566	0.177194
303 Pancreas	304 Pancreas	305 Pancreas	306 Pancreas	307 Pancreas	308 Pancreas		309 Pancreas	340 Danaraga	ा बारा हवें व	311 Fancreas	312 Pancreae	on on one	Pancreas	Pancreas		315 Pancreas	316 Pancreas	317 Pancreas	1	318 Pancreas	319 Pancreas	320 Pancreas	321 Pancreas	322 Pancreas	323 Pancreas	324 Pancreas	Pancreas	326 Pancreas
303	304	305	306	307	308		309	310	2 2	31.1	312	1	313	314		315	316	317	(318	319	320	321	322	323	324	325	326

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

FIG. 11M

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327 Pancreas	as 0.1765499	0.4377639	0.363297	0.2310578	U41766_s_a t	U41766_s_a Metalloprotease/disintegrin/cysteine-rich protein precursor (MDC9) t
328 Pancreas	as 0.1753717	0.4376566	0.363239	0.23086834 1_at	184_rna	FLII gene
329 Pancreas	as 0.1740268	0.4375736	0.363182	0.23070936 U15131	at	HTS1
330 Pancreas	as 0.1739228	0.4372805	0.362984	X 0.2306095	X68733_rna 1_at	Alpha1-antichymotrypsin, exon 1
331 Pancreas	as 0.173609	0.4371579	0.362964	0.23040158	X57579_s_a t	Activin beta-A subunit (exon 2)
0					D45917_s_a	
332 Pancreas	as 0.1733888	0.437153	0.362743	0.23032051	- 1	TIMP-3, partial cds (C-ferminus region)
333 Pancreas	as 0.171895	0.43707	0.362719	0.2302363 66_	_AA1131 _at	EST: zm27e01.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526872 3', mRNA sequence, (from Genbank)
334 Pancreas	ıs 0.1718943	0.4368998	0.362514	0.23009038	U27326_s_a t	FUT3 Albha (1.3/1.4) fucosyltransferase
				derrocking and a second	HG2994-	
1 0					HT4850_s_a	
335 Pancreas			0.362326	0.2299985		Elastin, Alt. Splice 2
336 Pancreas	is 0.1706867	0.4366488	0.362181	0.2297499 L36645	L36645_at	Receptor protein-tyrosine kinase (HEK8) mRNA
337 Pancreas	-	0.435845	0.362181	0.2296057 M93036	M93036 at	MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN GA733-2 PRECURSOR
338 Pancreas	is 0.1696099	0.4358323	0.362061	0.22946241 U27333	U27333_at	Alpha-1,3 fucosyltransferase 6 (FCT3A) mRNA
330 Dancrese	0 1605303	0 4257040	0.064740		D00003_s_a	
340 Dancreas	t	1	0.301712		1	CYP3A3 Cytochrome P450 IIIA3 (nifedipine oxidase chain 3)
o40 rancies	\dagger	0.4356631	0.361691	0.22932297	D87071_at	KIAA0233 gene
341 Pancreas	s 0.1693031	0.4356532	0.361642	0.22915365 t	//19267_s_a	TPM1 Tropomyosin alpha chain (skeletal muscle)
342 Pancreas	IS 0.1690814	0.4355716	0.361459	RC_A 0.22902328 76_at	A1906	EST: zp89g09.s1 Stratagene HeLa cell s3 937216 Homo sapiens
343 Pancreas			0.361145	0.22888122 D50532	D50532 at	Macrobana lactin 2
344 Pancreas		0.4347507	0.361065	0.22877204 L04270	1)	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR
345 Pancreas	s 0.1688594	0.4344482	0.361012	0.22861604 M25629 at	M25629_at	Kallikrein mRNA, clone clone phKK25
, ,					A0789	EST: zm95f07.s1 Stratagene colon HT29 (#937221) Homo sapiens
346 Pancreas	T	-	0.360701	0.22852479 32_at		cDNA clone 545701 3', mRNA sequence. (from Genbank)
347 Pancreas	s 0.1686/12	0.4337262	0.360543	0.22840263 X75342	t2_at	SHB SHB adaptor protein (a Src homology 2 protein)
348 Pancreas	s 0.1684651	0.4334429	0.360504	0.22816657 C00476 at	C00476 at	EST: HUMGS0007866, Human Gene Signature, 3'-directed cDNA sequence, mRNA sequence. (from Genbank)
					M11313 s.a	
349 Pancreas		0.1681121 0.4331623	0.360444	0.22799188		A2M Alpha-2-macroglobulin

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FIG. 11N

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350 Pancreas	0.1679768	0 4330843	0.360311	10 22782714 1128240 at	MAT8 profesio
351 Pancreas	0.1676114	- 1	0.360228	0.22765163 U03056 at	Hyali ronodi rosaminidase 1 (HVAI 1) mRNA
352 Pancreas	0.1675607		0.360063		
353 Pancreas	0.1668353		0.360023		
354 Pancreas	0.1665658		0.359929	0.22731425 D17793 at	DDH1 Dihydrodiol dehydrogenase
L L	6				
355 Pancreas	0.1665002	9	0.359594	0.22722998 U67849_at	Beta-galactoside alpha2,6-sialyltransferase (SIAT1) mRNA, exon W
356 Pancreas	0.1663914	0.432159	0.359256	0.22706501 L20826_at	I-plastin mRNA
1				RC_AA4549	EST: zx99d10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
35/ Pancreas	0.1662391	0.4321106	0.359233	0.22684869 78_at	811891 3', mRNA sequence. (from Genbank)
358 Pancreas	0.1660601	1	0.359153	0.22679117 U16306_at	CSPG2 Chondroitin sulfate proteoglycan 2 (versican)
359 Pancreas	0.1651519		0.359128	0.22654821 W31097_at	Homo sapiens COX4AL mRNA, complete cds
360 Pancreas	0.1648087	i	0.35897	0.22643818 X81420 at	MLN137 mRNA
361 Pancreas	0.1644733	0.4314531	0.35853	0.2263567 U03688 at	CYP1B1 Cytochrome P450 IB1 (dioxin-inducible)
362 Pancreas	0.1634512	0.4311937	0.358367	0.22618711 U48707 at	Protein phosphatase-1 inhibitor mRNA
	0				Y07829_xpt3 Exon A1 from H.sapiens gene encoding RING finger
363 Pancreas	0.1633332	0.4307453	0.358285	0.22612299 at	protein./ntype=DNA /annot=exon
364 Pancreas	0.1620863	0.4306892	0.358064	0.22601184 M34309 at	ERBB3 V-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3 (alternative products)
365 Pancreas	0.1619619	0.4306732	0.358035	0.22583023 65 at	EST: zk46h09.s1 Soares pregnant uterus NbHPU Homo sapiens
366 Pancreas	0.1619335	1 1	0.35787	0.22574383 L04733 at	KINESIN LIGHT CHAIN
				Z19574 rna	
367 Pancreas	0.1616663	•	0.357694	0.2256286 1_at	Cytokeratin 17
368 Pancreas	0.161317	0.4300522	0.357533	0.2254944 M69023_at	Globin gene
					EST: aa01a12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
369 Pancreas	0 160555	0.4300077	0.357501	AA455860_s	
		1	100.00.0	N.22301110 at	(III offi Gendank)
370 Pancreas	0.1598018	0.4298748	0.357331	0.22518858 HT3688 at	Niclear Factor NEII6
371 Pancreas	0.1596494	0.4298276	0.357304		RNS1 Ribonuclease A (pancreatic)
372 Pancreas	0.1592098	0.4298215	0.357159	0.22489779 X76105 at	DAP-1 mRNA
373 Pancreas	0.1592042	0.4297251	0.357082	0.22475794 68 at	EST: zo23g08.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 587774.3' mRNA segments (from Cenhank)
374 Pancreas	0.1588987	0.429719	0.356935		LAMB1 Laminin B1 chain
375 Pancreas	0.1587369	0.4296986	0.356819	0.22448462 J02758 s at	at Apolipoprotein A-IV precursor
376 Pancreas	0.1585681	0.4296492	0.356803	0.22438303 HT1098 at	Cystatin D
377 Pancreas	0.1582393	0.4295513	0.35655	0.2243046 U49260 at	Mevalonate pyrophosphate decarboxylase (MPD) mRNA

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instructional stand finds temp.	K-Cl cotransporter (hKCC1) mRNA	S100P S100 calcium-binding protein P	IGL@ Immunoglobulin lambda light chain			Short-chain dehydrogenase/reductase 1	EST: yh81g01.r1 Homo sapiens cDNA clone 136176 5' similar to	GEBDE Insuling Its arough for 1 1 1 1 1 1 1 1 1 1	EST: 2v47h07.s1 Soares overv tumor NhHOT Homo services obtain	clone 756829 3', mRNA sequence. (from Genbank)	Phosphatidylinositol-glycan-class C (PIG-C)	EST: zo48h03.r1 Stratagene endothelial cell 937223 Homo sapiens	t lelement: mRNA societies (f. 2007)		cDNA 5' end, mRNA sequence. (from Genbank)	EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1 PRECURSOR	Protein Dhoenhatoes Inciting 11	Total Hashington Homolog	AFFX-LysX-M at (endodenolis control)	AFFX-I ve X-M at (miscollanosus cont-1 1111	CD59 CD59 antiren p18-20 (antiren identification)	antibodies 16.345, EJ16, EJ30, EL32 and G344)	OSK2 Drandolis control (No.70)	contain convertase subtilisin/kexin type 2	Interferon, alpha-inducible protein 27	Death domain receptor 3 (DDR3) mRNA, alternatively spliced form 2,	Al PHA-ACTININ 1 OVTOSKEI FTAL 1905-05.	Homo sapiens follistatin-related protein FLRG (FLRG) mRNA,	cumplete cas	clone 383179 51 mRNA sequence (from Control)	20-kDa myosin light chain (MI C-2) mRNA	Mac-2 binding protein mRNA
		Abbo14 at	X57809_at	0.22376604 M76665 at		at	R33301 nt		RC_AA4266	40_at	0.2231326 D85418 at	AAEESAE	1 1	AA314587_a	1	M57730 at	HG3570- HT3773 at	AFFX-LvsX-	M_at	-ysX-		at	to or	1612	s at		T	AA2279	71223 a	· ·		
0.994009471166064	0.22409247	0.0000/40 0.0000	0.22383262 X57809	0.223/6604	720736660	0.22304071	0.22350217 R33304	0.22338259		0.22329882 40 at	0.2231326		0.22305468	10000	1,008082777.0	0.22288442 M57730	HG3570- 0.22270949 HT3773 at		0.22262543 M at	0.22257286 M at-2		0.22234379 M84349	0.22224523 305252		0.2220705 92	0.22192991 U83600 at	0.2218258 M95178	0 22162992 56	0.55.105.05	0.22146438 t	0.22135113 J02854 at	0.22124396 L13210 at
0 356/27	3 6			-	0.356417		0.355984	0.3		0.355/35	0.555555		0.35554	0.385008	0.00000	0.354846	0.354781		0.354647	0.354553		0.354484	0.354436		0.354431	0.354307	0.354128	0.354066		0.354059	0.353944	0.353582
3 0 429282F		-	- 1	,	0.4290619	1	0.4289388	0.4289348	0.4200442	- 1			0.4286616	0.4286403		0.4281668	0.4278688		0.4276867	0.4276668		0.4274579	0.4272135	47000-	178074.0	0.4262222	0.4261222	0.4261217		0.4257195	0.4257063	0.4255509
0.1580268	0.1578262	0.4577343	0.151.045	70101.0	0.1562685		0.156221	0.1561164	0.15/0851	0 154768			0.1546832	0.1534232		0.1528883	0.1526794	1	0.1519917	0.1519917	0 4 7 4 0	0.1518/72	0.1516542	0.4507802	0.1001002	0.1506744 0.4262222	0.1504689	0.1494065		0.1487714 0.4257195	0.1482132 0.4257063	0.140034 0.4255509
378 Pancreas	379 Pancreas	380 Pancreas	381 Pancreas		382 Pancreas		383 Pancreas	384 Pancreas	385 Pancreas	386 Pancreas			387 Pancreas	388 Pancreas		389 Pancreas	390 Pancreas		rancreas	392 Pancreas	303 Danaraa	rancieas	394 Pancreas	395 Pancreas		-+	os/ Fancreas	398 Pancreas	 	+	400 rancieas 404 Dancias	anoreas
378	376	380	381		382		383	384	385	386			387	388		389	390	204	80	392	303	Cec	394	395		396	1/60	398 F	0	388	400 5	

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402 Pancreas	0.1465931	0.4254811	0.353412	0.22108869 L40371_at	Thyroid receptor interactor (TRIP4) mRNA, 3' end of cds
403 Pancreas	0.1465808	0.4253718	0.353263	0,22101992 D16154 at	Cytochrome P-450c11, exon 3-9
404 Pancreas	0.1465383	9	0.353122	0.22078371 HT4385_at	Olfactory Receptor Or17-210
405 Pancreas	0.1448025	0.425101	0.353001	0.22063361 M14218_at	ASL Argininosuccinate lyase
			1	RC_AA4906	RC_AA4906 EST: zw99f10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
406 Pancreas	0.1447358		0.352915	0.22054137 70_at	clone 785131 3', mRNA sequence. (from Genbank)
407 Pancreas	0.1446189		0.352885	0.22036909 J03764 at	PA11 Plasminogen activator inhibitor, type I
408 Pancreas	0.1445339	_	0.352817	0.22028802 D55696 at	Cysteine protease
409 Pancreas	0.1440039	0.4248809	0.352547	0.22010562 X92814 at	Rat HREV107-like protein
				RC_AA4550	EST: aa04d11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
410 Pancreas	0.1432172		0.352419	0.2200262 78_at	812277 3', mRNA sequence. (from Genbank)
411 Pancreas	0.1431273	0.4246844	0.352225	0.21986967 V00563_at	
				AA456471_s	EST: zx74g11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
412 Pancreas	0.1426979		0.352015	0.21982433 at	clone 809540 5', mRNA sequence. (from Genbank)
413 Pancreas	0.142507	0.4245292	0.351879	0.21961014 D45213 at	Homo sapiens mRNA for zinc finger protein, complete cds
				U01317 cds	Epsilon-globin gene extracted from Human beta globin region on
414 Pancreas	0.1420584	0.4245271	0.351839	0.2195332 1_at	chromosome 11
415 Pancreas	0.1416256	0.4243606	0.351757	HG880- 0.21943115 HT880 at	Mucin 6. Gastric (Gb:1 07517)
416 Pancreas	0.1397498	0.4243606	0.351622		Interferon-induced leucine zipper protein (IFP35) mRNA, partial cds
417 Pancreas	0.1392388	0.4243341	0.351565	0.21919066 S57132 s a	s at COL16A1 Alpha-1 type XVI collagen
				RC AAA167	ECT: 71:00003 cd Copror tootic MLT Llows contour about
418 Pancreas	0.1388932	0.4242676	0.35154	0.21911976 42_at	42_at 731380 3', mRNA sequence. (from Genbank)
419 Pancreas	0.1387572	0.424144	0.351491	M16707_ma 0.21902552 1_at	Histone H4 gene, clone FO108
420 Pancreas	0.1383305	0.4239167	0.35143	L08044_s_at	· · · · · ·
421 Pancreas	0 1383305	0.4238932	N 351/11	08044	+ TEE Trafell feature (1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-
		1	10000	n	TTS Helbii laciol s (intestintal)
422 Pancreas	0.1377552		0.351393	0.2186529 L38487_at	Estrogen receptor-related protein (hERRa1) mRNA, 3' end, partial cds
423 Pancreas	0.1371543	- 1	0.351355	0.21842928 L33799 at	PCOLCE Procollagen C-endopeptidase enhancer
424 Pancreas	0.1371511	0.4230616	0.351351	0,21838579 D31883 at	KIAA0059 gene
425 Pancreas	0.1371464	0.423006	0.351201	0.21824138 M80359 at	PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78
426 Pancreas	0.1370405	0.423003	0.351173	0.21815978 M86849 at	Connexin 26 (GJB2) mRNA
1			1	RC_AA4062	
427 Pancreas	0.1366365	0.4229905	0.351012	0.21808575 18 at	742886 3', mRNA sequence. (from Genbank)

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Mad protein homolog (hMAD-3) mRNA	COL4A2 Collagen, type IV, alpha 2	EST: zw65e01.s1 Soares testis NHT Homo sapiens cDNA clone 781080 3', mRNA sequence. (from Genbank)		Human tumor susceptibility protein (TSG101) mRNA, complete cds	L-arginine:glycine amidinotransferase [human, kidney carcinoma cells, mRNA, 2330 ntl	DSG2 Desmodein 2	Transmembrane receptor (ror2) mRNA	H2A/k gene	Human 1 alpha,25-dihydroxyvitamin D3 24-hydroxylase (CYP24)	Gardinoembronic antiden family member 2 CCM2	Pancreatic linase related protein 1 (Pt RP1) mRNA	Smoothelin	MMP2 Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)	AA043160_a EST: zk48g01.r1 Soares pregnant uterus NbHPU Homo sapiens	cDNA clone 486096 5', mRNA sequence. (from Genbank)	Potassium channel KCNO1 mRNA	RPS13 RNA polymerase II polypeptide B (140 kD)		cDNA clone 592307 3', mRNA sequence. (from Genbank)	SIP-1 mRNA	Solute carrier family 9 (sodium/hydrogen exchanger), isoform 3	regulatory factor 2	Chemokine	(clone S171) mRNA	Tazarotene-induced gene 2 (TIG2) mRNA	Homeotic Protein Hox-42	Integrin alpha 6 (or alpha E) protein gene extracted from Human	EST: 202g02.s1 Soares pregnant uterus NbHPU Homo sapiens	cDNA clone 491186 3', mRNA sequence. (from Genbank)	Alpha 2 adrenergic receptor gene
U68019 at		RC_AA4299 98_at	AA156838_a	1	S68805 at	II .		Z80777 at	U60669_ma	X98311 at			M55593 at			U90065_s_a t	X04297_at		at	U82108_s_a t	U82108_s_a	t-2	D43767_at	L40393_at	U77594 at	HG3884- HT4154 at	X53586_rna	 AA1370	73_at	M23533_at
0.21794756 U68019	0.21772872 X05610	RC_A 0.21767052 98_at	1707 1170 0	U.Z1 /54344 t	0.21735202 S68805	0.21723673	0.21711375 M97639	0.21705256 Z80777	U606	0.2167595 X98311	0.21665491 M93283	0.216568 Z49989	0.21641165 M55593	Partition of the Partit	0.21627662	0.21615298	0.21607332 X04297	0	0.21590476 19	0.21579467		0.21564145 t-2	0.21556382 D43767	0.21546201	0.21538307	HG3884 0.21522285 HT4154	0.24540404	0.5101010	0.21499509 73	0.21487539 M23533_at
0.350966	0.350932	0.350798	2000	U.350501	0.350338	0.350296	0.350171	0.349997	0.349303	0.349303	0.348979	0.348765	0.348756		0.348707	0.348676	0.348663	000000	0.348629	0.348285		0.348154	0.348057	0.347994	0.34797	0.347913	0 347852	100	0.347754	0.347708
0.4229495	0.4229094	0.4228163	0.400070	0.422373	0.4222394	0.1345958 0.4221798	0.1336637 0.4220383	0.4218547	0.4215976	0.4215976	0.42,15236	0.4213508	0.4210648		0.4209068	0.4208304	0.4208304	7007007	0.4204084	0.4204049		0.4203105	0.4203105	0.4202434	0.42024	0.4201832	0.4199822		0.4199315	0.4199202
0.1364298	0.1363869	0.1360926	0 1350802	0.1333002	0.1351346	0.1345958	0.1336637	0.1331809	0.1330381	0.1319078	0.1319019	0.1318878	0.1317985		0.1313918	0.1305154	0.1300213	0 4 20 4 20 2	0.1234232	0.1286612				0.1277934	0.1276084	0.1268105	0.1261273	1		0.1256432
428 Pancreas	429 Pancreas	430 Pancreas	Dancrose	ר מוכותם	432 Pancreas	433 Pancreas	434 Pancreas	435 Pancreas	436 Pancreas	437 Pancreas	438 Pancreas	439 Pancreas	Pancreas		Pancreas	442 Pancreas	443 Pancreas	AAA Danoroos	- वालक्व	Pancreas	1	446 Pancreas	447 Pancreas	448 Pancreas	449 Pancreas	450 Pancreas	Pancreas		452 Pancreas	453 Pancreas
428	429	430	131	2	432	433	434	435	436	437	438	439	440		441	442	443	77		445		446	147	148	149	150	451		22	503

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454 Pancreas	0.1256295	0.419746	0.347654	0.21469477 49 at	le EST: zx66b02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796395 3', mRNA sequence, (from Genbank)
455 Pancreas	0.1254913	0.41962	0.347641	0.21453787 at	1
456 Pancreas	0.1247778	0.41962	0.347318	42	
457 Pancreas	0.1242701	0.4195918	0.347231	0.21438734 J03258 at	
458 Pancreas	0.1238554	0.4194851	0.347217	0.21424824 L19872 at	
459 Pancreas	0.1237912	0.4194425	0.347054	0.21408753 L23116 at	
460 Pancreas	0.1236062	0.4194204	0.346948	M33493_s_ 0.2139876 t	Tryptase-III mRNA, 3' end
461 Pancreas	0.1222131	0.1222131 0.4190792	0.346641	0.21383649 at	<u>_</u> .
462 Pancreas	0.1220419	0.4188728	0.3465	11-	T
463 Pancreas	0.1217272	0.4187281	0.346456	0,21369001 D89016 at	
464 Pancreas	0.1214543	0.4187148	0.346368	0.21347573 U70867 at	
465 Pancreas	0.1210791	0.4186941	0.34619	0.21340513 M23254_at	
466 Pancreas	0.1201572	0.4186941	0.346087	D83174_s_0.21328305_t	Ø.
767 P.	0 4004400		0000	RC_AA4890	+
407 Fancieas	0.1201439	0.4185918	0.346038	0.21320248 b3_at	IMAGE:824/1/3, mKNA sequence. (from Genbank)
468 Pancreas	0.1197977	0.4185861	0.345924	0.2129841 J05200 s	at Ryanodine receptor 1 (skeletal)
469 Pancreas	0.1196643	0.418361	0.345881	0.212945 L27080 at	Melanocortin 5 receptor (MC5R) gene
470 Pancreas	0.11923	0.4182988	0.345665	AA252581 0.2128496 t	Ø
471 Pancreas	0.1191973	0.4182084	0 345622	RC_D59847	·
				4	(rioti Galidalin)
472 Pancreas	0.1183518	0.4181297	0.345532	0.21260984 L11369_at	Protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8
473 Pancreas	0.1180387	0.4179826	0.345332	AA491376_a 0.21233512 t	a EST: aa65e11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825836 5', mRNA sequence. (from Genbank)
474 Pancreas	0.11794	0.4179387	0.345241	0.2122144.1 s. at	
475 Pancreas	0.1178205		0.345226	0.21217644 D76444 at	HKf-1 mRNA
476 Pancreas	0.1177303	0.4175842	0.34513	0.21216248 R39374 at	EST: yh95a06.r1 Homo sapiens cDNA clone 137458 5' similar to gb:M55542 INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (HUMAN); (from Genbank)
477 Pancreas	0 1179379	0.4175842	0.345098	0.94903093\W9743E at	
478 Pancreas	0.1168284		0.345067	0.21198222 X69090 at	
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InsP3 5-phosphatase	CDH3 Cadherin 3 (P-cadherin)	TAK1 binding protein 1 (TAB1) mRNA	SCA1 Ataxin 1	Chemokine HCC-1	Apolipoprofein All	AA381902_a EST: EST95112 Activated T-cells I Homo sapiens cDNA 5' end.	mRNA sequence. (from Genbank)	Cancellous bone osteoblast mRNA for GS3786		Fibronectin, Alt. Splice 1	Hepatocyte growth factor-like protein gene	Brain-expressed HHCPA78 homolog [human, HL-60 acute	promyelocytic leukemia cells, mRNA, 2704 ntl	ECT: wondone of Conson Melinam. Cd 11.	644600 of circilotte OM: Doct Date 1 Horno Sapiens CUINA GIOILE	NO_AM4030 011000 3 SIMIIII O 3W;Kbz3_KABII F40029 KAS-KELATED 61 af PROTFIN RAB-25 · mRNA sequence (from Genhank)	AF000561 a Homo sapiens HIV-1 inducer of short transcripts binding protein	(FBI1) mRNA, complete cds		Guanine Nucleotide-Binding Protein Hsr1	Carboxypeptidase Z precursor, mRNA	M6PR Mannose receptor	BGN Biglycan	SPARC SPARC/osteonectin	Heat shock protein hsp40 homolog mRNA	Tob family	HRC Histidine-rich calcium binding protein		Transmembrane protein mRNA	Breast tumor autoantigen mRNA, complete sequence	EST: zl20h08.s1 Soares pregnant uterus NbHPU Homo sapiens	COLVA CIONE SOCSET S, HINNA SEQUENCE, (HOLL GENSAIN)	LAMB2 Laminin, beta 2 (laminin S)
X77567_s_a	0.21179631 X63629_at	3 U49928 at	7 X79204_at	6 Z49269 at	X04898_rna 2 1 at	AA381902_a	9 t	0.21108493 D87120 at	HG3044-	H13/42_s_a 3 t	U37055_ma 0.2108611 s_at		8 S73591_at		00 444 70	761 at	AF000561 a	6t _	HG3227-	0.21039824 HT3404_at	5 U83411_at	2 M93221_at	1 J04599_at	0.2099505 J03040_at	7 U40992_at	3 D64109_at	0.2095504 M60052 at	AF000959_a	5 t	0.20939425 U24576_at	RC_AA1568	X79683 c a	2 t
0.211863821	0.2117963	0.21159413 U49928	0.21153237	0.21145776 Z49269	0.21138282 1 at	da and appropriate and adapting starts, 1970, 19	0.21127579 t	0.2110849		0.21093573	0.21086		0.21069598 S73591			0.21063247 61 at		0.21060526		0.2103982	0.21018955 U83411	0.21005812 M93221	0.21000981 J04599	0.209950	0.20980817 U40992	0.20964763 D64109	0.209550		0.20949535 t	0.2093942	RC_A	767607.0	0.209202
0.345037	0.345007	0.344777	0.344776	0.344638	0.344147		0.344047	0.343907		0.343736	0.343648		0.343567			0.343451		0.343245		0.343123	0.343	0.343	0.342879	0.342873	0.342857	0.342696	0.342587		0.342578	0.342447	1210131	0.042404	0.342279
0.4174888	0.4174105	0.4173543	0.4171035	0.4170411	0.4170252		0.4169194	0.4168361		0.4168026	0.4167035		0.416477			0.4163693		0.4163249		- 1	1	0.4162073	0.4160898		0	0.415697	0.4154531		0.4154259	0.4154259	0.415384	100014.0	0.4152254
0.1164274	0.1159584	0.1158195	0.1155414	0.1155159	0.1148278		0.1144981	0.1142331		0.1140519	0.1138885		0.1134855			0.1130875		0.1126792		0.1126343	0.1115712	0.1114354	0.1114248	0.1113904	0.1103433	0.1100771	0.1100137		0.1098329	0,1098121	0 1095284	0.1000401	0.1093876
479 Pancreas	480 Pancreas	481 Pancreas	482 Pancreas	483 Pancreas	484 Pancreas		485 Pancreas	486 Pancreas		487 Pancreas	488 Pancreas		489 Pancreas			490 Pancreas		491 Pancreas		492 Pancreas	493 Pancreas	494 Pancreas	495 Pancreas	496 Pancreas	497 Pancreas	498 Pancreas	499 Pancreas		500 Pancreas	501 Pancreas	502 Pancreas	200	503 Pancreas

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors the state of the s

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	E Heat shock 70kD protein 6 (HSP70B') HSPA6 Heat shock 70kD protein 6 (HSP70B')		Defensin 6 (HD-6) gene	EST: zw66b09.s1 Soares testis NHT Homo sapiens cDNA clone 781145 3', mRNA sequence, (from Genhank)	MGAT1 N-acetyldlucosaminyltransferase I	Soluble protein Jagged mRNA, partial cds	LCAT Lecithin-cholesterol acyltransferase			}	-	HOXB1 Homeo box B1	+	Utal-specificity tyrosine-(Y)-phosphorylation regulated kinase 1 INTER! FLIKIN-1 RECEPTOR TYPE DEFCLIBEOD	EST: yz76d04.r1 Homo sapiens cDNA clone 288967 5' similar to			CYP27 Cytochrome P450, subfamily XXVII (steroid 27-hydroxylase, cerebrotendinous xanthomatosis)	EST: zx46a12.s1 Soares testis NHT Homo sapiens cDNA clone 795262 3', mRNA sequence, (from Genhank)	MST1R Profein-fyrosine kinase RON	MFAP2 Microfibrillar-associated protein 2	Insulin receptor substrate-1 forman skeletal miscrla mRNA 5828 at	Effector cell protease receptor-1 (EPR-1) gene, partial cds	Regulator of G-protein signalling 5	Caveolin-2 mRNA
C00038_s_a t	0.20894991 X51757 at-2 0.20885721 X51757 at	17	1 at	KC_AA4461 88_at	M55621 at	U73936 at	X13839_at	J04076 at	U95740_ma 2_at	H61361_s_a t	X16666_s_a t-2	X16666_s_a t	U58496_s_a	M27492 at		N78437_at	K03008_cds 2_at	20721747 X59812 at	RC_AA4539 97_at	X70040 at	U19718_at	.20681229 S62539 at	L32866_at	AA081209_a t	U32114_at
0.209035141	0.20894991 X51757 0.20885721 X51757		0.208739981 at	0.2086626 88_	0.20852609 M55621	0.20848976 U73936	0.20836902 X13839	0.20827596 J04076 at	0.20806 2_at	0.20795113	X1 0.20790625 t-2	0.20785482	101077000			0.2075356 N78437	K030 0.207352 2_at	0.20721747	RC 0.20711195 97	0.2070228	0.20701785 U19718	0.20681229	0.20671234 L32866_at	0.2066905	0.20654275 U32114_at
0.34225	0.342206	17000	0.341945	0.341941	0.341869	0.3418	0.341769	0.341633	0.341491	0.341477	0.341352	0.341202	0.244020	0.341039		0.340988	0.340714	0.340706	0.340614	0.340577	0.340516	0.340514	0.340281	0.340139	0.340118
o	0.41497	,	0.414/052					0.4144106	0.4142174	0.4141842	0.4140984	0.4140593	0.4130687	0.413943		0.4138496	0.4137324	0.4136788	0.4134644	0.4134043	0.4133453	0.4132289	0.4132258	0.4129247	0.4127833
0.1092651	0.1090078	0.4000072	0.1009073	0.1084821	0.1082371	0.108202	0.1079309	0.107587	0.1074948	0.106733	0.1062176	0.1062176	0 1061917	0.1051414	0.404.04.0	0.1046546	0.1042106	0.1036883	0.1034349	0.1031755	0.1030601	0.1027545	0.1020946		0.1018037
504 Pancreas	505 Pancreas 506 Pancreas	507 Dancreas	oor I allorgas	508 Pancreas	509 Pancreas	510 Pancreas	511 Pancreas	512 Pancreas	513 Pancreas	514 Pancreas	515 Pancreas	516 Pancreas	517 Pancreas	518 Pancreas	F40 D200000	o i s Faircreas	520 Pancreas	521 Pancreas	522 Pancreas	523 Pancreas	524 Pancreas	525 Pancreas	526 Pancreas	527 Pancreas	528 Pancreas

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520	590 Dancreas	0.4043070				M55682_s_a	
043	r all cras	0.1013076	1	ر دن	0.20048128 t		CRTM Cartilage matrix protein
530	530 Pancreas	0.1011229	- 1	0	0.20635456 M98343	8343_at	Amplaxin (EMS1) mRNA
234	531 Pancreas	0.1008726	0.4123334	0.339715	0.20623834 X17651	7651_at	MYOG Myogenin (myogenic factor 4)
C L		0					Ovarian cancer downregulated myosin heavy chain homolog (Doc1)
532	Pancreas	0.1006438	0.4121501	0.339641	0.20615427 U53445	3445_at	mRNA
533	533 Pancreas	0.1005173	0.4119512	0 330417	J00098	J00098_cds	
534	534 Pancreas	0 1004105	- 1	0.330411	0.2000109118	מון	Apolipoprotein C-III::apolipoprotein A-I
	200	0.1001.0	- 1	0.0339030	บ	469 at	Mitochondrial creatine kinase (CKMT) gene
535	535 Dancreas	0.4009534			RC	<u>_1</u>	EST: zv15e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
200	Foe Dongress	0.1002331	۱-		0.2059537940	s at	753742 3', mRNA sequence. (from Genbank)
250	ן מוכומא	0.0990173	0.411843	0.338754	0.20582399 U11313	1313_at	SCP2 Sterol carrier protein 2
1	C	1			AA4	AA496215_a	
23/	Pancreas	0.0995893	0.4117179	0.338747	0.20572168 t		clone 796822 5', mRNA sequence. (from Genbank)
520	F39 Dangroom	0.0000		0	RC.	RC_AA1428	EST: zl40h02.s1 Soares pregnant uterus NbHPU Homo sapiens
000	ralicieas	0.0893346	- 1	0.338688	0.20554462 49 at	at	cDNA clone 504435 3', mRNA sequence. (from Genbank)
200	oos raicreas	0.0893295	0.411/005	0.338631	0.20548584 X83228	1228_at	Ll-cadherin
270	000000000000000000000000000000000000000	00000					GJB1 Gap junction protein, beta 1, 32kD (connexin 32, Charcot-Marie-
040	040 Fallcreas	0.0883019	0.4116893	0.338562	0.20533413 X04325	1325 at	Tooth neuropathy, X-linked)
571	541 Dancreae	0.0000440		10000	RC RC	A4560	EST: aa03f02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
770	Denoteds	0.0390.149	- 1	0.338365	0.2052891 55_at		812187 3', mRNA sequence. (from Genbank)
246	242 Fancreas	0.0988109	. 1	0.338358	0.2051208 M86406	at J	ACTN2 Actinin alpha 2
543	543 Pancreas	0.0986825	9	0.338004	0.20502268 U53446	at	Mitogen-responsive phosphoprotein (DOC-2) mRNA
544	544 Pancreas	0.0981786		0.337974	0.20494626 U33	U33267 at	Glycine receptor beta subunit (GLRR) mRNA
545	545 Pancreas	0.098084	0.4110865	0.337969	0.20482378 D38305	्व	Tob
	1				RC	RC_AA4959	EST: zw06e06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
546	546 Pancreas	0.0976737		0.33796	0.20468907 94_at		768514 3', mRNA sequence. (from Genbank)
24/	547 Pancreas	0.0976723	0.4106137	0.337952	0.20452134 X76534	at	NMB Neuromedin B
2/8/2	5/18 Donoroon	0.0075000		1	AA2	AA232837_a	EST: zr44g03.r1 Soares NhHMPu S1 Horno sapiens cDNA clone
2	वाशस्त्र	0.09/3029	0.4106137	0.33/931	0.20445386 t		666292 5', mRNA sequence. (from Genbank)
549 F	Pancrase	0.0027000		100100	RC_	A4959	EST: zw05h01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
2	all closes	0.03/2004	0.4103970	0.33/66/	0.20435306 26		768433 3', mRNA sequence. (from Genbank)
550 F	550 Pancreas	0.0971799	0.4104979	0.337565	0.20419675 7 at	17_rna	Hypothetical protein 384D8 7 gene extracted from Chromosome
551 F	Pancreas	0.096436	0.4104713	0.337517	0.20405622 X79440 at		NADP+-dependent malic enzyme
(1	,				RC	RC_AA3938	EST: zv64c05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
1700	Fancreas	0.0959474	0.4103843	0.337513	0.20399094 03_a	at	clone 758408 3', mRNA sequence. (from Genbank)
553 F	553 Pancreas	0.0958899	0.4101951	0.337424	0.20388122 X66945 at		FGFR1 Basic fibroblast growth factor (bFGF) receptor (shorter form)

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

				H. that tail H term tail		Vered Viant Auge and treef Veref Veref
						EST: zt98b05.s1 Soares testis NHT Homo sapiens cDNA clone
				11	BC AA4700	SOUTHAGE THIOESTEDAGE MEDITIM CHAIN: "DAY SOCIORIES
554 Pancreas	0.0957991	0.40987	0.337334	0.20386134 66 at	36 at	(from Genbank)
555 Pancreas	0.0952122	0.409845	0.337307	0.20369741 Y00318	700318_at	IF I factor (complement)
				7	e 170203A	EST: zx55h09.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
556 Pancreas	0.0		0.337061	0.20362344 t	P 1 1 200 21 V	element;; mRNA sequence; (from Genbank)
557 Pancreas	0.09493	0.4097378	0.336981	0.20350453 U25997	J25997_at	Stanniocalcin precursor (STC) mRNA
558 Pancreas	0.0943425	0.4097345	0.336918	0.20337877 N48927 at	148927 at	EST: yy/5e09.r1 Homo sapiens cDNA clone 279400 5'. (from Genbank)
559 Pancreas	0.0941559	0.4006106	0 336017	1	AA306051_a	
	0.001 100.0	1	0.000917	0.2032343[- 1	KIAAU683 gene product
560 Pancreas	0.0939614	0.4094395	0.336865	RC_A 0.20315278 69_at	A4280	EST: zw57b01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 774121 3', mRNA sequence, (from Genbank)
	•				HG4679-	
561 Pancreas	0.093534	0.4092763	0.336722	0.20311129 HT5104	1T5104_at	Oncogene Ret/Ptc, Fusion Activated
562 Pancreas	0.093391	0.4092578	0.336275	* 05650500 U	X54667_s_a	0.4.1
		200	0.00010	0.20000000		CO 14 Cystaur S
563 Pancreas	0.0926611	0.4092093	0.336223	0.20292598 N31127	V31127 at	EST: yx52e01.r1 Homo sapiens cDNA clone 265368 5'. (from Genbank)
564 Pancreas	0.0922383	1 1	0.335995	0.20288192 U14391	11	Myosin-IC mRNA
565 Pancreas	0.0921624	0.4088525	0.335978	0.20269935 D50582		Inward recifier K channel
566 Pancreas	0.0921418	0.408699	0.335913	0.20259373 D86961		KIAA0206 gene partial cds
					E!	Protein immino-reactive with anti-DTH notyclosed certification and NA
567 Pancreas	0.0916047	0.4085547	0.335878	0.20248578 U28831	J28831_at	partial cds
568 Pancreas	0.0915589	0.4084188	0.335718		Z35402_rna 1_s_at	Gene encoding E-cadherin, exon 3 and joined CDS
						+
569 Pancreas	0.0911742	0.4082805	0.335573	0.20220631 23	at	EST; ae49e10,s1 Stratagene lung carcinoma 937/218 Homo sapiens cDNA clone 950250 31 mRNA secuence (from Genhank)
570 Pancreas	0.090908	0.4082049	0.335512	U.20213962 t	U33052_s_a	I iniciactivated protein binase DDIC2 mDNIA
571 Pancreas	0.090893	1	0.335474	0.2020836 \$75174	75174 at	E2F4 F2F transcription factor 4 n107/n130-hinding
572 Pancreas	0.0908435	0.4078955	0.335391	0.20178682 D43638	043638 at	ETO mRNA
573 Pancreas	0.0903513	0.4075186	0.335297	0.2017477 D14043	014043 at	PUTATIVE MUCIN CORE PROTEIN PRECURSOR 24
574 Pancreas	0.0902054	0.407365	0.335112	0.20164298 D84454 at)84454_at	UDP-galactose translocator
575 Pancreas	0.089557	0.4073069	0.335074	0.20161234 34 at	A4632	KjAA0792 gene product
576 Pancreas	0.089489	0.407287	0.335063	0.20157944 U66033	at	Glypican-5 (GPC5) mRNA

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599 Pancreas	0.0827454	0.405914	0.333063	0.1994687 [L3:	3930_s_at	0.1994687 L33930 s at CD24 signal transducer mRNA and 3' region
000	0000000		700000	- RC	AA2340	RC_AA2340 EST: z74b07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
604 Dengrade	0.0023039	0.4038448	0.333027	0.19943239 bb at	T	bog109 3, mRNA sequence. (from Genbank)
001 Fancieas	0.06231	_	0.332992	0.19932204 L37792 at	// 92_at	Syntaxin 1A mKNA
602 Pancreas	0.082285	- 1	0.332722	0.19916914 L77701	7701_at	COX17 mRNA
603 Pancreas	0.0819284	- :	0.332693	0.19913451 U63455_at	3455_at	SUR Sulfonylurea receptor (hyperinsulinemia)
604 Pancreas	0.0818573	0.4056875	0.332601	0.19902349 X65633	5633_at	ACTH-R gene for adrenocorticotropic hormone receptor
605 Pancreas	0.0818389	0.0818389 0.4056812	0.332522	0.19895706 J05257	5257_at	DPEP1 Dipeptidase 1 (renal)
						Cancellous bone osteoblast mRNA for serin protease with IGF-binding
606 Pancreas	0.0818003	0.4056769	0.332389	0.19891724 D87258 at		motif
607 Pancreas	0.0810012	0.4055005	0.332332	0.19881985 Y00064 at		CHGB Chromogranin B (secretogranin 1)
608 Pancreas	0.0805052	0.4054101	0.332293	0.1987502 U04898		RORA RAR-related orphan receptor A
609 Pancreas	0.0803671	0.4051523	0.332237	RC_A 0.19864947 73 at	RC_AA2783 73_at	Homo sapiens mRNA for KIAA0746 protein, partial cds
				AA	306264 a	AA306264 a EST: EST177232 Jurkat T-cells VI Homo sapiens cDNA 5' end,
610 Pancreas	0.079641	0.4049811	0.332216	0.19859292 t		mRNA sequence. (from Genbank)
					U60808_s_a	
611 Pancreas	0.0794707		0.332099	0.19839124 t		CDP-diacylglycerol synthase (CDS) mRNA
612 Pancreas	0.0789514	0.4048894	0.332077	0.19836743 Y09561 at	9561_at	P2X7 receptor
613 Pancreas	0.0787257	0.40.483.43	0 331000	AB 0.1082021E t	AB002316_a	OF CONTINUE AND A STATE OF CON
644 Dancrose	0.0705060		0.551.550	0.130202131		numan mikiya ior kilaaus is gene, partial cds. (from Genbank)
CAE DEFENDED	0.07070	- 1	0.331748	U.19814326 M97675	;st	Protein tyrosine kinase t-Ror1 (Ror1) mRNA
o 15 Fancreas	0.078423	0.4047233	0.331676	0.197988 U56998	6998_at	Putative serine/threonine protein kinase PRK (prk) mRNA
616 Pancreas	0.0776481	0.4046421	0.331413	ME 0.19791195 t	M58286_s_a t	TNFR1 Tumor necrosis factor receptor 1 (55kD)
617 Pancreas	0.0776421	0.4044043	0.33112	0.19782032 M65199 at	35199 at	EDN2 Endothelin 2
						EST: zs26b12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
618 Pancreas	0.0775303	0.0775303 0.4043191	0.330985	RC_A 0.19777517 87.3t	AZ0Z8	IMAGE: 086303 3' similar to contains Alu repetitive element;, mKNA seguence (from Ganbank)
619 Pancreas	0.0757827	0.4042187	0.330973	0.19763578 L41351	1351 at	Prostasin mRNA
620 Pancreas	0.0756736	0.4041202	0.330935	0.19755837 U05291_at	5291_at	FMOD Fibromodulin
621 Pancreas	0.0755747	0.4040855	0.330927	0.19745106 UZ	2028 r at	0.19745106 U22028 r at Cytochrome P450 (CYP2A13) gene
622 Pancreas	0.0752706	0.0752706 0.4040651	0.33071	0.19739838 M37435 at	17435 at	CSF1 Colony-stimulating factor 1 (M-CSF)
623 Pancreas	0.0751096	0.4040651	0.330642	0.19732223 X12901_at		VILLIN
624 Pancreas	0.0750878	0.4039925	0.330558	0.19723009 at	L41919_rna1 at	HIC-1 gene fragment
625 Pancreas	0.0749503	0 4035203	0.330552	HG2604- 0 19717816 HT2700	Ta	Dan_2
	2000	1	2000000	0.01.00	5	7.117.1

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65 EST: zq94e07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 649668 3', mRNA sequence. (from Genbank)	s_a PXMP1 Peroxisomal membrane protein 1 (70kD, Zellweger syndrome)	at COX7A1 Cytochrome c oxidase subunit VIIa nolynentide 1 (muscle)	at MALATE OXIDOREDUCTASE	at Lysophosphatidic acid acyltransferase-beta mRNA					at Protein-tyrosine phosphatase	a,		at	Sa Annovill II discondigual	Homo sapiens mRNA for villin-like protein complete cle (from			1				-	ज	1 IEX-1	a Nebulin mRNA. partial cds	-		Malianorin-5 (AODS) rene	
RC_AA2165 89_at	181182			U56418 a	RC_AA4436	67_at	D87438_a	M18079_e	D64053_a	U01691_s_t	Y12670_at	S69272 s	M62895_s_a		D88154_a	RC_AA3996	33 at	L42379_at	D82347_at	J00277 at			581914_at	U35637_s_ t	U78095_at	HG4052-	146569 at	U84569_al
RC_A 0.19707073 89 at	0.19697988 t	0.19690345 M83186	0.19684352 U43944	0.19679824 U56418		0.1967322 67_at	0.19662224 D87438_at	0.19652843 M18079_at	0.19641562 D64053	0.19622745	0.19612709	0.19607201 S69272 s	0.19601893		0.19587103 D88154 at		0.195/3468 33	0.195552561.42379	0.1955421 D82347	0.1954168 300277	0.00.00	0.1953942 216411	0.1952/598 S81914	0.19513087 t	0.19511808 U78095	HG4052-	0.19494246 1146569	0.19486268 U84569 at
0.330394	0.330286	0.330238	0.330163	0.330163		0.330064	0.329905	0.329892	0.329783	0.329601	0.329559	0.329464	0.32939		0.329371	7	0.329325	0.329191	0.329091	0.329025	0000000	0.328989	0.3288/6	0.328857	0.328832	0 328782	0.32872	0.328578
0.4034933	0.4034843	0.4033777		0.4033165		0.4033131	0.4032323	0.4031362	0.4030623	0.402816	0.4024667	0.4022011	0.4020826		0.402037	0 404 000 4	0.4010004	0.4018324	0.4017611	0.4016902	0.4046094	0.4010034	0.4013907	0.4012235	0.4012144	0.4011256	0.4010988	0.4007911
0.0745711	0.0745633	0.0743295	0.0742191	0.0740601	6	0.0736893	0.0731634	0.0728746	0.0727107	0.0724607	0.0724527	0.0722438	0.0718779		0.0713764	0.0744809		0.0703004	0.0708247	0.0707143	0.070350	- 1	0.01020		0.0697996	0.0694097	-	1 1
626 Pancreas	Pancreas	628 Pancreas	629 Pancreas	630 Pancreas	C	631 Pancreas	632 Pancreas	633 Pancreas	634 Pancreas	635 Pancreas	636 Pancreas	637 Pancreas	638 Pancreas		639 Pancreas	640 Dancreas	641 Pancreas	allocas	042 Fancreas	Pancreas	644 Pancreas	645 Pancreae	200	646 Pancreas	647 Pancreas	648 Pancreas	649 Pancreas	650 Pancreas
626	627	628	629	930	Š	631	0.32	633	634	635	929	637	638		639	640	641	100	740	643	644	645	2	646	647	648	649	650

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Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors

Inventors: Sridhar Ramaswamy, et al.

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651	Pancreas	0.0686109	0.4007261	0.328456	0.19478604	J84569_at-2	0.19478604 U84569_at-2 Chromosome 21 open reading frame 2
	1					J04152_rna1	J04152_rna1 M1S1 gene extracted from Human gastrointestinal tumor-associated
652	652 Pancreas	0.0678274	- 1	0.328266	0.19463858		antigen GA733-1 protein gene, clone 05516
653	653 Pancreas	0.0674938	1	0.328124	. 0.1946017 U21931_	_at	FBP1 Fructose-bisphosphatase 1
654	654 Pancreas	0.0667722	0.4003489	0.327991	0.19451174 U95367	at	Human GABA-A receptor pi subunit mRNA, complete cds
655	655 Pancreas	0.0667504	0.4003232	0.327877	0.19440651 X95876	aţ	G-protein coupled receptor
929	656 Pancreas	0.0666562	0.4003226	0.327844	0.19435789 D85429 at		DNAJ PROTEIN HOMOLOG 1
657	657 Pancreas	0.0665032	0.4002916	0.327819	0.19429946 M31013	Г	MYH9 Myosin, heavy polypeptide 9, non-muscle
658	658 Pancreas	0.06597	0.4002819	0.3278	0.19415566 M73720	at	CPA3 Carboxypeptidase A3 (mast cell)
629	659 Pancreas	0.0657443	0.3999901	0.327781	0.19409369	AB002380_a	KIAA0382 gene, partial cds
099	660 Pancreas	0.0656389	0.3999532	0.327731	0 194029851	X55019_s_a	CHRND Cholinerale recentor nicotinic delle notanentide
661	661 Pancreas	0.0656389		0.327577	X5: 0.19394241 t-2	5019_s_a	Cholineraic receptor nicotinic delta nolvaentide
662	662 Pancreas	0.0656329	0.3998449	0.327484	0.19378129 U73682 at	1	Meningioma-expressed antigen 6 (MEA6) mRNA
693	Pancreas	0.065575	0.3998072	0.327479	RC_A 0.19375148 88_at	A1714	Homo sapiens clone 24778 unknown mRNA
664	664 Pancreas	0.0654741	0.3997836	0.327478	0.19369625	S79854 at-2	0.19369625 S79854 at-2 Deiodinase, iodothyronine, type III
665	665 Pancreas	0.0654741	0.3996081	0.327453	0.19362615 S79854	S79854 at	Type 3 iodothyronine deiodinase
999	666 Pancreas	0.0650274	0.3992822	0.327346	0.19352014 L17128 at		GGCX Gamma-glutamyl carboxylase
299	667 Pancreas	0.0649902	0.3992768	0.327227	0.19337107 M64788_at		RAP1GA1 RAP1, GTPase activating protein 1
899	668 Pancreas	0.0648868	0.3991098	0.327027	0.19328368 Z26653 at		LAMA2 Laminin, alpha 2 (merosin, congenital muscular dystrophy)
699	669 Pancreas	0.0647603	0.3990901	0.326945	0.19325253 X89066_at		TRPC1 Transient receptor potential channel 1
670	670 Pancreas	0.0647027	0.3989755	0.326941	RC_A 0.19318736 54 at	RC_AA1325 54_at	RC_AA1325 clone 587486 3' similar to SW:MDCE_MOUSE P21271 MYOSIN-LIKE 54 at PROTEIN.; mRNA sequence. (from Genbank)
671	Pancreas	0.0644335	0.3989382	0.326722	RC_A 0.19307046 00_at	A4020	EST: zu55b03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741869 3' similar to TR:G452270 G452270 2-19 PROTEIN PRECURSOR.;, mRNA sequence. (from Genbank)
672	Pancreas	0.0643771	0.3985494	0.326635	RC_A 0.19302645 67_at	RC_AA4559 67_at	Neuronal PAS domain protein 2
673	673 Pancreas	0.0641495	0.3985007	0.32661	0.19286697 66 s at	RC_AA3484 66 s at	Regulator of G-protein signalling 5
674	674 Pancreas	0.0630208	0.398468	0	0.19278526	AA303711_a t	Ephrin-B1

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Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswanıy, et al.

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675 Pancreas	0.0627377	0.3982904	0.326399	0,19263771	AA295819_s at	AA295819_s EST: EST101121 Thymus III Homo sapiens cDNA 5' end, mRNA at
676 Pancreas	0.0619927	<u> </u>	0.326291	0.19251992	D83735 at	Adult heart mRNA for neutral calponin
677 Pancreas	0.0617258	0.3981172	0.326291	0.1924785 X05615	X05615_at	Thyroglobulin
670 Description			1		AA487015_s	
670 Dangges	+	- 1	0.326217	0.19238625	at	clone 841769 5', mRNA sequence. (from Genbank)
ory rancieas	5		0.326199	0.19225594 M59499 at	M59499_at	TISSUE FACTOR PATHWAY INHIBITOR PRECURSOR
bgu Pancreas	0.06124	0.3979077	0.32618	0.19214974 L13391	L13391_at	REGULATOR OF G-PROTEIN SIGNALLING 2
004 Denough	7.1.707.00				AA426304_r	EST: zw11g07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
00 Pallueas	0.0010174	0.39/8/36	0.326137	0.19206993	at	769020 5', mRNA sequence. (from Genbank)
000	100000		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		AB000897_a	
obs Pancreas	0.0603275		0.32605	0.19201934		Cadherin FIB3, partial cds
683 Pancreas	0.060263		0.326006	0.19197464 D82675	D82675_at	EST: similar to none, mRNA sequence, (from Genbank)
684 Pancreas	0.0601004	- 1	0.325751	0.19189379 X54162	X54162_at	64 KD AUTOANTIGEN D1
685 Pancreas	0.0600266	0.3974408	0.325682	0.19177243 M17466	M17466_at	F12 Coagulation factor XII (Hageman factor)
686 Pancreas	0.0592057	0.3974216	0.325567	0.19171983 \\ Y00317	Y00317 at-2	
687 Pancreas	0.0592057	0.397/179	0 325522	0.4046000		UDP-GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR,
	0.00000	L	0.02000	0.1910002 100317	rousi/_at	MICKUSOWAL
688 Pancreas	0.0587257	0.3973526	0.325521	0.19148682	AA095600_a t	L5079.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', mRNA sequence (from Genhank)
						Clone pSK1 interferon gamma receptor accessory factor-1 (AF-1)
689 Pancreas	0.0584491	0.3972171	0.325489	0.19141361 U05875	J05875_at	mRNA
						EST: zk97d12.r1 Soares pregnant uterus NbHPU Homo sapiens
						cDNA clone 490775 5' similar to gb:L32179 Human arylacetamide
690 Pancreas	0.0583136	0.3971216	0.325449	0.19129473		deacetylase mRNA, complete cds. (HUMAN);, mRNA sequence. (from Genbank)
0	1				M24122_s_a	
691 Pancreas	0.0578924	- 1	0.32542	0.19123964		MYL3 Myosin, light polypeptide 3, alkali, ventricular, skeletal, slow
692 Pancreas	0.05765	- 1	0.325414	0.1911619 L48513	.48513_at	Paraoxonase (PON2) mRNA
693 Pancreas	0.05/5461	0.3970162	0.325373	0.19105273 U79258	J79258_at	Clone 23732 mRNA, partial cds
694 Pancreas	0.0570444	0.3969659	0.32527	0.19090556 U64871	J64871_at	G protein-coupled receptor GPR-NGA gene
695 Pancreas	0.056731	0.3968439	0.325195	RC_A 0.19087186 84_at	RC_AA4238 84_at	Homo sapiens mRNA for KIAA0287 gene, partial cds
696 Pancreas	0.0566979	0.3968068	0.325079	0.19085953	D50855_s_a t	CASR Calcium-sensing receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism)
697 Pancreas	0.0566699	0.3967628	0.325048	0.1906883 M22960_at		PPGB Protective protein for beta-galactosidase (galactosialidosis)
698 Pancreas	0.0561367	0.3966727	0.324969	0.19067462 t	AC002077_a	AC002077_a GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-1 t
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						U20758_rna	
669 P	699 Pancreas	0.0560136	- 1	0.324911	0.19056943	_at	Osteopontin gene
700 P	700 Pancreas	0.0558856	0.3963859	0.324878	0.19051494 R60605	360605 at	Yh14b06.r1 Homo sapiens cDNA clone 37738 5', (from Genbank)
701 P	701 Pancreas	0.0552527	0.3961977	0.324813	0.19041143 U53786		EVPL Envoplakin
2002		L					
707 F	702 Pancreas	0.0551515		0.324686	0.190331/1 S/1018 at-2	_at-2	Peptidylprolyl isomerase C (cyclophilin C)
/03 P	ancreas	0.0551515	0.3960319	0.324561	0.19022691 S71018	,at	Cyclophilin C [human, kidney, mRNA, 883 nt]
1		1				12471_cds	Thrombospondin-p50 gene extracted from Human thrombospondin-1
704 P	704 Pancreas	0.0551309	0.3959803	0.324547	0.190173491	_at	gene, partial cds
						X13766_s_a	
705 P	705 Pancreas	0.0547465	- 1	0.32451	0.19006127 t		CSN2 Beta-casein
706 P	706 Pancreas	0.0546628	0.3956415	0.32451	0.18998659 S34389_at	334389_at	HMOX2 Heme oxygenase (decycling) 2
7		1			A	AA358888_a	EST: EST67818 Fetal lung II Homo sapiens cDNA 5' end, mRNA
101	ror Fancreas	0.0546542		0.324502	0.18989405		sequence. (from Genbank)
708 P	708 Pancreas	0.0545703	0.3954237	0.324455	0.18981382 M12125 at	//12125_at	Skeletal beta-tropomyosin
						AA033703_a	EST: zf01d10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA
709 P	709 Pancreas	0.054416	\sim	0.324428	0.18977097 t		clone 375667 5', mRNA sequence, (from Genbank)
710 P.	710 Pancreas	0.0542019	0.395284	0.324403	0.1896241 U28281	J28281 at	SCTR Secretin receptor
711 P.	711 Pancreas	0.0541305	0.3952656	0.324391	0.18953659 U49188	ll .	Placenta (Diff33) mRNA
712 P.	712 Pancreas	0.0539464	0.3952472	0.324258	0.18949248 M91083	äţ	DNA-binding protein (HRC1) mRNA
713 P.	713 Pancreas	0.0535458	0.3952055	0.324239	0.18942979 Y08136 at		ASM-like phosphodiesterase 3a
714 P.	714 Pancreas	0.0535063	0.3951488	0.324234	0.18934222 U78313 at	J78313 at	Myogenic repressor I-mf (MDFI) mRNA
						RC AA4044	EST: zw38a06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
715 P.	715 Pancreas	0.0533906	- 1	0.324161	0.18930747 87	17_at	clone 772306 3', mRNA sequence, (from Genbank)
716 P.	716 Pancreas	0.0529316	- 1	0.3241	0.18924192 U09860	J09860 at	PRSS7 Protease, serine, 7 (enterokinase)
717 P.	717 Pancreas	0.052749	0.3949802	0.32409	0.18909808 M21302 at	A21302 at	Small proline rich protein (sprll) mRNA, clone 174N
718 P _i	718 Pancreas	0.0525981	0.3949701	0.324059	0.18900725 t	M91368_s_a t	Na+/Ca+ exchanger (CNC) mRNA
719 P.	719 Pancraas	0.0518023	0.3040474	0.322005		AB002296_a	
		0.0010020	1 2 2 2 2 2 2	0.050300	0.10090332	07770	MIAAU298 gene product
720 P	720 Pancreas	0.0518132	0.394871	0.323713	0.18883476 1 s at	Auz419_ma 1 s af	IPA nene
79.4 Pg	791 Pancreae	0.0547804	0.3046969	003666	T 0000 0	3985	EST: 273b05.s1 Soares testis NHT Homo sapiens cDNA clone
7007	and and	0.0211004	0.0340030	0.323386	U.1880//03/33 at		72/953 3', mKNA sequence. (from Genbank)
177)	/ ZZ Pancreas	0.0517782	0.3946/45	0.323564	0.18861987 X64810	(64810_at	PCSK1 Proprotein convertase subtilisin/kexin type 1
723 Pa	723 Pancreas	0.0508785	0.3944626	0.323531	0.18853721 W27650_	V27650_at	EST: 36e12 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)
724 Ps	724 Pancreas	0.0508736	0 30/3030	0.322534	18846E73 L	HG3236-	Nourseffbromofonia 9 Tomor Ounaconne (Ch. 197065)
11.7	con con	0.000000	0.0040002	0,02000	0.100403131	113413 1 at	0.100403/3/11/34/3 1 at Ineuroribroniatosis z Turrior Suppressor (GD.LZ7003)

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705 Dancross	0.0608008	0 3043844	0 322510	HG3517		Almaho A Andidan maning Francis
700 1000	+	ŧ	0.022319	0.10030033	- 11	Alpha-1-Annuyban, o End
/ Zb Pancreas	7	7	0.323492	0.18830512 M59911	M59911_at	ITGA3 Integrin alpha-3 subunit
727 Pancreas		-	0.323478	0.18823019 M96789_at	M96789_at	GJA4 Gap junction protein, alpha 4, 37kD (connexin 37)
728 Pancreas	s 0.0502943	0.394157	0.323405	0.18816702 X93510_at	X93510_at	37 kDa LIM domain protein
					U45878 s a	
729 Pancreas	s 0.0498247	0.3938775	0.323309	0.18809421		Inhibitor of apoptosis protein 1 mRNA
730 Pancreas	s 0.0493286	0.3937683	0,323305	0.18798196 M96132	M96132 at	MHC class II HLA-DR-beta-1*09012 (HLA-DRB1*09012) gene, 3'end
	-					(genomic clones lambda-fSK2-T2, HS578T1; cDNA clones RS-f3.4, 61)
731 Pancreas	s 0.0491917	0.3937386	0.323068	0.18782736 V00574 s	V00574_s_at	at c-Ha-ras1 proto-oncogene, complete coding sequence
732 Pancreas	s 0.0491057	0.3936019	0.323064	0.18776813	AA418143_a	AA418143_a EST: zv97b09.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
733 Pancreas	╁┈	1	0.32264	0.18768327 X97058 at	X97058 at	P2Y6 receptor, short solice variant mRNA
					X60673_rna	
734 Pancreas	s 0.0487488	0.3935328	0.322351	0.18765172	1 at	AK3 mRNA for adenylate kinase 3
					HG2755-	
/35 Pancreas	s 0.048641	0.3934996	0.322332	0.18757597 HT2862	HT2862_at	T-Plastin
						Hypothetical human protein R31240_2 gene extracted from Homo
						sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272
000			- 1	*	4D000092_c	AD000092_c and R28549 containing the EKLF, GCDH, CRTC, and RAD23A
/36 Pancreas	s 0.0485113	0.3934173	0.322328	0.18757421 ds2_at	ds2_at	genes, genomic sequence
1			;		AA464051_s	EST: zx86d04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
/3/ Fancreas	\dashv	0.3933761	0.322276	0.18735895	at	clone 810631 5', mRNA sequence. (from Genbank)
738 Pancreas	\dashv	0.3932881	0.322081	0.18726256 L36033	L36033_at	SDF1 Stromal cell-derived factor 1
739 Pancreas	s 0.0483683	0.3932245	0.321989	0.18721056 X78706_at	X78706_at	CRAT Carnitine acetyltransferase
				/	AF001548 r	815A9.1 gene (myosin heavy chain) extracted from Homo saniens
740 Pancreas	s 0.0481097	0.3930922	0.321475	0.18712951 na1	at	chromosome 16 BAC clone CIT987SK-815A9 complete sequence
					RC_D25942	EST: Human colon 3'directed Mbol cDNA, HUMGS06716, clone
741 Pancreas	+		0.321413	0.18705058	rat	cm2781, mRNA sequence. (from Genbank)
742 Pancreas	\neg		0.3214	0.18695353 D28137	D28137_at	RPS11 Ribosomal protein S11
743 Pancreas			0.321345	0.18681973 U73377	J73377 at	SKI V-ski avian sarcoma viral oncogene homolog
744 Pancreas	s 0.0474275	0.3928776	0.321279	0.18671212 U90905	J90905_at	Clone 23574 mRNA sequence
745 1300000			0	1	RC_AA4914	EST: ab01d12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
140 กลาดเคลร	2		0.3212	0.18668373 63_at	og_at	clone 839543 3', mRNA sequence. (from Genbank)
746 Pancreas	\dashv	- 1	0.321177	0.18656825 D31887_at	J31887 at	KIAA0062 gene, partial cds
747 Pancreas	s 0.0467393	0.3927784	0,321175	0.18653668 D43968	D43968_at	CBFA2 Proto-oncogene AML1 {alternative products}
748 Pancreas	s 0.0458387	0.3926974	0.321026	0.18644363	M27749 r at	0.18644363 M27749 r at Immunoglobulin-related 14.1 protein mRNA
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749 Pancreas	0.0454475	0.3926883	0.320905	0.18636368 X53416_at	El N1 Filamin 1 (actin-binding protein-280)
750 Pancreas	-		0.320852	0.1863169 U07664 at	HB9 homeobox gene
1		1	-	X61755_rna	
751 Pancreas	1		0.320764	0.18625695 1 s at	HOX3D gene for homeoprotein HOX3D
752 Pancreas	0.0446037	0.3924094	0.320726	0.18619926 M90696_at	CTSS Cathepsin S
753 Pancreas	0.0441947	0.3923088	0.32069	X58298_s_a 0.18607153 t	IL6R Interleukin 6 receptor
				RC AA4963	EST: zv37c09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
754 Pancreas			0.320522	0.18603428 66_at	clone 755824 3', mRNA sequence. (from Genbank)
755 Pancreas	-		0.320457	0.18595268 L02648_at	
756 Pancreas	-	0.3920745	0.320356	0.18583295 X72308_at-2	
757 Pancreas	-	0.3920402	0.320237	0.18578789 X72308_at	MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR
758 Pancreas	0.0422934	0.3918841	0.320117	0.18572955 D84110 at	RBP-MS/lype 1
750 Dancreas	80866700	0.3048400	0 240044	HG2724-	
1 33 1 31 10 533	+			0.1630609 H12620 at	
760 Pancreas	0.0421554	0.3916346	0.319902	KC_AA4300 0 18563306 36 at	EST: Zw65r10.s1 Soares tests NHT Homo sapiens cDNA clone 781099 3' mRNA ceruance (from Genhank)
761 Pancreas	1	1		0.18554850 X70200 at	Homo cholone mDNA for SVT SSV protein
	+		0.0	0.10304039 X19200 at	POLA and extracted from Human la acamino Habain O P A rouise
762 Pancreas	0.0416487	0.3916132	0.319733	0.18540572 5_at	A: gamma-3 5' flank
		L		HG3415-	
763 Pancreas	0.0415134	0.3914889	0.319603	0.18531708 HT3598_at	Poliovirus Receptor
	-			RC_AA4875	EST: ab23e01.s1 Stratagene lung (#937210) Homo sapiens cDNA
764 Pancreas	-		0.319581	0.18530028 58_at	clone 841656 3', mRNA sequence. (from Genbank)
765 Pancreas		- 1	0.31938	0.1852204 L22548 at	COL18A1 Collagen, type XVIII, alpha 1
766 Pancreas	0.0414315	0.3913104	0.31929	0.1852084 U12535 at	Epidermal growth factor receptor kinase substrate (Eps8) mRNA
767 Pancreas	0.0413034	0 3040084	0 340085	AF015950_a	TTTT/
768 Pancreas	+-		0.319167	0.18502258 D25274 at	Randomly sequenced mRNA
	\vdash		The state of the s		Transforming growth factor-beta induced gene product (BIGH3)
769 Pancreas	0.0411955	0.3911472	0.319141	0.184944 M77349_at	mRNA
() ()					Germline Ig alpha mutant chain gene C-alpha-3 region of the secreted
770 Pancreas	-	. !	0.31913	0.18483837 M85220_at	protein, 3' end
771 Pancreas		0.3910221	0.319023	0.18472582 X71125 at	Glutamine cyclotransferase
772 Pancreas	0.0		0.318967	0.1846892 U77180_at	EBI1-ligand chemokine
773 Pancreas	0.0407	0.3909498	0.318924	0.18460506 D87434_at	KIAA0247 gene
!				M97925_rna	
774 Pancreas	0.0406888	0.3907001	0.318829	0.18451984 1_at	Defensin 5 gene
775 Pancreas	0.0401114	0.3903465	0.318764	0.18444523 U09210 at	SLC18A3 Solute carrier family 18 (vesicular acetylcholine), member 3
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776 Pancreas	0.0398312	0.3902517	0.318744	0.18440726 U45285 at	
777 Pancreas	0.0397135	0.390192	0.318743	0.18431243 U40380	
778 Pancreas	0.0387974	0 3901587	0318565	RC_AA4194	
200		200000	2001	0.1041001401 al	INDAMESTRACION OF THE CONTROL OF THE
779 Pancreas	0.0385597	0.3901347	0.318405	AAZ8/ / 49_a 0.1841216 t	49_a zs51b11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700989 5', mRNA sequence. (from Genbank)
780 Pancreas	0.0377284	1	0.318386	0.1840631 M36803	at
781 Pancreas	0.0373459	0.3900852	0.31831	0.18403506 U52100	at
782 Dangrage	0.0360604	00000000	007070	U68135_	s a
1021 allords	0.0303034	1	0.318109	0.183962051	S1c, mKNA sequence
783 Pancreas	0.0365574	0.3899592	0.318104	0.18377244 1_s_at	rna Receptor tyrosine kinase DDR gene
784 Pancreas	0.035841	0.3895468	0.318052	0.18372366 Z68228	0.18372366 Z68228 s at JUP Junction plakoglobin
				RC_AA	RC_AA4781 EST: zt89e03.s1 Soares testis NHT Homo sapiens cDNA clone
785 Pancreas	0.0352118	0.3894484	0.317833	0.18364914 12 at	729532 3', mRNA sequence. (from Genbank)
786 Pancreas	0.0346144	0.3893405	0.31782	0.18356068 at	59_s GLUT1 C-terminal binding profein
787 Pancreas	0.0344629	0.3892617	0.31782	0.18353364 Z24725	at
0					T
/88 Pancreas	0.0344202	0.3892587	0.317811	0.18341781 W25945 at	
789 Pancreas	0.0343859	0.380108	0 247740	AB002325_a	
790 Pancreas	0.0342803		0.347704	0.1000000001	\top
200	0.0001 020	- 1	0.317701	0.1032/224 U3944/ at	٦,
791 Pancreas	0.0334188	0.3891069	0.317633	RC_AA2341 0.18315534 12 at	:341 EST: zr74a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669104 3', mRNA sequence. (from Genbank)
792 Pancreas	0.0333544	0.3890183	0.317568	0.1830357 U40434	at
C C				HG429-	
/93 Pancreas	0.0333063	0.0333063 0.3888591	0.317526	0.18297827 HT429	1t
794 Pancreas	0.0330798	- 1	0.31746	0.18290998 U02556	at RP3 mRNA
795 Pancreas	0.0329533	1	0.317316	0.18282567 Y08639 at	at Nuclear orphan receptor ROR-beta
796 Pancreas	0.0328809		0.317273	0.18273741 U67171	at
797 Pancreas	0.032871	0.3884676	0.317206	0.18266168 U91903	at Frezzled (fre) mRNA
798 Pancreas	0.0326147	0.388227	0.317117	AB002332 0.1825429 t	w.
799 Pancreas	0.0326079	0.3880671	0.31704	M13452_s_a	S_a LMNA Lamin A
800 Pancreas	0.0324061	0.3879441	0,316879	0.18245973 D14823 at	
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Heat shock profein (hsp 70) gene	DNA-BINDING PROTEIN MEL-18	EST: zv22d06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	754379 3' similar to contains Alu repetitive element;contains L1.t3 L1	repetitive element ;, mRNA sequence. (from Genbank)	EST: zt52g05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 726008 3', mRNA sequence. (from Genbank)	Clone 23759 mRNA, partial cds	DRA Down-regulated in adenoma		clone 784128 3', mRNA sequence. (from Genhank)	EST: HUMRTPGEM Homo sapiens cDNA (from Genhank)	Type II iodofhyronine deiodinase mRNA	EST: zs15h06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	Mesothelial kenatin K7 (tuna II) wanta a	mesonicia na anii N (iybe ii) iiiRNA, 3 end	Claudin 4	IFN-omega 1 gene for interferon, omogo 4		BAC clone GS244B22 from 7q21-q22, complete sequence		NF-IL6-beta profein mRNA	100	Outcoulong releasing normone receptor 1	Dysirogrycan (DAGT) IIIRNA	Cpg-Enriched Dna, Clone S19	ERBB2 V-erb-b2 avian erythroblastic leukemia viral oncogene	remarge (incurve) in the deliver of the population of the populati	I and the state of	Metallothionaln isoform 2	STS Steroid sulfatase (microsomal)	RC_AA6217 EST: af54e12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 14_at clone 1035502 3', mRNA sequence. (from Genbank)
M11717_ma 1 at	D13969 at		RC_AA4361	74_at	RC_AA3941				44320		M91392_at	U53506 at	12435	7	1	_atat	. ma	150_a		83667_ma	s at	X72304_s_a	ta			(03363_s_a	lG4683-	T5108_s_a	T	\top	3C_AA6217 14_at c
0.18040824 1 at	0.18039578 D13969			0.18039241 74 at		0.18027721	0.1802232 U79241	0.18013038 L02785 at		0.18004806 74_at	0.17994042 M91392	0.17992336 U53506	RC_A 0 179826 62 34	0.17971656 M13955 at		0.17968687	X58822 0.17963299 1 s at		0.1796093	i	0.179516021	0 17942718	0.17935938 19711		0.17935938 HT4265_at	X 0.1792777†t		0 17913444	0.17907988 V00594 at	0.17906326 M16505 at	0.1790029114_at
0.315454	0.315412		· c	0.31539				0.315228			0.314943	0.314932	0.314897	0.314814		0.31476	0.314752		0.314725	0.704.40.70	0.314053	0.314628	0.31453		0.314416	0.314377		0.314314	0.314192	0.314158	0.314108
0.3861498	0.3861168		0 30602	\bot	0.3860465	- 1	l.	0.3859116		0.363909	0.027665 0.385/677	0.02/3305 0.385/462	0.3857426	0.3857287		0.3857287	0.3857121		0.3836923	O 3856960		0.3856348	0.385612		0.385607	0.385607		0.3854704	0.3854447	0.3854392	0.3854319
0.0283829	0.0283379		782287	0.020201	0.0281155	0.0201133	0.0273944	0.021/8/1	0.0277647	0.0277000	0.027665	0.02720.0	0.0270495	0.02702		0.0269895	0.026901	0.009000	0.020000	0.0266984	1000000	0.0266384	0.0266116		0.0265/1	0.0264226		0.026225	0.0262104	0.0258902	0.0255124
825 Pancreas	826 Pancreas		827 Pancreas	cas de la casa	828 Pancreas	879 Pancrose	830 Dangraga	oso r alloreas	831 Pancreae	830 Deportors	822 Departed	जन्म जाताच्या जन्म	834 Pancreas	835 Pancreas		836 Pancreas	837 Pancreas	838 Pancrase	choin loop	839 Pancreas		840 Pancreas	841 Pancreas	042	042 FallCreas	843 Pancreas		844 Pancreas	845 Pancreas	846 Pancreas	847 Pancreas

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors the state that the season and the state of t

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswa.ny, et al. EST: ze76a01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA SOX9 SRY (sex-determining region Y)-box 9 (campomelic dysplasia, AA011479_a|EST: zi01b10.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens EST: HUMGS0003774, Human Gene Signature, 3'-directed cDNA EST: Human HL60 3'directed Mbol cDNA, HUMGS01145, clone CTNNA1 Catenin (cadherin-associated protein), alpha 1 (102kD) EST: zs80f03.s1 NCI CGAP GCB1 Homo sapiens cDNA clone Gamma-Aminobutyric Acid (Gaba) A Receptor, Alpha Subunit Mitogen-activated kinase kinase 5 (MAPKKK5) mRNA PTPN12 Protein tyrosine phosphatase, non-receptor type 12 EST: HUMRTPGEAL Homo sapiens cDNA. (from Genbank) Homo sapiens mRNA for putative Sqv-7-like protein, partial cDNA clone 429499 5', mRNA sequence. (from Genbank) Intestinal peptide-associated transporter HPT-1 mRNA IMAGE:703805 3', mRNA sequence. (from Genbank) APOLIPOPROTEIN AI REGULATORY PROTEIN-1 clone 364872 3', mRNA sequence. (from Genbank) Cell division cycle 42 (GTP-binding protein, 25kD) sequence, mRNA sequence. (from Genbank) pm2260, mRNA sequence. (from Genbank) (HepG2) glucose transporter gene mRNA Oncogene Aml1-Evi-1, Fusion Activated AFFX-LysX-5_at (endogenous control) Snk interacting protein 2-28 mRNA MEOX1 Homeobox protein mox1 PRKCD Protein kinase C, delta autosomal sex-reversal) Pur (pur-alpha) mRNA DLX-2 (DLX-2) gene Cystatin SN 0.1776285 C01811 f at HT2660_s_a AA431505_a RC_AA0244 U07969_s_a RC AA2783 U51003_s_a RC D20171 AFFX-LysX-RC AA4880 0.17754743 M96684 at 0.17749256 K03195 at 0.1785819 HT4328 at 0.17842634 M93425 at 0.1780755 M64497_at 0.17804883 M91493 at 0.17795952 U67156 at 0.17771026 M19169 at 0.17746082 D10495 at 0.1783034 U10492 at 0.1780225 U03100_at 0.17820074 Z46629_at 0.17770809 U85611 at HG2564tat HG4058-0.17888783|82 at 0.17863908 74 at 0.17738783|5 at 0.17839518 at 0.17892605 29 0.17823067 t 0.17812856|t 0.17877142 0.17778233| 0.17880717 0.312511 0.314049 0.313868 0.313719 0.313719 0.313442 0.313216 0.312916 0.313663 0.313292 0.313274 0.313124 0.313847 0.313562 0.313357 0.313117 0.313024 0.312934 0.312863 0.312822 0.31269 0.312684 0.312584 0.312887 0.0238274 0.3846764 0.0239828 0.3849711 0.0228041 0.3840572 0.0223422 0.3839934 0.0207598 0.3834124 0.0248002 0.3854228 0.0246769 0.3853476 0.3840275 0.0215241 0.3837043 0.0251997 0.3854319 0.0249567 0.3854254 0.0210133 0.3834915 0.023641 0.3842898 0.3840372 0.385281 0.385217 0.384407 0.0228214 | 0.3842488 0.0221932 0.3839398 0.383853 0.0214896 0.3836268 0.0212778 0.3835089 0.024243 0.3851121 0.021531 0.3838234 0.0246648 0.0224255 0.0243452 0.0237864 0.0220404 0.0223697 856 Pancreas 855 Pancreas 849 Pancreas 850|Pancreas 851|Pancreas 852 Pancreas Pancreas 860 Pancreas 861 Pancreas 862 Pancreas 863 Pancreas 864 Pancreas 865 Pancreas 867|Pancreas 868 Pancreas 848|Pancreas 853 Pancreas 854 Pancreas 858 Pancreas 859|Pancreas 866 Pancreas 869|Pancreas 870 Pancreas 871 Pancreas

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al*.

0.0207598 0.3833924 0.312483 0.17737393 5_at-2 AFFX-LysX-5_at (miscellaneous control - 11k chips)	0.3833924 0.31	0.3832988 0.312378 0.17719974 X73029 at	X89986_s_a	0.3832488 0.312359 0.	0.3832371 0.312289 0.177019 M33308_at	0.3831261 0.312266 0.17700893 M37763 at	EST: zk34e10.s1 Soares pregnant uterus NbHPU Homo sapiens RC AA0376 cDNA clone 484746 3' similar to DIR: \$18878 \$18878 in a notein	0.3829823 0.312222 0.17697026 51 at	0.3829823 0.312177 0.17692587 HT3749 at	0.3829767 0.312165 0.17681041 N56451 at	0.3828223 0.344089 0.47667542222 2.	0.38281 0.311899	0.38277230 0.3447E7 0.47EE46.43 34	0.3021139 0.311131 0.110340	0.3827105 0.311746 0.17650795	X98534 s.a	0.3826/26 0.311/09 0.17638993	0.0176302 0.3825615 0.31166 0.17629634 HT174 at Desmoplakin I	0.382545 0.311592 0.17625247 GMCSF at	0.3823973 0.311586 0.17621383 S65738 at	0.0173534 0.3823854 0.311458 0.17608044 Y00815_at PTPRF Protein tyrosine phosphatase, receptor type, f polypeptide	0.3823151 0.311342 0.17604436 U37146 at	0.0170954 0.382247 0.311198 0.17594041 t Genbank)	 HT1803_s_a 0.0170875; 0.3822207 0.311105 0.17500031	0.3821062 0.311173 0.17577389 X95191 at	0.3820921 0.31114 0.17574449 X00038 at	
0.0207598 0.3		0.0201764 0.3		- 1		0.0192371 0.3		0.0190351 0.3	0.0189054 0.3	0.0188678 0.3	0.0186373	1	0.0180150.03	- 1	0.0179569 0.3		0.01/12/4 0.3	0.0176302 0.3		0.0174386 0.3	0.0173534 0.3	0.0171226 0.3	0.0170954 0.	0.0170875 0.3	- 1		
872 Pancreas	873 Pancreas	874 Pancreas		875 Pancreas	876 Pancreas	877 Pancreas		878 Pancreas	879 Pancreas	880 Pancreas	884 Pancreas	882 Pancreas	883 Dancrese	บบบ r นาเกเซล	884 Pancreas	005 000	ooo rancreas			888 Pancreas	889 Pancreas	890 Pancreas	891 Pancreas	892 Pancreas	893 Pancreas	894 Pancreas	ROE DOBOTOOS

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890 Pancreas	\dashv	- 1	0.311085	0.17562294 D87463 at	- 1	KIAA027.3 gene
897 Pancreas	0.0166389	0.3818834	0.310858	0.17557068 M94250_at	M94250_at	MDK Midkine (neurite growth-promoting factor 2)
()						Human Ras-like small GTPase RIBA mRNA, alternatively spliced,
898 Pancreas	0.0163755	0.381864	0.310845	0.17541833 U78166	U78166_at	complete cds
					HG1496-	
899 Pancreas	0.0162663	0.3818345	0.310769	0.17537308	HT1496_s_a t	Adrenal-Specific Protein Do2
	\vdash	ł	-			
900 Pancreas	\neg	9	0.310672	0.1753571	s_at	at Paraoxonase 3
901 Pancreas	0.0159504	0.381728	0.31065	0.17528461 D86960	at	KIAA0205 gene
902 Pancreas	0.0159152	0.3816479	0.310649	0.17524263	AA429793_a	EST: zw57d06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
903 Pancreas	\vdash		0.310602	0.17508924 X17098	X17098 at	PSG6 Pregnancy-snecific hefa-1 alyconrotein 6
904 Pancreas	0.0157441	0.3814851	0.310581	0.17499995 M28713		NADH-CYTOCHROME B5 REDUCTASE
008			L	1	D17570_s_a	
and FallCleas	0.0150694	0.3814664	0.310539	0.1749758 t-2	[-2	Human mRNA for zona-pellucida-binding protein (sp38), complete cds
906 Pancreas	0.0156694	0.3813849	0.310486	0.17489211	D17570_s_a t	Zona-pellucida-binding protein (sp.38)
907 Pancreas	0.0155905	0.3813748	0.310355	HG273 0.17481355 HT273	HG273- HT273 at	I vmnhorvte Antiren Hla-G3
908 Pancreas	0.0154867	0.3811627	0.310261	0.17473437[173191	173191 at	Inward rectifier notasselling channel (Kird 3)
909 Pancreas	T		0.310248	0.17466988 X99920	X99920 at	S100 calcium-hinding profession A13
910 Pancreas	0.0153782	0.3811277	0.310218	0.17458709121954	121954 at	PERIPHERAL TYPE RENZONIAZEDINE DECEDADO
911 Pancreas	0.0150023	1	0.310195	0.1745037 M63603 at	M63603 at	PLN Phospholamban
						EST. 31/70h00 of Course total foths Nh311E0 A.: Usung goniese about
					RC AA4240	clone 759905 3' similar to WP:B0024.13 CE05157 · mRNA
912 Pancreas			0.310139	0.17440295 06_at		sequence. (from Genbank)
913 Pancreas	0.0147269	0.3810111	0.309995	0.17434274 U48959	U48959_at	Myosin light chain kinase (MLCK) mRNA
914 Pancreas	0.0146187	0.3809514	0.309951	0.1742641	AA251078_a	EST: zs01b12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
L L	1				U08854_s_a	marcondo o marcondonos (non contrain)
915 Pancreas	0.0145964	0.3809514	0.309853	0.17419758		UDP glucuronosyltransferase precursor (UGT2B15) mRNA
916 Pancreas	0.0145888	0.38093	0.309845	0.17413391	U50822_ma 1 s at	Neurogenic helix-loop-helix protein NEUROD (neurod) gene
917 Pancreas		0.3809081	0.309826	0.17402822 X86693	X86693 at	High endothelial venule
918 Pancreas		0.3808982	0.309783	0.17396589 1.13278	L,13278_at	CRYZ Crystallin zeta (quinone reductase)
919 Pancreas		0.3808469	0.309747	0.17390133 C14915_at	C14915_at	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12
920 Pancreas	0.0140228	1	0.309709	0.17387846 M63138 at	M63138_at	CTSD Cathepsin D (lysosomal aspartyl protease)
921 Pancreas	0.0137339	- 1	0.309676	0.17379501 M55210	M55210_at	LAMC1 Laminin, gamma 1 (formerly LAMB2)
922 Pancreas	0.0136/58	0.3807679	0.309562	0.1737371	U89942_at	Lysyl oxidase-related protein (WS9-14) mRNA

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						EST: zt60f12.s1 Soares testis NHT Homo sapiens cDNA clone
000					RC_AA3982	726767 3' similar to contains MER13.b3 MER13 repetitive element;
923 Pancreas	0.0136356	0.3807412	0.309509	0.17360435 90_at	90_at	mRNA sequence. (from Genbank)
924 Pancreas	0.0134755		0.309458	0.17354436 X81372	X81372_at	Biphenyl hydrolase-related protein
925 Pancreas	0.0132196	- 1	0.30945	0.17354208 M23294	M23294_at	HEXB Hexosaminidase B (beta polypeptide)
926 Pancreas	0.013061	0.3804676	0.309434	0.17342441 M63256	M63256 at	CDR2 Cerebellar degeneration-related protein (62kD)
927 Pancreas	0.0428850	0.2002045	0000		RC_AA4774	EST: zu42f03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
928 Dancroos	0.0126639		0.309358	0.17340198	32_s_at	clone 740669 3', mRNA sequence. (from Genbank)
340 railoreas	7016210.0	0.3803458	0.309228	0.17324902		Annexin II, 5'UTR (sequence from the 5'cap to the start codon)
929 Pancrese	0.0122572	0.2000004	70000		M20778_s_a	
930 Pancreas	0.012046	- 1	0.309211	0.1731849	0.1/31849 t	Homo sapien, alpha-3 (VI) collagen
931 Pancreae	0.0120275	.1 .	0.000100	0.11.012043	wzosou al	Chromogranin B (secretogranin 1)
200	0.0120213	- 1	0.309105	0.1730738 U58516	U58516_at	Breast epithelial antigen BA46 mRNA
932 Pancreas	0.0119055	0.3800434	0.30906	0.1730264	AA478129_a	
933 Pancreas	0.0118301	0.3799817	0.309027	0.1729786 D17516	D17516 at	PACAP receptor
934 Pancreas	0.0114276	0.3798537	0.309026	0.17295383 U69114	U69114 at	EST: Human Down syndrome region, YAC 152F7, mRNA sequence. (from Genbank)
700					RC_AA1871	EST: zp62b01.s1 Stratagene endothelial cell 937223 Homo saniens
900 Paricreas	0.0112642		0.308992	0.17289628 33_at	33_at	cDNA clone 624745 3', mRNA sequence (from Genhank)
950 Paricreas	0.0112601	0.3798097	0.308919	0.17287809 Z35307	Z35307_at	ECE1 Endothelin converting enzyme 1
aoi Failcreas	0.0109491	0.3797908	0.308815	0.17278089 L34219 at	L34219_at	RLBP1 Cellular retinaldehyde-binding protein
938 Pancreas	0.0109036	0.3797874	0.308753	RC 0 17263697 53	RC_AA4365	EST: zv08c11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
939 Pancreas	0.010878	0.3796868	0.308742	0.17257673 X77307 at	X77307 at	5-HVDDOXYTBYDTAAMIE 30 DESERTED
940 Pancreas	0.0098719	0.3795845	0.308719	0.17251839 U90552	U90552 at	Butvrophilin (BTE5) mRNA
941 Pancreas	0.0098491	0.3795497	0.308682	0.17246318	Z24459_xpt5 at	Z24459_xpt5 Exon2A from H.sapiens MTCP1 gene, exons 2A to 7 (and joined at mRNA)./ntvpe=DNA /annot=exon
942 Pancreas	0.009683	0.3794782	0.308563	RC 0.17239702 82	_AA2814 at	EST: zt03e10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
943 Pancreas	0.0095531	0.3791548	0.308551	0.17237099	M26041_s_a t	HLA-DOA1 MHC class II DO alpha
944 Pancreas	0.0094053	0.379135	0.308511	0.17224282 M99438	M99438 at	Transducin-like enhancer protein (TI E3) mRN∆
945 Pancreas	0.0093573	0.3791104	0.308503	0.1722058	M29277_s_a t	CELL SURFACE GLYCOPROTEIN MUC18 PRFCURSOR
946 Pancreas	0.0093008	0.3791104	0.308444	HG3893- 0.17220096 HT4163 at		Phosphodiucomutase 1 Alf Shice
947 Pancreas	0.0092136	0.378905	0.308444	0.17205693 U49278 at	,	Putative DNA-binding protein mRNA, partial cds
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	Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.
Clone 23587 mRNA sequence GRN Granulin TUBULIN ALPHA-4 CHAIN Cysteine-rich heart protein (hCRHP) mRNA RBP1 Cellular retinol-binding protein Leukemia virus receptor 1 (GLVR1) mRNA Transthyretin (prealburnin, amyloidosis type I) EST: aa61c10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825426 3', mRNA sequence. (from Genbank) PTPRM Protein tyrosine phosphafase, receptor type, mu polypeptide PTAFR Platelet activating factor receptor	Continued to the cont
0.1719559 U90914 at 0.17188223 X62320 at 0.1718628 X06956 at 0.17175265 U09770 at 0.17169529 M11433 at 0.17165744 L20859 at 0.17160176 M11844 at RC_AA5042 0.1714249 70 at 0.17142138 X58288 at 0.17142138 X58288 at 0.17142138 X58288 at 0.17142138 X58288 at 0.17142138 X58288 at 0.17142138 X58288 at 0.17142138 X58288 at	94 r at W19984 at W19984 at K02215 at D49357 at Y13492 s at RC_AA4196 09 at M19154 at U13369 at D17400 at D17400 at D17400 at D17400 at D17400 at CAA1868 97 at RC_AA1868 97 at RC_AA3500 30 at RC_AA3500 30 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at RC_AA357 at
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FIG. 11M2

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50 protoin mDNA 21 and	OF PROBILITIONAL S CITE	ייי יייי יייי יייי ייייי ייייי יייייי יייי	ADPR Unydropteridine reductase	314 yeile ioi 314 Uncoretal antigen	at SOD3 Superoxide dismutase 3, extracellular	EST: yl96f11.r1 Homo sapiens cDNA clone 45943 5' (from Contract)	EST: zn53e03.s1 Stratagene muscle 937209 Homo sapiens cDNA	EST: aa44c09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	EST: EST12479 Uterus tumor I Homo sapiens cDNA 3' end, mRNA	EST: ab03d12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA	Golfe 639733 3, mKNA sequence. (from Genbank)	Orphan G protein-coupled receptor (RDC1) mRNA partial cds	PRKCZ Protein kinase C. zeta	EST: yi96e02.r1 Homo sapiens cDNA clone 147098 5'. (from Genbank)	Tyrocylprotein cultotronofees	yrosyprotein suitottaise z	MMP2 Matrix metalloproteinase 2	CC chemokine LARC precursor	EST: zx96a12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 811582 3. mRNA sequence (from Canhant)	Succinate Dehydrogenase Elavoprotein Subunit	22a6 Human retina cDNA randomly primed sublibrary Homo sapiens	CDINA, IIIKNA sequence. (Irom Genbank)	ELP-1 mRNA sequence	EST: zl74e07.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 510372 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genhank)	THBD gene extracted from Human thromhomodulin gene	ביים ביים ביים ביים ביים וימוו מוו סוווססוווססחוווו לפוופ
0.1701967 19267 at	0 1701876 126710 at	0 1701374 M16447 of	0.1101371 M 10447 at		0.16996583 JU294/ s at	0.16986887 H09058_at	RC_AA0856 8 76 at	RC_AA4902 5 62 at	RC_AA2996	RC_AA5048	3 L14787 at		Z15108_at	R80351_at	RC_AA4593	D86331 s a	-	0.1691872 U64197_at	AA4545 s at	. at	7	ה ל	at :		J02973_ma1 at	
L	L		\perp		0.1099658		RC_A 0.16984868 76_at			RC A 0 1695673 00 at	0.16953933 1.14787	0.16950552 U67784	0.16945219 Z15108	0.16932535 R80351	RC_A 0.16930793 89_at		0.16923861	0.1691872	RC 0.16909096 97	HG2602. 0.16905203 HT2698	0 16900474 14/26187	0.16891864 1136922	0.16878948 M88458	RC 0.16874222 60	0.16867444	
3 0.306664	1		\perp		\perp	0.306468	0.306435	0.306426	0.3063	1		0	0.30619	0,306075	0.306028	10 mm m m m m m m m m m m m m m m m m m	0.305968	0.305908	0.305808	0.305805	0.305801	0.30577	0.305718	0.305711	0.305665	
0.3759746		3 0.3755874		J		0.3753988	0.3752322	0.3751638	0.3751578	0.3751535	1	1	0.3749511	0.3748851	0.3748787		0.3748153	0.3747873	0.3747445	0.374696	0.3746279	0.3745216	0.3745115	0.3745095	0.3745001	
0.0061341	0.0053417	0.0051793	0.0051524	0.005104		0.0049885	0.0048985	0.0047371	0.0046622	0.004536	0.0044392	0.0042782	0.0038888	0.0039818	0.0039155		0.0038674	0.0035995	0.0035149	0.0034695	0.0033017	0.0027846	0.0025467	0.0025293	0.0021767	
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97	97	97	97.	979		88	981	982	983	984	386	986		988	686	Ċ	930	66	992	993	994	995	986	266	866	

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors region with gary when the region and the country and the region of the r

 0.0020229	0.3745001	0.305637	X 0.0020229 0.3745001 0.305637 0.168606741	X62515_s_a t	HSPG2 Heparan sulfate proteoglycan
 .0016461	0.3744899	0.305616	0.16851833 W	/56463_at	0.0016461 0.3744899 0.305616 0.16851833 W56463_at cDNA clone 326459 5', mRNA sequence. (from Genbank)

FIG. 1102

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	1.2056562	0.7462531	0.651255	0.49000722	RC_AA1769 75 s at	Himan prostotic coordances and a feet and a
	1.150031	0.6942502	0.603854	0.4573873 X07730 at	07730 at	APS Prostate specific antiden
1	1.1072491	0.6685929	0.582254	0.4402699 t	M34376_s_a t	MSMB Beta-microseminoprotein (prostate secreted)
j	1.0564668	0.6536669	0.566208	RC_A 0.4287084 63_at	RC_AA4169 63_at	EST: zt69h05.s1 Soares testis NHT Homo sapiens cDNA clone 727641 3' similar to gb:X14850_cds1 HISTONE H2A.X (HUMAN);, mRNA sequence, (from Genhank)
- 1	1.0498478	0.6413899	0.555247	U 0.41923457 t	U22178_s_a t	MSMB Beta-microseminonrotein (proctoto cocreto)
- 1	1.0272197	1.0272197 0.6314022	0.546222	0.41171598 M24902 at	124902 at	ACPP Acid phosphatase, prostate
- 1	1.0131627	0.6237198	0.540418	RC_A 0.40537417 26_at	RC_AA1956 26_at	EST: zr38h09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665729 3', mRNA sequence, (from Genhank)
			-		HG2261- HT2361 6 6	
1	1.0064116	0.617686	0.53471	0.39937273	8 - 16671	Antigen, Prostate Specific Alt Solice Form 2
	0.9983715	0.6117601	0.530192	0.39433932	AA099391_s at	EST: zk85e12.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489646 5' mRNA sequence (from Ganhank)
	0.9497854	0.6091605	0.525377	0.39051536 90_at	C_AA0472)_at	RC_AA0472 EST: zk74f05.s1 Soares pregnant uterus NbHPU Homo sapiens 90_at cDNA clone 488577 3', mRNA sequence (from Genhank)
	0.9145066	0.6044182	0.52174	0.38678116 t	C01409_s_a t	EST: HUMGS0008391, Human Gene Signature, 3'-directed cDNA sequence, from Genbank)
	0.8882394	0.6030476	0.517905	A 0.3831058	AA234665_a t	Supervillin
	0.8852299	0.5962434	0.514562	RC_A	A0171	RC_AA0171 361524 3' similar to contains element PTR7 repetitive element;
$I \cup I$	0.8648246	1 1	0.512382	0.37685722 X59766 at	36 at	AZGP1 Zinc-aluha-2-divronmen 4
	0.8643197	0.5876886	0.509529	RC_AA(0.3741907 49_r_at	6	EST: zj99f01.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469177 3', mRNA sequence. (from Genbank)
				<u> </u>	1058	EST: zu57g11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 742148 3' similar to TR:G780241 G780241 AU-BINDING DEOTERMIENCY CONTINUENCY
	0.861838	0.861838 0.5842731	0.507509	0.3719474 32 at		Genbank)

FIG. 124

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EST: 12g3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence. (from Genbank)	KLK1 Kallikrein 1 (renal/pancreas/salivary) {alternative products}	EST; zx65e12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 796366 3', mRNA sequence. (from Genbank)	EST: zw65e01.s1 Soares testis NHT Homo sapiens cDNA clone 781080 3', mRNA sequence. (from Genbank)	AE001548 r 81540 1 gene (minein heavy zhain) extracted from Homo canians	chromosome 16 BAC clone CIT987SK-815A9 complete sequence		EST: ab12a04.s1 Stratagene lung (#937210) Homo sapiens cDNA	Enteric smooth muscle gamma-actin gene, 5' flank and	RC_AA1871 EST: zp62b01.s1 Stratagene endothelial cell 937223 Homo sapiens 33 at cDNA clone 624745 3', mRNA sequence. (from Genbank)	NF-H gene, exon 1 (and joined CDS)			Phosphodiesterase 9A	MYH11 Myosin, heavy polypeptide 11, smooth muscle	Clone A9A2BRB2 (CAC)n/(GTG)n repeat-containing mRNA	0.34514582 U00943 at-2 Human clone A9A2BRB2 (CAC)n/(GTG)n repeat-containing mRNA	BRAIN SPECIFIC POLYPEPTIDE PEP-19	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0503	EST: zv27d12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 754871 3', mRNA sequence. (from Genbank)		
W26769 at	S39329 at	RC_AA4561	35 <u>_</u> at	RC_AA4299 98_at	AE001548 r	na1 at	9	RC_AA4878	0.3558713 D00654 at	RC_AA1871 33_at	X15306_ma 1 at	RC_AA4565	RC_AA1289	97_at	D10667_s_a t	0.34659663 U00943_at	U00943 at-2	0.34363896 U52969 at	RC_AA6091 13_at	RC_AA4115 32 at	RC_AA4300	RC_AA4963 66_at
0.3697102 W26769	0.36733624 S39329		0.3650193 35_at	RC_A 0.36277044 98 at		0.36110395 na1	0.3594728 t	RC_A 0.35773683_79_at	0.3558713	RC_A 0.3540116 33 at	X 0.352284161	RC_A 0.35091248 98. at		0.34926105 97	0.3481089 t	0.34659663	0.34514582	0.34363896	0.34231102 13	0.34123212 32 at	RC_A 0.34006175 47 at	RC_A 0.3387454 66_at
0.504399	0.500787		0.499316	0.497976		0.496438	0.49364	0 49259	0.490684	0.489226	0.488052	0.485825		0.484755	0.483382	0.48175	0.480478	0.479351	0.477309	0.47656	0 475776	0.474368
0.5810913	0.5788426	I	0.5758644	0.5740604		0.5721853	0.5697741	0.5683232	0.566691	0.5634838	0.5619771	0.5604654		0.559049	0.7857197 0.5563237	0.7834053 0.5544608	0.5540588	0.5535718	0.5517426	0.5491698	0 5484343	1 1
0.8583609	0.8567439		0.8544304	0.8508199		0.8503591	0.8487131	0.8481424	0.8479604	0.8473496	0.8106132	0 7970863		0.7859255	0.7857197	0.7834053	0.7834053	0.7809461	0.7801142	0.7770838	0.7764195	0.7761946
17 Prostate	18 Prostate		19 Prostate	20 Prostate		21 Prostate	22 Prostate	23 Prostate	24 Prostate	25 Prostate	26 Prostate	27 Prostate		Prostate	29 Prostate	30 Prostate	31 Prostate	32 Prostate	33 Prostate	Prostate	35 Prostate	36 Prostate
17	18		20	20		21	22	73	24	25	26	77	i '	78	29	8	34	32	33	8	35	36

Docket No.: 2825.2020-002

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					2C DAME10	EST: 2063040 of Source total fetus NEOLIFO 0. 11
37 Prostate	0.7723309	0.5450091	0.473031	0.33763986	16_at	86_at clone 796170 3', mRNA sequence. (from Genbank)
38 Prostate	0.768858	0.5419448	0.471731	0.33615154	RC_D59971	EST: Human fetal brain cDNA 3'-end GEN-078E12, mRNA sequence.
			; 		-3 at HG2261-	(riotit Gerbank)
39 Prostate	0.765341	0.5411084	0.470842	0.3351907 HT2352	T2352_at	Antigen, Prostate Specific, Alt. Splice Form 3
40 Prostate	0.7642014		0.469657	0.334210041	AA047151_a	EST: zk74f05.r1 Soares pregnant uterus NbHPU Homo sapiens
41 Prostate	0.7641559	0.5385019		0.33338007 U48959	J48959 at	Myosin light chain kinase (MI CK) mRNA
42 Prostate	0.7630378	0.5383377	0.467798	0.33245933 t	AA037316_a	EST: zc52h08.r1 Soares senescent fibroblasts NbHSF Homo sapiens
43 Prostate	0.7613946	0.538004	0.4664	0.3313788 M99487	äŧ	PROSTATE-SPECIFIC MEMBRANE ANTIGEN
44 Prostate	0.7604477	0.5369695	0.465384	RC_A	A4180	EST: zv94h02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
45 Prostate	0.7590286	1 1	0.464409	0.32965672 X91868	91868 at	SIX1 protein
46 Prostate	0.7572511	0.5332657	0.463036	0.3289377 N40141	140141 at	Homo sapiens mRNA for JM27 protein, complete CDS (clone IMAGE 145745 and IMAGE 257878)
47 000000	7			R	A4357	EST: zt79e05.s1 Soares testis NHT Homo sapiens cDNA clone
40 Prostate	0.735638	1	0.462426	0.3279926 48_at		728576 3', mRNA sequence. (from Genbank)
46 Prostate	0.749978	- 1	0.461185	0.32723513 U39840 at		Hepatocyte nuclear factor-3 alpha (HNF-3 alpha) mRNA
49 Prostate	0.7490042	- 1	0.460694	0.32650223 M22430 at		PLA2G2A Phospholipase A2, group IIA (platelets, synovial fluid)
ou Prostate	0.747659	0.5315405	0.460338	0.32563075 M12125 at		Skeletal beta-tropomyosin
- F	1				D17408_s_a	
or Prostate	0.7473589	0.5308155	0.459396	0.32478625 t		Calponin
52 Prostate	0.7391968	0.5299506	0.458432	RC 0.323658 27		Homo sapiens NADP-dependent isocitrate dehydrogenase (IDH) mRNA, complete cds
53 Prostate	0.7329932	0 5200732	0 457546	R	A1284	EST: zm24e06.s1 Stratagene pancreas (#937208) Homo sapiens
	700070	1	0+010+0	0.3223004 86 at	Ou OO	CUNA clone 526594 3', mRNA sequence. (from Genbank)
54 Prostate	0.7308382	0.5286248	0.457037	0.32205924 03	_AA2358 i_at	EST: zs4zg06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 687898 3', mRNA sequence. (from Genbank)
55 Prostate	0.7307606	0.5281515	0.456172	0.32141533 t	U92314_s_a t	Hydroxysteroid sulfotransferase SULT2B1a (HSST2) mRNA
56 Prostate	0.7307606	0.5270093	0.455333	0.32052302 t-2	2314_s_a	Sulfotransferase family 2B, member 1
57 Prostate	0.7303116	0.5263293	0.454279	RC 0.31973705/09	_AA4302	Homo caniane I IM pratoin mDNA
58 Prostate	0.7290818	0.7290818 0.5244746	0.453399	A 0.31890127	033766_s	EST: zk19b12.r1 Soares pregnant uterus NbHPU Homo sapiens
		2	20000			CONTRACTOR 410913 3, IIIRNA Sequence. (Irom Genbank)

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EST: zn19a04 s1 Stratagene neugoepithelium NT2DAMI 037234	RC_AA0846 Homo sapiens cDNA clone 547926 3', mRNA sequence. (from 02 at	(Augusta	Transforming growth factor heta 1 induced transcript 1	(clone \$240ii117/zan112) mpMA	Thymosin heta-d m.BNA	AA082546 a EST: ze88h10.r1 Soares fetal heart NhHH10M Linguistics	clone 366115 5', mRNA sequence, (from Genbank)	EST: zv17e07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	/53924 3, mRNA sequence. (from Genbank)	Homo canione mDNA for solution 17	EST: 2w57d06 r1 Soares total fetus Nb2HE8 0 Hemo considered		EST: hbc3204 Homo sapiens cDNA clone hbc3204 5'end. (from	EST: af48c08.s1 Soares total fettis Nh2HF8 Ow Homo sepiens conta	clone 1034894 3', mRNA sequence. (from Genhank)	EST: zs46d03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700517 3. mRNA sequence (from Genbank)	(HOLL CALIDATIV)	EST: zq69c06.s1 Stratagene neuroepithelium (#937231) Homo	sapiens convacione 646858 3, mRNA sequence. (from Genbank)	Transmembrane 7 superfamily member 2		PERIOD, DROSOPHILA, HOMOLOG OF, 2	EST: zl13g07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 501852 3', mRNA sequence. (from Genhank)	EST: HUMGS0003384, Human Gene Signature, 3'-directed cDNA	EST: EST83940 Parathyroid gland tumor I Homo sapiens cDNA 3'	end, mRNA sequence. (from Genbank)	EST: zv54f03.s1 Soares testis NHT Homo sapiens cDNA clone 757469 3', mRNA sequence. (from Genhank)	EST: zn85a12.s1 Stratagene lung carcinoma 937218 Homo sapiens	cDNA clone 564958 3', mRNA sequence. (from Genbank)
	RC_AA0846 02 at	RC_ AA2332	57 at	L40399 at	0.3164816 D85181 at	AA082546 a	1	RC_AA4790	30 at	AA402971_S	AA429793 a	+	T48536 at	A6216		2911		A2057	00110	at	NB002345_a		A1279		0	01010	A4372	A1264	
	0.31826204 02		0.31750128 57 at	0.31703424 L40399	0.3164816		0.31577867 t	0.345467.06	0.010101	0.31441122		0.31382555 t	0.31319913 T48536 at		0.31234014 34 at	RC_AA. 0.31196657 59_r_at		RC_A 0.31119442 24_at	71.011.00	0.3106203 58	7	0.310219881	RC_A 0.30944642 64_at	0.30891645 C00358 at	1	0.3002303 18 at	0.30780503 58_at	3	0.30128148 12 at
	0.452613		0.452064	,	0.450765		0.450357	0 449244	5	0.448685		0.447742	0.447323		0.446659	0.445428		0.445371		0.445083	0.444	0.44450	0.443158	0.443123	0.444024	4761440	0.4414	0.444004	4001 +4-0
	0.5233697		- 1	- 1	0.5217126		0.5215629	0.5208399		0.5197024	,	0.5193453	0.5182234		0.5180734	0.5167005		0.515649		0.5152378	0 5144485	704441000	0.5143696	0.5136402	0.513193	2	0.5126681	0.5116018	O+00110.0
	0.7266153		0.7226381	0.7212004	0.7208732	1	0./149324	0.7100186		0.7076368		0.706525	0.7024102	70001	0.7023528	0.7015156		0.7011182		0.700474	0.6951623	2010000	0.6941831	0.6929858	0.691104		0.6906615	0.690201	
	59 Prostate	- 1	60 Prostate	61 Prostate	62 Prostate	0	os Prostate	64 Prostate		65 Prostate		oo Prostate	67 Prostate	68 Droctoto	o riosiale	69 Prostate		70 Prostate		71 Prostate	72 Prostate		73 Prostate	74 Prostate	75 Prostate		76 Prostate	77 Prostate	
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RC AA1323 EST: zo28d09.s1 Stratagene colon (#937204) Homo canions on NA	clone 588209 3', mRNA sequence. (from Genbank)		+	EST: zs46d03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700517.3', mRNA sequence (from Genhank)	EST: yc42e04.r1 Homo sapiens cDNA clone 83358 5: (from Genbank)		20-KDa myosin linht chain (MLC-2) mDNA	SORD Sorbifol debydrogenese	APOA2 Apolipoprofein A-II	S-adenosylmethionine decarboxylase 1	EST: zr81e12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	EST: 779405 st Soares testis NITT Home continue Continue	728553 3' similar to TR:G452276 G452276 NPDCF-1.; mRNA	sequence. (from Genbank)	Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antiden MAGF I IKE	gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase)	LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032	EST: zw52g09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	Glone 773728 3' similar to WP:R11D1.11 CE06316 MOUSE ADIPOCYTE P27 PROTEIN LIKE;, mRNA sequence. (from	Genbank)	MAGE:667196 3', mRNA sequence	EST: zu19b03.s1 Soares NHHMPu S1 Homo sapiens cDNA clone	CPI.H mRNA		EST: zt57h04.s1 Soares testis NHT Homo sapiens cDNA clone	726487 3', mRNA sequence, (from Genbank)
RC AA1323	2 66 at	N75870_s_a 4 t	RC_AA1565 3 32 at	RC_AA2911 8 59_f_at	0.30486175 T68510 at	D79791_s_a	7 J02854 at		0.30308852 D14695 at	0.30238143 W63793 at	RC_AA2564	, n	RC_AA4357	. 40 al			RC_AA4516 80_at		RC_AA4339	40 at	56 at	RC_AA4056	1 19783 at		RC_AA3992	71_at
	0.30680072 66	0.3064534	RC_A 0.3059563 32_at	0		0,30442053	0.30414927	0.30356243 L29008			0.30199936/85 at	2000	0.30170682/40	7000710000			RC 0.30115393 80		RC 0 30045247 46	0.300402.0	0.3001968 56 at	0.20085258 63	0.29953346 19783	0.2000462	701070	0.2987609 71
	0.440284	0.439416	0.439234		0.438305	0.438027	Li	0.437174	0.436605	- 1	0.435253		0.434721	\perp			0.434469		0.433818	0.0001.0	0.433587	0 432832	0.432422	0.431851		0.431508
	0.5107673	0.5101306	0.5096272	0.509364	0.509044	0.5083146	0.6762923 0.5075067	0.6741846 0.5067304	0.5059861	0.5055976	0.5050273		0.5044967	_1			0.5042999		0.5031441	4	0.5030469	0.5021772	1	0.5010664		0.5005027
	0.6893996	0.6883029	0.6862451	0.6836953	0.6822293	0.6807238	0.6762923	0.6741846	0.6713697	0.6699484	0.6693808		0.6684371				0.6664848		0.6636378		0.663594	0.6632475	0.6616011	0.6614391		0.6586252
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. 111	KIAA0331 gene product	+			Genbank)		Gone 773401 3', mRNA sequence. (from Genbank)	EST: zu54b12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	EST: 275902.s1 Soares NHMMPu S1 Homo sapiens cDNA clone	669266 3', mRNA sequence. (from Genbank)	EST: zr66c06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	668362 3', mRNA sequence. (from Genbank) EST: z102a10 s1 NCI CGAB CCB4 11.	IMAGE:711930 3', mRNA sequence, (from Genhank)	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR	EST: zv23c07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	Human apM2 mRNA for GS2374 (unknown product specific to	adipose tissue), complete cds	EST: ze22b07.s1 Soares fetal heart NhHH10W Home continued to the continued	clone 359701 3', mRNA sequence, (from Genbank)	Myodlohin gene (evon 1) (ond Latin 1900)	EST: zk09g09.s1 Soares pregnant uterus NbHPU Homo sapiens	EST: zr77f04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	งงร4วร ว, mknA sequence. (from Genbank)	cene encoding E-cadherin, exon 3 and joined CDS	KIAA0331 gene product
	RC_AA6095 76 at	RC_AA4194 61_at	AA479266_a t	N71513_s_a	731605 at	RC_AA4260	M69225 at	RC_AA4029	RC_AA2364	10	A2345	A2821			A4103	782	ţ	<u> </u>		17 ma		A2534	35402 ma	A4969	
	0.29841784	RC_A 0.29797372 61 at	0.29760277	0.20716057	0.29676324 731695 at	RC A	0.29582968 M69225 at	RC_A 0.29556254 68 at	0.00507004	0.23307.384.35 s. at	RC A RC A	0.23430030	0.2940378 38_at	0.29365513 M27492 at	RC_A 0.29314995 11 at	F	0.29245773 X13830		0.29199937 76 at	0.2917363 1 at	0.2912448 41	RC AA2534	0.200k2k02	0.2002.002 R	0.29019535 80 at
	0.430452	0.43029	0.429985	0.429647	0.429326	0.428744	0.428364	0.427941	0.427915	0.42732	0.427263	0.12120	0.42685	0.420709	0.426277	0.425904	0.425431		0.425074	0.424772	0.424629	0.423876	0.423369		0.423151
	0.5002668	0.4991493	0.498833	0.6570579 0.4985224	0.6568294 0.4984954	0.4982454		0.4980562	0,4978114	0.4976958	0.4973906		0.4971947	000000000000000000000000000000000000000	0.4951832	0.4951832	0.4946998	0,10,00	0.4343146	0.4931663	0.492733	0.4922514	0.4916819	0.4049409	70101647
	0.6583689	0.6579552	0.6575186	0.6570579	0.6568294	0.6558126	0.6517711	0.6512691	0.6510165	0.6506759 0.4976958	0.6493998	0000000	0.6493036		0.6492758	0.6485527		0.6470500	- 1	0.6474449 (0.6465631	0.6465359	0.6457118	0.6452014	
	97 Prostate	98 Prostate	99 Prostate	100 Prostate	101 Prostate	102 Prostate	103 Prostate	104 Prostate	105 Prostate	106 Prostate	107 Prostate	108 Droctate	109 Prostate		110 Prostate	111 Prostate	112 Prostate	113 Prostata	+	114 Prostate	115 Prostate	116 Prostate	117 Prostate (118 Prostate	
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Inventors: Sridhar Ramaswamy, et al. Breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial RC_AA4301 | EST: zw61a11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA RC_AA4016 EST: zv65b11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA RC_AA4496 | EST: zx07b04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA AA447410_s EST: zw93c10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA RC_AA1016 Homo sapiens herpesvirus entry protein B (HVEB) mRNA, complete J04152_rna1 M1S1 gene extracted from Human gastrointestinal tumor-associated EST: zv28g12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: zb33d08.r1 Soares parathyroid tumor NbHPA Homo sapiens RC_AA0352 EST: zk25b02.s1 Soares pregnant uterus NbHPU Homo sapiens Human pre-B cell enhancing factor (PBEF) mRNA, complete cds EST: zs94d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone EST: Human aorta cDNA 5'-end GEN-347F12, mRNA sequence. EST: af17b03.s1 Soares testis NHT Homo sapiens cDNA clone EST: af04e03.s1 Soares testis NHT Homo sapiens cDNA clone N34737_s_a EST: yx82f11.r1 Homo sapiens cDNA clone 268269 5'. (from DPP4 Dipeptidylpeptidase IV (CD26, adenosine deaminase Thyroid autoantigen (truncated actin-binding protein) mRNA cDNA clone 471531 3', mRNA sequence. (from Genbank) cDNA clone 305391 5', mRNA sequence. (from Genbank) IMAGE:705133 3', mRNA sequence. (from Genbank) clone 758493 3', mRNA sequence. (from Genbank) clone 785743 3', mRNA sequence. (from Genbank) clone 774524 3', mRNA sequence. (from Genbank) clone 755014 3', mRNA sequence. (from Genbank) clone 784530 5', mRNA sequence. (from Genbank) 1030684 3', mRNA sequence. (from Genbank) 1031885 3', mRNA sequence. (from Genbank) 22kDa smooth muscle protein (SM22) mRNA antigen GA733-1 protein gene, clone 05516 H.sapiens ARS gene, component B complexing protein 2) FN1 Fibronectin 1 (from Genbank) Genbank) 0.28778097 08_at RC_AA4221 RC_AA2812 D58115 s a RC_AA6088 0.28858697 X99977 at RC_AA6097 0.28677955 M76378_at RC_AA4890 0.2871002 M95787_at 0.2861282 M62994 at 0.28511065 W23474 at 0.28996736 U41060 at 0.28952515|X60708_at 0.28822535 77 at 0.2879647 84 at 0.2889202|33 at 0.28726017 46 at s at 0.28934842 01 at 0.2858967 45 at 0.28381932 23 at 0.2847816 12 at 0.28362876 02 at aţ 0.285586151 0.28645197 0.2841175 0.2843933 0.422795 0.422433 0.421749 0.421642 0.420925 0.420512 0.416619 0.421402 0.421105 0.419416 0.419724 0.419131 0.418772 0.418674 0.418453 0.416728 0.421487 0.420041 0.417429 0.417344 0.417681 0.643281 | 0.4895182 0.6445446 | 0.4908056 | 0.6435612 0.4899734 0.6420888 | 0.4892011 0.641219 0.4888274 0.641183 0.488632 0.6376609 | 0.4878603 0.6445197 | 0.4904437 0.6382334 0.4882474 0.6360824 | 0.4872048 0.6412803 0.4889637 0.6407533 0.4886051 0.6349918 | 0.4870953 0.6298189 | 0.4857845 0.6428337 0.4895182 0.637006 0.4875477 0.6348161 | 0.4868452 0.6342157 | 0.4865417 0.6341479 | 0.4864672 0.6332777 | 0.4861375 0.6312944 | 0.4858992 | 119|Prostate 121 Prostate 20 Prostate 134 Prostate 122|Prostate 136 Prostate 123 Prostate 124 Prostate 125|Prostate 126 Prostate 127 Prostate 130 Prostate 131 Prostate 132 Prostate 133 Prostate 135 Prostate 138 Prostate 128 Prostate 129 Prostate 137 Prostate 139 Prostate

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2825.2020-002

Title: Genetic Markers for Tumors

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EST: zs59e08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701798 3', mRNA sequence. (from Genbank)	ANPEP Alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13)		Endothelin converting enzyme 1	Non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds		Transmembrane receptor (ror2) mRNA	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFYI)	Fatty acid amide hydrolase mRNA		304U3Z 3, MKNA sequence. (from Genbank) ALDH6 Aldehvde dehvdrogenase 6		Claudin 4	EST: zt71a04.r1 Soares testis NHT Homo sapiens cDNA clone			Homo sapiens growth arrest and DNA-damage-inducible protein GADD45gamma mRNA, complete cds	Golgi SNAP receptor complex member 1	EST: zw38a06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 772306 3', mRNA sequence. (from Genbank)	AA028171_a clone 364865 5' similar to contains element MER35 repetitive element to mRNA sequence. (from Genbank)	Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease)	EST: zx05e10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785610 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)
RC_AA2927 3 17_at	0.2830048 M22324_at	RC_AA0184 253 at	RC_AA0629 3 15_at	3 U83115 at	RC_AA6090	2 M97639 at	C16248 at		RC_AA0215	0.28045684 U07919 at	AA427468_s			1	3 56_at	RC_AA4022 324_at	RC_AA4814 3 14_at	RC_AA4044	/ 87_at	AA028171_a	1X66785 f at	_AA44@
RC_A 0.28323716 17_at	0.283004	0.282602 53	0.28226548 15	0.28197953 U83115	0 28464443 53	0.2813932 M97639	0.28120813 C16248	0.28098103 U82535	723030000	0.28045684 U079		0.28027204	0.27995634		0.27961266 56_at	RC 0.27928016 24	RC_A 0.27890116 14_at		0.2786579787	0.27839088 t	0.2779724 X66785	RC 0.27780527 55
0.41626	0.415935	0.415699	0.415188	0.415004	0.414709		0.414138	0.413451	0.449499	0.413405		0.412805	0.412735		0.412627	0.411906	0.411832		0.41149	0.411437	0.41086	0.410792
0.485503	0.4850179	0.4847548	0.4846771	0.4840952	0.4838995		0.4832098	0.4828006	0.4827780	- 1	í	0.4817271	0.4817121	1	0.4815701	0.4811368	0.4809717		0.4806446	0.4801837	0.4800968	0.6112962 0.4799881
0.6290444	0.6290371	0.6268249	0.6262843	0.6256754	0.6255443	0.6249026	0.6219987	0.6209018	0.6194904	0.6190519		0.6172585	0.6155099		0.6150956	0.6147652	0.6142747	1	0.613595	0.6123323	0.6116102	0.6112962
140 Prostate	141 Prostate	142 Prostate	143 Prostate	144 Prostate	145 Prostate	146 Prostate	147 Prostate	148 Prostate	149 Prostate	150 Prostate		151 Prostate	152 Prostate		153 Prostate	154 Prostate	155 Prostate		156 Prostate	157 Prostate	158 Prostate	159 Prostate
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RC_AA4900 EST: ab05d09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA 69 at clone 8399213', mRNA sequence. (from Genbank)		KIAA0018 gene	Outochrome h581 rene		College three VII slope 1 (onlegen by III)	definition of the state of the	RC_AA4343 EST: zw31a06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 770866 3', mRNA sequence. (from Genbank)		_		EST: ze19f06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 359459 3', mRNA sequence. (from Genbank)	CPE Carboxypeptidase E	MaxiK potassium channel beta subunit mRNA		clone 774707 3', mRNA sequence. (from Genbank)					antigen 2	EST: zw64f03.s1 Soares testis NHT Homo sapiens cDNA clone		EST: zp74c05.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 625928 3', mRNA sequence. (from Genbank)	at Homo sapiens mRNA for smoothelin. (from Genbank)	RC_AA0404 EST: 2k46h09.s1 Soares pregnant uterus NbHPU Homo sapiens	ANX3 Annexin III (lipocortin III)	AA410529_s EST: zv23a01.r1 Soares NhHMPu S1 Homo sapiens cDNA clone at 754440 5', mRNA sequence. (from Genbank)
0.27747253 69 at	0.27723765 03 f at	0.27700478 D13643_at	U29463_s_a	. 일 :	000 42 at	0.2761838 L02870 s at	RC_AA4343	0.27594388 90_at	RC_AA0265 0.27569866 97 at	RC AA0555	0.27545 60 r at	RC_AA0106	'274 65_at	0.2749901 X51405 at	0.27468523 U25138_at	RC_AA4420	712 71_at	AA418921_a		0.2740255 84_at	AA114949_a		RC_AA4460	0.2733808805_at	RC_AA1868 0.27317977 97_at	0.27297464 Y13492 s a	RC_AA0404	0.27237383 L20591 at	
0.27747	0.27723	0.27700	0.2766968	76.0	0.21	0.2761		0.27594	0.27569		0.27		0.27517	0.2749	0.27468		0.27451712 71	(0.27425542	0.2740		0.27367917	1	0.2/338	0.27317	0.27297	0.9725	0.27237	0.27214924
0.410558	0.41026	0	0.409971	7070707	17160+0	0.40943		0.409049	0.408604		0.408603		0.408317	0.408066	0.407598		0.407427		0.40/415	0.406835		0.406686		0.406428	0.405812	0.405712	0.405282		0.404844
0.4795347	0.4793637	0.4792782	0.4785797	1	-	0.4773963	1	0.4771512	0.4770647		0.4767934		0.4765101	0.4761858	0.4760726	ļ	0.4759167	0.00	0.475613	0.475487		0.4753977		0.4741243	0.4736542	0.4734552	0.4730634		0.4728706
0.6112632	0.6104791	0.6094204	0.6090662	0.6063696	0.0000020	0.6060374		0.6038646	0.602949		0.6025259		0.6009183	0.6004708	0.6001433		0.5984812	1000	0.5978817	0.5978021		0.5970512	0000	0.39/0480	0.5966892	0.5957331	0.5947304	0.5943906	0.5934044
160 Prostate	161 Prostate	162 Prostate	163 Prostate	164 Prostata	200	165 Prostate		166 Prostate	167 Prostate		168 Prostate		169 Prostate	170 Prostate	171 Prostate		172 Prostate	-	1/3 Prostate	174 Prostate		175 Prostate	0.00	i / o r i ostate	177 Prostate	178 Prostate	179 Prostate	180 Prostate	181 Prostate
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0.5913555 0.4722694 0.404173 0.2716269 85 at a control of the control o	182 Pro	state	0.5925654		0.404601	0.27184728	N77716_s_a t	Homo sapiens mRNA for low molecular mass ubiquinone-binding protein, complete cds
0.5913445 0.4721748 0.404031 0.27139384 33 at AA447439 0.5913063 0.4715289 0.403558 0.2710902 0.0717 at AA447439 0.5909669 0.4712761 0.403023 0.2708465 at AA447439 0.588317 0.4710031 0.402465 0.2708465 at AA47439 0.588217 0.4710031 0.402465 0.2708465 at AA43884 0.588217 0.4706759 0.4019 0.2696854 0.2703684 0.588340 0.4704774 0.402465 0.2703684 0.58048 0.4704774 0.402465 0.2703684 0.588360 at O.5882217 0.4704573 0.4019 0.26968554 0.070311 at AA194815 0.5882217 0.4704573 0.401428 0.2695277 0.2695277 0.470485 0.5887937 0.4704573 0.401128 0.26952577 0.44058 0.5887937 0.4704573 0.401128 0.26879364 0.440578 0.5887937 0.440937 0.400654 0.26854077 at 20.5864977 at 20.586895 0.4698977 0.400654 0.26829576 at 20.5863636 0.4688612 0.400104 0.26782957 at 20.5865955 0.5885951 0.4685086 0.2685957 at 20.5885955 0.4685086 0.39981 0.26732737 at 20.5865955 0.5885951 0.2685953 0.26859953 0.26859993 0.26859953 0.26859953 0.26859953 0.26859953 0.268	183 Pro:	state	0.5913555	3	0.404173	0.2716269	RC_AA6214 85_at	KIAA0575 gene product
0.5913063 0.4715289 0.403658 0.2710902 L09717_at 0.5909669 0.4715125 0.403521 0.2708465_at AA447439_s 0.5809669 0.4712761 0.403023 0.2707807 V00815_at 0.588317 0.4710031 0.402745 0.2703664 U35048_at 0.5883071 0.4709901 0.402465 0.2703664 U35048_at 0.588371 0.4706789 0.4019 0.26965188 Z83806 at 0.5882937 0.4706779 0.4019 0.26965188 Z83806 at 0.58879937 0.4706779 0.4019 0.26965188 Z83806 at 0.5871372 0.470377 0.401428 0.2695271 at 0.5871372 0.4704776 0.401128 0.26995355 U12778 at 0.5871372 0.4700534 0.40102 0.26879364 39 at 0.5864977 0.4698977 0.400669 0.26829576 1 at-2 0.5865655 0.4688512 0.400104 0.26758299 2 at-2 0.5865955 0.4688512	184 Pro	state	0.5913445	,	0.404031	0.27139384	RC_AA1556 33_at	Insulin-like growth factor 1 receptor
0.5910223 0.4715125 0.403521 0.2708465 at attacked by the control of the	185 Pros	state	0.5913063	- 1	0.403658	0.2710902		LAMP2 Lysosome-associated membrane protein 2 {alternative products}
0.5899669 0.4712761 0.403023 0.2707807 Y00815_at 0.589317 0.4710031 0.402745 0.2703664 U35048_at 0.5885118 0.4709901 0.402465 0.2701583 44_at 0.5884084 0.4707774 0.402335 0.26995188 Z83806_at 0.5884084 0.4707774 0.402335 0.26995188 Z83806_at 0.5882077 0.4706789 0.401643 0.26968554 K01911_at A194815_s 0.5882217 0.4706778 0.401643 0.26952174_at A194815_s 0.5875172 0.4704573 0.401128 0.2695271 39_at 0.58751372 0.4702776 0.401128 0.2695277 39_at 0.58751372 0.4700534 0.401128 0.26879364 39_at 0.5871372 0.4700235 0.400654 0.26879364 39_at 0.5871372 0.4700235 0.400654 0.26829576 1_at 0.5864977 0.4694937 0.400314 0.26781183 t 0.5864977 0.4698512 0.400104 0.26782183 t 0.5855955 0.4688512 0.400104 0.26732737 41_at 0.5855955 0.4688512 0.400104 0.26732737 41_at 0.5885955 0.4688512 0.400104 0.26732737 41_at 0.5885337 0.5881315 0.4682981 0.39967 0.26711115 23_at 0.5841315 0.4682981 0.39967 0.26711115 23_at 0.5841315 0.6582981 0.39967 0.26711115 23_at 0.5841315 0.6582981 0.39967 0.26711115 23_at 0.57411115 23_at 0.5841315 0.4582981 0.39967 0.26711115 23_at 0.57411115 23_at 0.5841315 0.4682981 0.39967 0.26711115 23_at 0.574111111111111111111111111111111111111	186 Pros	state	0.5910223		0.403521		AA447439_s _at	
0.589317 0.4710031 0.402745 0.2703664 U35048 at DA50894 0.5885118 0.4709901 0.402465 0.2701583 44 at DA50894 0.5884084 0.4707774 0.402335 0.26995188 283806 at DA4094 0.5882017 0.4706759 0.4019 0.26968554 K01911 at DA4194815 0.588086 0.4704573 0.401376 0.26952174 AA194815 0.5879937 0.470377 0.401128 0.2695271 39 at D04636 0.5871372 0.4702776 0.401128 0.26879364 39 at D04636 0.5871372 0.4700235 0.400654 0.268879364 39 at D04636 0.5871372 0.4700235 0.400654 0.26829576 1 at D04636 0.5864977 0.4698977 0.400659 0.26829576 1 at D04636 0.5863636 0.4688512 0.400104 0.2675829 97 at D04659 0.5865955 0.4688512 0.400104 0.2675829 97 at D04659 0.5865956 0.4688508 0.39981 0.267327374 41 at D04659	187 Pros	state	0.5909669		0.403023	0.2707807	Y00815 at	PTPRF Protein Vrosine nhosnhatase recentor two f notweatide
0.5885118 0.4709901 0.402465 0.2701583 RC_AA5984 0.5884084 0.4707774 0.402335 0.26995188 283806 at at at at at at at at at at at at at	188 Pros	state	0,589317	0.4710031	0.402745	0.2703664	U35048 at	TSC-22 protein mRNA
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0.588371 0.4706789 0.4019 0.26968554 K01911 at 0.5882217 0.4706759 0.401643 0.26952174 at AA194815 s 0.588086 0.4704573 0.401376 0.2695271 39 at RC_AA1485 0.5879937 0.470377 0.401128 0.26879364 39 at U04636 ma 0.5871372 0.4700234 0.40102 0.26879364 39 at U04636 ma 0.5874372 0.4700235 0.400654 0.26879364 39 at U04636 ma 0.5864977 0.4698977 0.400569 0.26829576 1 at X66276 s a 0.5863636 0.4688512 0.400104 0.26781183 t RC_AA4539 0.5855955 0.4685086 0.39981 0.26732737 41 at RC_AA5051 0.5841315 0.4682981 0.39967 0.26711115 23 at	190 Pros	state	0.5884084		0.402335	0.26995188	Z83806 at	Axonemal dynein heavy chain (partial, ID holhcg)
0.5882217 0.4706759 0.401643 0.26952174 at 0.588086 0.4704573 0.401376 0.2692271 at 0.5879937 0.470377 0.401128 0.26905355 U12778 at 0.5875179 0.4702776 0.401128 0.26879364 39 at U04636 ma 0.5871372 0.4700234 0.40102 0.26879364 39 at U04636 ma 0.5871372 0.4700235 0.400654 0.26854077 1 at U04636 ma 0.5864977 0.4698977 0.400569 0.2680042 t Accondage and 0.5863636 0.4688512 0.40014 0.26781183 Accondage and 0.58636365 0.4688512 0.400104 0.2678183 Accondage and 0.58636365 0.4688512 0.400104 0.2678183 Accondage and 0.58636365 0.46885086 0.39981 0.26735737 At at 0.5841315 0.4682981 0.39987 0.26731377 At at	191 Pros	state	0.588371		0.4019	0.26968554		NPY Neuropeptide Y
0.588086 0.4704573 0.401376 0.2692271 RC_AA1485 0.5879937 0.470377 0.401128 0.26905355 U12778_at 0.5875179 0.4702776 0.401128 0.26879364 39_at 0.5871372 0.4700534 0.40102 0.26879364 39_at 0.5871372 0.4700235 0.400654 0.26854077 1 at-2 0.5864977 0.4698977 0.400569 0.26829576 1 at 0.5863636 0.4688512 0.400144 0.26781183 KC_AA4539 0.5865955 0.4685086 0.39981 0.26732737 41_at 0.5841315 0.4682981 0.39967 0.26731115 23_at	192 Pros	state	0.5882217		0.401643		AA194815_s at	EST: zr35f03.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 665405 5', mRNA sequence, (from Genhank)
0.5879937 0.470377 0.401128 0.26905355 U12778_at 0.5875179 0.4702776 0.401128 0.26879364 39_at 0.5871372 0.4700534 0.40102 0.26854077 1 at-2 0.5871372 0.4700235 0.400654 0.26829576 1 at 0.5864977 0.4698977 0.400569 0.2680042 1 0.5863636 0.4688512 0.400104 0.267581183 1 0.5863655 0.4685086 0.39981 0.26732737 41_at 0.5841315 0.4682981 0.39967 0.26732737 41_at 0.5841315 0.4682981 0.26732737 41_at	193 Pros	state	0.588086		0.401376	0.2692271	RC_AA1485	EST: 2106e05.s1 Soares pregnant uterus NbHPU Homo sapiens
0.5875179 0.4702776 0.401128 0.26879364 39_at 0.5871372 0.4700534 0.40102 0.26854077 1 at-2 0.5871372 0.4700235 0.400654 0.26829576 1 at 0.5864977 0.4698977 0.400569 0.2680042 t 0.5863636 0.4698977 0.400144 0.26781183 t 0.5863656 0.4688512 0.400104 0.2675829 97_at 0.5865955 0.4685086 0.39981 0.26732737 41_at 0.5841315 0.4682981 0.339967 0.267711115 23_at	194 Pros	state	0.5879937		0.401128	0.26905355	U12778 at	ACADSB Acyl-coA dehydrogenase
0.5875179 0.4702776 0.401128 0.26879364 39_at 0.5871372 0.4700534 0.40102 0.26854077 1 at-2 0.5871372 0.4700235 0.400654 0.26829576 1 at 0.5864977 0.4698977 0.400569 0.2680042 1 0.5863636 0.4688512 0.400104 0.26781183 1 0.5865955 0.4685086 0.39981 0.26732737 41_at 0.5841315 0.4682981 0.39967 0.26711115 23_at								
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0.5864977 0.4688512 0.400034 0.2675829576 1 at C00038 s.a 0.5865955 0.4688512 0.400104 0.2675829576 1 at C00038 s.a 0.5863636 0.4688512 0.400104 0.26781183 1 CAA4539 0.5855955 0.4685086 0.39981 0.2675829 97 at At at At at At at At at At At at At At At At At At At At At At At At At	196 Pros	state	0.5871372		0.40102	0.26854077	U04636_rna	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase
0.5864977 0.4698977 0.400569 0.2680042 t 0.5864977 0.4694937 0.400314 0.26781183 X66276_s_a 0.5863636 0.4688512 0.400104 0.2675829 97_at 0.5855955 0.4685086 0.39981 0.26732737 41_at 0.5841315 0.4682981 0.39967 0.26711115 23_at	197 Pros	state	0.5871372	1	0.400654	0.26829578	U04636_rna	din cyclodygelase)
0.5864977 0.4694937 0.400314 0.26781183 t X66276_s_a 0.5863636 0.4688512 0.400104 0.2675829 97_at 0.5855955 0.4685086 0.39981 0.26732737 41_at 0.5841315 0.4682981 0.39967 0.26711115_23_at	198 Pros	state	0.586886	1	0.400569	0.2680042 t	38 s_a	EST: HUMGS0003443, Human Gene Signature, 3'-directed cDNA sequence (from Genhank)
0.5863636 0.4688512 0.400104 0.2675829 PC_AA4539 0.5855955 0.4685086 0.39981 0.26732737 41 at 0.5841315 0.4682981 0.39967 0.26711115 23 at	199 Pros	itate	0.5864977		0.400314	0.26781183 t		MYBPC1 Myosin-binding profein C. slow-tyne
0.5855955 0.4685086 0.39981 0.26732737 41 at 0.5841315 0.4682981 0.39967 0.26711115 23 at	200 Pros	tate	0.5863636		0.400104	0.2675829	A4539	EST: zx46a12.s1 Soares testis NHT Homo sapiens cDNA clone 795262 3', mRNA sequence, (from Genhank)
0.5841315 0.4682981 0.39967 0.26711115 23 at	201 Pros	tate	0.5855955	1	0.39981	0.26732737	A5051	EST: aa65e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825822 3', mRNA sequence. (from Genbank)
	202 Pros	tate	0.5841315		0.39967	0.26711115	A1913	EST: zp83b09.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 626777 3', mRNA sequence. (from Genbank)

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પાતમ પંતામ પાતારે મારામ મારામ પહેલો પાતારે પહેલા	RC_AA4853 EST: ab09a07.s1 Stratagene lung (#937210) Homo sapiens cDNA	Golle 040270 3, mKNA sequence. (from Genbank) Hkf-1 mRNA	Kinase A anchor profein	TDM1 Tronominals alsh 1 ' ' ' ' ' ' ' '	EST: zw35h03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 771317 3', mRNA sequence. (from Genbank)	E31: E3182247 Prostate gland I Homo sapiens cDNA 3' end, mRNA sequence. (from Genhank)	Lower strate 4 or :	JUNB Jun B proto-programs	EST: HUMGS0008379, Human Gene Signature, 3'-directed cDNA sequence, from Carbooks	EST: zu55b03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	Diole 741009 3: Similar to 1R:G452270 G452270 2-19 PROTEIN PRECURSOR: :: mRNA segmence /from Ganhant)	KIAA0268 gene, partial cds		0.26439974 1182613 at -2 Indinan DNA-binding protein ABP/ZF mRNA, complete cds	MCP Montress afects	order institutatie cotactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)		Short-chain dehydrogenase/reductase 1	Actin depolymerizing factor [human, fetal brain, mRNA, 1452 nt]	Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse HN1 (Hemathlorical and Namelogical society)	of a putative CpG island. Contains ESTs and GSSs	2000	Costathionine Reta Southage Alt Coling a	EST: EST49299 Gall bladder I Homo sapiens cDNA 3' end, mRNA	Sequence. (from Genbank)	NIAAU I Ub gene	Homo sapiens mRNA for KIAA0776 protein, partial cds
	RC_AA4853	D76444 at	X97335 at	M19267_s_a	RC_AA4762	A 27.03	A37.03	00573_r	345 at			>		107243 210	182613 at F	ธี		\$_87677		T				H14824_s_a t	A3435	+0 0	912	at
hir that their is but that	RC_A	0.26659372 D76444	0.26646683 X97335			0.2659507 35 at	0.26579258 53_at	0.26557875 nat	0.2654417 X51345	0.26520842 C01397 at		0.26501727 00 at	0.26469582 D87742 at	0.26450705	0.26439974 1182613		0.2641381 X59405_at	1	0.20333047 at	0.50212030	LĹ	0.26355585 12 at	<u></u> .	0.26337394 t	7	0.2030262/ 14 at	7.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2	0.26249048 69
	0.399317		0.398938	0.3984	0.308460	0.330108	0.397856	0.397822	0.397777	0.397631		0.396751	0.396495	0.396269	0.396173		0.395851	0 30568	0.395397			0.39522		0.39512	0.305440	0.395103		0.394641
	0.4679814	1 1	0.4664888	0.4663544	0.4662611		0.4660753	0,4658954	0.4658386	0.465359		0.4653239	0.37080 0.4651363	0.4650046	0.4647957		0.4647071	0.4646206	0.4643598			0.4641366		0.4639533	0.4638834	0.463758		0.4636937
	0.5838199	0.5827327	0.5814714	0.5814693	0.5790319		0.5790135	0.5781454	0.5780271	0.5775183		0.5771865	0.57080	0.576651	0.576651		0.5764993	0.5757962	3			0.574474 (0.574224 (0.5742155 (- 1		0.572737 (
	203 Prostate	204 Prostate	ZU5 Prostate	206 Prostate	207 Prostate		208 Prostate	209 Prostate	210 Prostate	211 Prostate		212 Prostate	- Coldic	214 Prostate	215 Prostate		216 Prostate	217 Prostate	218 Prostate		-	Prostate		220 Prostate	221 Prostate	-		223 Prostate
	203	204	202	206	207		208	209	210	211		212	1	214	215	(216	217	218		Č	7 8 7		220 F	221 F	222 F	(1677

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224 Prostate	0.5726978	0.463195	0.394534	0.2622724	3C_D20888	RC_D20888 EST: Human HL60 3'directed Mbol cDNA, HUMGS01869, clone
225 Prostate	0.5719746	0		0.26213694	131383 at	G profein gamma-10 subunit mRNA
				2	RC_AA4119	
226 Prostate	0.5715209	0.4628296	0.394113	0.26199704	4_at	
227 Prostate	0.5712687	0.4626799	0.393897	A. 0.2617884	AA195179_s at	
228 Prostate	0.5709684	0.4623777	0.393595	0.26142707	RC_AA5984 53 s at	H.sapiens mRNA for refrotransnoson
229 Prostate	0.5708897	0.462335	0.39336	0.26123214	A4286	EST: zw69c08.s1 Soares testis NHT Homo sapiens cDNA clone
230 Prostate	0.5703667	0.4620423	0.393068	0.261094	A4180	
231 Prostate	0.5702447	0.4617716	0.392632	RC A 0 2607551 40 at	A4814	EST: zv45a05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
232 Prostate	0.5701376	ļ	0.392415	0.26056284 X75756	π	DRKCM Protein kings C m
233 Prostate	0.5695193	0.4606413	0.392186	0.2604212 Z24727	; to	TPM1 Transmyosin alpha chain (ekolofal musala)
234 Prostate	0.5692244		0.391931	0.26007408 Z49989	क्र	Smoothelin
235 Prostate	0.5691826	0.460608	0.391747	0.25984997 D14533	at	XPA Xeroderma pigmentos im complementation group A
236 Prostate	0.5689654	0.4604097	0.39148	RC_A 0.25965405 50_at	A0322	EST: zk19f06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 471011 31 mRNA semience (from Combant)
237 Prostate	0.5687566	0.4600774	0.391363	0 25943884 t	7685_a	Deemonlokin (DDI DDI)
238 Prostate	0.5687344	0.4600278	0.391127	0.25926986 R66230	t	EST: yi34d06.r1 Homo sapiens cDNA clone 141131 5'. (from
239 Prostate	0.5682151	0.4599342	0.390861	RC_A	952	EST: zr36g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
240 Prostate	0 5685760	0.4507700	002000	W	02027_s_	EST: za57c08.r1 Soares fetal liver spleen 1NFLS Homo sapiens
	0.0000	0.4331123	0.330709	0.25885978 at	1 4 4 3 0 8 4	cDNA clone 296654 5', mRNA sequence. (from Genbank)
241 Prostate	0.5652082	0.4597072	0.390571	0.25870547 97	at	EST: ztb9a08.s1 Soares testis NHT Homo sapiens cDNA clone 726614 3', mRNA sequence. (from Genbank)
242 Prostate	0.564452	0.4596437	0.390347	RC_A 0.258506.25 at	A0349	EST: zk25e01.s1 Soares pregnant uterus NbHPU Homo sapiens
243 Prostate	0.5641075	0.4596017	0.390108	0.25838092 D13315	at	GLO1 Glyoxalase I
244 Prostate	0.5630525	0.4594392	0.389974	W3 0.25816056 at	W31738_s_ c	EST: zb93b06.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320339 5' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)
245 Prostate	0.5619864	0.459054	0.38981	0.25788718 M57730 at	i	EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1
246 Prostate	0.5617257	0.4587861	0.389758	0.25770676 X83425_at		LU gene for Lutheran blood group glycoprotein

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Inventors: Sridhar Ra.naswamy, et al. YWHAZ Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase RC_AA4045 Homo sapiens herpesvirus entry protein B (HVEB) mRNA, complete Pyrroline-5-carboxylate dehydrogenase (P5CDh) mRNA, long form EST: zv10d03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA4180 EST: zv94f11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA4822 | EST: ab15c03.s1 Stratagene lung (#937210) Homo sapiens cDNA RC_AA4476 EST: aa18c12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone RC_AA3473 EST: EST53685 Fetal heart II Homo sapiens cDNA 3' end, mRNA EST: zr75c01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone Tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, EST: aa41e07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone 0.2573073/46 at cDNA clone 501807.31 mRNA sequence (from Ganacia) 669216 3' similar to TR:G755466 G755466 TRANSMEMBRANE RC_AA2619 EST: zs17d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone Fatty acid synthase {3' region} [human, breast and HepG2 cells, PROTEIN PRECURSOR.;; mRNA sequence. (from Genbank) cDNA clone 501807 3', mRNA sequence. (from Genbank) GFPT Glutamine-fructose-6-phosphate transaminase IMAGE:815844 3', mRNA sequence. (from Genbank) IMAGE:685447 3', mRNA sequence. (from Genbank) Guanine nucleotide regulatory protein (tim1) mRNA clone 840868 3', mRNA sequence. (from Genbank) 753221 3', mRNA sequence. (from Genbank) 767469 3', mRNA sequence. (from Genbank) 813622 3', mRNA sequence. (from Genbank) Caldesmon 1, Alt. Splice 3, Non-Muscle LIM protein (LPP) mRNA, partial cds activation protein, zeta polypeptide Clone 23720 mRNA sequence sequence. (from Genbank) 0.253581|S80437_s_at|mRNA Partial, 2237 nt] pseudoinflammatory) X123 mRNA, 3' end Golgin-245 mRNA KIAA0108 gene TPRD RC_AA4063 RC AA4852 RC_AA2364 U49957_s_a 0.25746408 D78134 at 0.25633585|HT2845_at 0.25666118 U02082 at 0.25642875 U79272 at 0.2560607 U24266_at 0.2559091 R73299 at 0.25450677 M90516 at 0.25529474 D30756 at 0.25521585 D84294 at 0.25553864 U41740 at 0.25493225 L27479 at HG2743-0.25690687 77 i at 0.25316197|24 f at 0.25708506 07 at 0.2557616 43 at 0.2546918 76 at 0.25442073 88_at 0.25415593|86 at 0.25376058 93 at 0.25333914 07 at 0.25393826 0.389617 0.3892050.388934 0.38943 0.388198 0.5594444 0.4575253 0.388517 0.5588209 0.4575253 0.388232 0.388144 0.388125 0.387136 0.387136 0.387841 0.387701 0.386688 0.386585 0.388071 0.387831 0.386423 0.5493456 | 0.4546997 | 0.385537 0.386397 0.386294 0.386055 0.385553 0.457627 0.5586749 | 0.4569283 0.5561669 0.4562562 0.4581895 0.5565282 0.4564447 0.5543262 0.4559726 0.5578245 | 0.4564635 0.456138 0.5541329 0.4559328 0.5529212 0.4551171 0.4581961 0.4579037 0.5583576 0.4567877 0.553995 0.4556782 0.5538735 0.4552889 0.5494102 0.4548665 0.4549871 0.45486650.4549871 0.4549741 0.56135790.5611047 0.5597033 0.5560176 0.5599628 0.5515243 0.5500592 0.5503541 0.5496034 247 Prostate 248 Prostate 249 Prostate 250 Prostate 253|Prostate 251 Prostate 252 Prostate 254 Prostate 255|Prostate 256|Prostate 257 Prostate 258 Prostate 259 Prostate 260 Prostate 261 Prostate 262 Prostate 263 Prostate 264 Prostate 265 Prostate 267|Prostate 266|Prostate 268 Prostate 269|Prostate

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors

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270	270 Prostate	0.5492716	0.4545837	0.385476	0.2529523 t	M24736_s_a t	SELE Selectin E (endothelial adhesion molecule 1)
271	Prostate	0.5487302	0.4542674	0.384923	RC_A 0.25279826 96_at	RC_AA4117 96_at	Homo sapiens clone 24631 mRNA sequence
272	272 Prostate	0.5484247	0.4542443	0.384876	0.25265172 t	U72518_s_a t	Human destrin-2 pseudogene mRNA, complete cds
273	273 Prostate	0.547724	0.4541701	0.38473	RC_A 0.25244185 15_at	RC_AA1332 15_at	Homo sapiens mRNA encoding RAMP1
274	274 Prostate	0.5470277	0.4539807	0.384725	RC 0.2523243 51	RC_AA4969 51 at	EST: aa42e08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 823622 31 mRNA sequence (from Genhank)
275	275 Prostate	0.5469666	0.5469666 0.4534964	0.384629	0.25203088 D11151	011151 at	EDNRA Endothelin receptor type A
276	Prostate	0.5465493	0.4534719	0.384534	0.25176066 t	M83216_s_a t	CALD1 Caldesmon
277	277 Prostate	0.5463292	0.4532066	0.38444	RC_A 0.25157344 04_at	C_AA4533 4_at	RC_AA4533 EST: zx32b10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 04_at clone 788155 3', mRNA sequence. (from Genbank)
278	278 Prostate	0.5463022	0.4528663	0.384035	M83667 0.251339 1_s_at	M83667_rna 1_s_at	NF-IL6-beta protein mRNA
279	279 Prostate	0.5456138	0.452676	0.383755	RC_A 0.2512209 56 at	3C_AA4258 36 at	Homo sapiens mRNA for KIAA0908 protein partial cds
280	280 Prostate	0.5454785	0	0.383675	0.25106984 M83822 at	/83822 at	Beige-like protein (BGL) mRNA, partial cds
281	Prostate	0.545441	0.4525109	0.383386	RC_A 0.25083986 63_at	RC_AA4914 63_at	EST: ab01d12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA
282	Prostate	0.5447523	1 1	0.383371	0.2506934 U51711	J51711_at	DESMOCOLLIN 2A/BB PRECURSOR
283	283 Prostate	0.5445942	0.4522296	0.383243	0.25055718 49 at	A4050	EST: zu19g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 738486 3' mRNA sequence (from Genhank)
284	284 Prostate	0.5440533	1	0.383186	0.25033736 00 at	RC_AA4783	CD39-like 2
285	285 Prostate	0.5437453	0.4518799	0.382972	0.25008348 70 at	RC_AA2817 70_at	Seven in absentia (Drosophila) homolog 1
286	286 Prostate	0.5436813	0.4515054	0.382823	0.24995187 t	VA485585_a	AA485585_a EST: zx90e01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA t
287	287 Prostate	0.5436299	1 1	0.382561	0.2498199 U88871	J88871_at	Peroxisome targeting signal 2 receptor (Pex7) mRNA
288	288 Prostate	0.5430307	0.4513028	0.382257	0.24966027 M38690_at	1	CD9 CD9 antigen
289	Prostate	0.5430216	0.4505165	0.382019	0.24946603 40_s_at	534	EST: z/6h03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669365 3', mRNA sequence. (from Genbank)
290	290 Prostate	0.5429966	0.4500143	0.381532	RC_A 0.24925146 62_at	561	EST: zr79b07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 681877 3', mRNA sequence. (from Genbank)
291	291 Prostate	0.5424957	0.4498984	0.381334	RC_A 0.24916528 98_at	A4056	EST: zu66e10.s1 Soares testis NHT Homo sapiens cDNA clone 742986 3', mRNA sequence. (from Genbank)

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EST: 43f5 Human retina cDNA randomly primed sublibrary Homo	sapiens cDNA, mRNA sequence. (from Genbank)	Transcription factor SIM2 long form mRNA	Clone HSH1 HMG CoA synthase mRNA, partial cds	EST: zw03b06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	768179 3', mRNA sequence. (from Genbank)	EST: HUMGS0003762, Human Gene Signature, 3'-directed cDNA	AA488793 a Aa54d11.r1 NCI CGAP GCR1 Home saniens chula clong	IMAGE:824757 5', mRNA sequence, (from Genhank)	TAK1 binding protein 1 (TAB1) mRNA	Niclear localization signal daloted in volcescritisfacial and a	KIAA0251 gene partial cds	EST: yl02e03.r1 Homo sapiens cDNA clone 138076 5'. (from Genbank)	EST: zx43g04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 789270 3', mRNA sequence. (from Genbank)	Clone 783764 3' mRNA sequence from Canhous	EST: zl33f12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA	cione 303/39 3, IIIKNA sequence. (Irom Genbank)	a AGL Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)	M35851_s_a AR Androgen receptor (dihydrotestosterone receptor; testicular teminization; spinal and bulbar muscular atrophy. Kennedy disease)	EST: zx08f10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	element MER22 repetitive element ;, mRNA sequence. (from	Genbank)	Placenta copper monamine oxidase mRNA	SCP2 Sterol carrier protein 2	EST: EST45795 Fetal kidney I Homo sapiens cDNA 3' end, mRNA segmence (from Genbank)	EST: zn93h01.s1 Stratagene lung carcinoma 937218 Homo sapiens
-	at	at	at	A4248		C01803_s_a E	AA488793 a /	. = 1		A4610	18 at		_AA4502	s at	_AA4469 at	_AA1300	5	J84011_s	/35851_s_a	<u> </u>	AA4494		स्र	te,	_AA3405 at	_AA1358
fr find direction of the control of	0.24902043 W28151_at	0.24885654 U80456	0.24857931 X83618		0.24848191 49_at	0.24836177		0.24817023	0.24798755 U49928 at	RC_A 0.24773268 57_at	0.2476032 D87438	0.24748597 R53717 at		0.24737182 94	RC 0.24703121 44	0 24697034 89	10010013.0	0.24675086 t	0.24657524 t			0.24638523 75	0.24615584 U39447	0.24608794 U11313	0.24588968 39	RC
	0.381322	0.381211	0.381009	1	0.380775	0.380684		0.380576	0.380523	0.38039	0.380343	0.380235		0.380078	0.379942	0.379802	700	0.379388	0.379236			0.37903	0.378904	0.378589	0.378548	01010
	0.4498854		0.4497663		0.449/064	0.4496755	1	0	0.448764	0.4484839	0.4483686	0.4482804		0.4481291	0.448094	0.4480678		0.4480511	0.4479351			0.4477828	0.4477741	0.4477734	0.4473016	0.4472020
0000	0.5423896	0.5421512	0.5414596	77	0.3412862	0.5410488		0.5404763	0.5401263	0.5400038	0.5399782	0.5396916	7.000	0.5390546	0.5387057	0.5385253		0.5383057	0.5376237		6	0.536918		0.5367519	0.5364852	0 5364504
	zyz Prostate	293 Prostate	294 Prostate	205 Drootsto	riosiale	296 Prostate		297 Prostate	298 Prostate	299 Prostate	300 Prostate	301 Prostate	0,000	ooz Frostate	303 Prostate	304 Prostate		305 Prostate	306 Prostate			\top	1	309 Prostate	310 Prostate	311 Proctate
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նչում մոու Հոգի տումի գումի Վետի Վետի		EST: zu36h10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740131 3', mRNA sequence, (from Genbank)	Tob		Pilot mRNA	Transcript ch138 [human, RF1,RF48 stomach cancer cell lines, mRNA, 235 nt]	Protein kinase mitogen- activated 13	Homo sapiens KIAA0439 mRNA, partial cds	Desmin gene	EST: zr25c10.s1 Stratagene NT2 neuronal precursor 937230 Homo	Methyl sterol oxidase (ERG25) mRNA	ERBB3 V-erb-b2 avian erythroblastic leukemia viral oncogene	homolog 3 {alternative products}	AA292234_a EST: zt50h06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA to clone 725819 5', mRNA sequence. (from Genbank)	RTP		Beta2-syntrophin (SNT B2) mRNA	Homo sapiens mRNA for HYA22, complete cds	Unknown product		Genuarik)	EST: zx06a12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 785662 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;, mRNA sequence. (from Genbank)
	RC_AA6209 65_at	RC_AA4795 33_at	D38305 at	X63741_s_a	+	S77393 at	AF004709_a t	RC_AA4585 78_at	M63391_ma 1_at	RC_AA2321	U60205 at		M34309 at	AA292234_a t	D87953_at	RC_AA2554	U40572 at		0.2428748 D28124 at	RC_AA4594	02 ร สเ	RC_AA4490 76_at
H. Unit Suit B. Cont. Savi	RC 0.24543941 65	RC_A 0.24525052 33 at	0.24509293 D38305		0.24492504 t	0.24479586 S77393_at	0.24457563 t	RC 0.2444855 78	M63: 0.2442783 1_at	RC 0 24408878.87	0.24403477 U60205		0.24385318 M34309	0.243611251	0.24345869 D87953_at	RC_A	0.2431215 U40572	0.24297151 D88153	0.2428748	0.0000000000000000000000000000000000000	0.24212910 02 5	RC 0.24252342 76
my An	0.37787	0.377733	0.377698		0.37763	0.377602	0.377323	0.377206	0.377109	0.376906	0.376712		0.376646	0.376522	0.37647	0.076460	0.376366	0.376285	0.376	בטביזבני ט	0.373707	0.375513
	0.4464575	0.4461213	0.4461089	Ì	0.4460386	0.4460049	0.4459347	0.445543	0.4454449	0 5346963 0 4453443	0.5341402 0.4451794	1	0.4451002		0.4447177	0 4444000	- 1	0.4438101	0.4433218	!	0.4432703	0.4430404
	0.5358225	0.5357221	0.5356431		0.5356014	0.5354915	0.5353308	0.5351836	0.5350846	0.5346963	0.5341402		0.5341062	0.5330498	0.5328742	0 5207007	0.5320264	0.5319198	0.5312803	0 6206646	0.3303313	0.5302557
	312 Prostate	313 Prostate	314 Prostate		315 Prostate	316 Prostate	317 Prostate	318 Prostate	319 Prostate	320 Prostate	321 Prostate		322 Prostate	323 Prostate	324 Prostate	205 0.000	326 Prostate	327 Prostate	328 Prostate		oza Fiustate	330 Prostate
	312	313	314		315	316	317	318	316	320	321	000	324	323	324	300	326	327	328	000	323	330

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IS cDNA	nit, alpha	ne					SDNA	7

331	Prostate	0.5299988	0.4426315	0.375476	0.24243796	RC_AA6214 40_at	RC_AA6214 EST: af35g10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA 40_at clone 1033698 3', mRNA sequence, (from Genhank)							
332	332 Prostate	0.5290062	0.4422808	0.375072	0.24232268 R69417	R69417 at	EST: yj83f12.r1 Homo sapiens cDNA clone 155375 5'. (from Genhank)							
333	333 Prostate	0.5289936	0.4422798	0		11 1	KRT15 Keratin 15							
334	334 Prostate	0.5285142	0.4419763	0.374859	0.24201627	RC_AA4500 10_at	EST: xx33f04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 788287 3. mRNA sequence (from Ganhank)							
335	335 Prostate	0.5277329	0.4419254	0.374727	0 24168041 14778 \$		PPP3CA Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha							
336	336 Prostate	0.5275849	1 (0.3		U90552 at	Butymphilin (BTES) Bulymphilin (BTES) Butymphilin 337	Prostate	0.5271085	0.4416855	0.374561	0.24132104	AA279359_a t	AA279359_a EST: zs84d01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone t
338	338 Prostate	0.5265877	0.4416533	0.374539	W 0 24113257 at	W38226_s_	(Alibaration (Caragamy)							
339	339 Prostate	0.5263924	1 1	1		U78294 at	Arachidonata 15 linovyramasa sooma tuss							
340	340 Prostate	0.5263754	0.4414145	0.373733			EST: yv29a08.r1 Homo sapiens cDNA clone 244118 5'. (from Genbank)							
341	341 Prostate	0.5258607	0.4413914	0.37373	0.2406929	M63509_s_a t	Glutathione S-transferase M2 (m.eclo)							
342	342 Prostate	0.5257589	0.4409685	0.373571	0.02853 528300	t	EST: yi82b05.r1 Homo sapiens cDNA clone 145713 5. (from							
343	343 Prostate	0.5255864	1	0.373414	0.24049558 M21154 at		MAIN C Account this							
344	344 Prostate	0.5245456	0.4406291	0.373311	0.24041334 40401 at		(close zand 29) m DNA 21 c. 1.							
345	345 Prostate	0.5245456	0.4405527	0.373268	0.2401133 L40401	0	Homo sanians (clone 22012) m DNA 21 222 222							
346 F	346 Prostate	0.5245253	0.4405329	0.373224	0.24004823 61 at	A4775	EST: zu41f11.s1 Soares ovary tumor NbHOT Homo sapiens cDNA							
347 F	347 Prostate	0.5241652	0.4404768	0.373169	0.239785391	AA037192_a	AA037192_a Dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-							
348 F	348 Prostate	0.5241537	0.4404557	0.372968	0.23958275 79	AA2583	Angiotensin recentor-like 2							
349 F	349 Prostate	0.5227521	0.4404486	0.372967	0.239412491	W477891_a	AA477891_a EST: zu34e12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA t clone 739918 5' mRNA sequence (from Canhank)							
350 F	Prostate	0.5227351	0.4403846	0.37269	RC_A 0.23931338 83_at	A1207	Eukaryotic translation initiation factor 2 subunit 3 (namma 52kD)							
351 P	Prostate	0.5223597	0.440243	0.372668	0.23929104 1 at	717_rna	Heat shock profein (hsn 70) gene							
352 F	352 Prostate	0.5220991	0.4400503	0.372588	0.23914976 61	AA0545 at	EST: zk83h03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 489461 3. mRNA sequence (from Genhank)							
353 F	353 Prostate	0.5220723	0.4399834	0.372379	A 0.23903655 t	A227621_a	AA227621_a EST: zr57e11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone t 667532 5', mRNA sequence. (from Genbank)							

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TNF-related anontosis inducing ligand TRAII anDNA	Chromogranin A (parathyroid secretory protein 1)			EST: 2t55b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 726225 3', mRNA sequence. (from Genhank)	;	CDINA CIOITE 469227 3, MKNA Sequence. (from Genbank)		mRNA sequence. (from Genbank)	ID2 Inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	Human striated muscle contraction regulatory protein (Id2B) mRNA, at-2 complete ads	FST: ah14d08 s1 Stratagene lung (#037240) Home canions obNA		sequence. (from Genbank)	EST: za92c10.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 300018 5' mRNA seguiance (from Ganbank)	GUANYLATE CYCLASE SOLUBLE: AI PHA-3 CHAIN	Stress responsive serine/threonine protein kinase Krs-1 mRNA	EST: zx68b01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796585.3" mRNA seguence (from Cenhank)	dense record of interest and included the condense of the cond	EST: zm87a05.r1 Stratagene ovarian cancer (#937219) Homo	EST: HUMGS0002430. Human Gene Signature 3'-directed conva	sequence, mRNA sequence. (from Genbank)	EST: zw70d08.s1 Soares testis NHT Homo sapiens cDNA clone	PEANING EDAME OF VORSES - STANDARD COME VI	Genbank)	EST: zu56e12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 742030 3', mRNA sequence. (from Genbank)	EST: ze79b09.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	Civile 303 Lt. 3, IllikivA sequence. (Irom Genbank) Prostate enecific membrane anticon (alternativol) anticon (human	at primary prostatic tissues, mRNA Partial, 251 nt]
23892976 U37518 at	RC_AA4615 59 at	HG4126-	23034083 H14396 at	RC_AA2930 96_at	RC_AA0565	مر ما مر	RC_AA4303	88_at	0.237862 M96843 at	M96843		RC_AA4860	92_at	0.23749638 W07142 at	X66534 at	U26424 at	RC_AA4614 44_at	5-	AA075427_a		C00337_at		BC 44/3/13	at	A4014		A0248		s at
0.23892976	0.23873119 59	0 2267605		RC_A 0.23839231 96_at	0 23846113 57			0.23798092 88 at	0.237862	0.2377651		,	0.23760425 92	0.23749638	0.23733936 X66534	0.23716441 U26424	RC_A 0.23705405 44 at		A 0.23692276+		0.23672333 C00337		,	0.23662771 17		0.23657416 52 at	RC_A	0.500051 00	0.23629376 S76978
0.372151	0.372003	0.374846	0.07 1040	0.371757	0.371582	100		0.371549	0.371245	0.371117	The state of the s		0.37087	0.370719	0.370419	0.370259	0.370191		0.370077		0.370068			0.369981		0.369967	0.360517		0.369404
0.4399368	0.4399333	0.4398906	0.400000	0.4398903	0.4395452			0.4394583	0.439154	0.438893		1	0.4388778	0.4380459	0.4380455	0.4379379	0.4378173		0.4374064		0.4372525			0.4367335		0.4366573	0.4365458		0.4362349
0.521638	0.5215861	0.5214881	10011700	0.5212281	0.5201612		7	0.5201383	0.5193806	0.5193806		2007	0.5182194	0.5179917	0.5179279	0.5174235	0.5173146		0.5171329 0.4374064		0.5165435			0.5165025		0.5161634	0.5155192	1	0.514276

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373 Prostate	0.5141313	0.436129	0.369276	M: 0.23602082 t	M27436_s_a t	F3 Coagulation factor III (thromboplastin, tissue factor)
374 Prostate	0.513948	0.4360542	0.369176	0.23577218 t	AB002344_a t	Human mRNA for KIAA0346 gene, partial cds
375 Prostate	0.513438	0.4359814	0.36898	RC_A 0 2356551 18 at	RC_AA4477	EST: aa20c10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
376 Prostate	0.5129824		0.368935	0.23548256 X04434 at	7434 at	IGF1R Insulin-like growth factor 1 recentor
377 Prostate	0.5129111	0.4358144	0.368877	RC_A 0.23545301 44_at	RC_AA4599 44_at	EST: zx66a08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796406 3', mRNA sequence (from Genhank)
378 Prostate	0.5126345	0.4357514	0.368752	RC_A 0.23536316 93 at	RC_AA2528 93_at	EST: zr76e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 669336 3', mRNA sequence (from Genhank)
379 Prostate	0.5122163	0.4357111	0.36872	0.23513953 R77200_at	77200_at	EST: yi65g05.r1 Homo sapiens cDNA clone 144152 5". (from Genbank)
380 Prostate	0.512036	0.4356674	0.368693	RC_A 0.23487738 30_at	RC_AA4339 30_at	EST: zw52e11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773708 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)
381 Prostate	0.5119253	0.435622	0.368138	RC_AA2 0.2347673 35_s_at	AA2325 s_at	EST: zr24a12.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664318 3', mRNA sequence. (from Genbank)
382 Prostate	0.5118731	0.4355272	0.368047	0.23471372 Hz	26326_f_at	0.23471372 H26326 f_at Ribosomal protein S20
383 Prostate	0.5118585	0.4355272	0.367978	0.23456888 W45259 at	45259 at	EST: zc24e10.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323274 5', mRNA sequence, (from Genbank)
384 Prostate	0.5117744	0.4354133	0.367793	RC_A 0.23435543 14 at	A1910	EST: zp85g03.s1 Stratagene HeLa cell s3 937216 Homo sapiens
385 Prostate	0.5115058	0.4351819	0.367526	0.23426354 S74728_at	4728_at	Antiquitin
386 Prostate	0.5112071	0.4351701	0.36745	RC_A 0.2340989427_at	RC_AA4821 27 at	Homo saniens mRNA for DAK4 protein
387 Prostate	0.5103671	0.4351701	0.367215	0.23400894 D82344	2344_at	NBPhox
388 Prostate	0.5103671	0.4351673	0.367211	0.23384629 D8	2344 at-2	0.23384629 D82344 at-2 Paired mesoderm homeohox 2h
389 Prostate	0.5097561	0.4350255	0.367121	0.23378049 U44111 at	4111_at	Histamine N-methyltransferase
390 Prostate	0.5088751	0.4349452	0.366978	0.2336974 U33921	ä	HSU33921 Clontech adult lung cDNA library (HL1158a) Homo sapiens cDNA clone L1-204, mRNA sequence
391 Prostate	0.5087709	0.4347852	0.366966	AA 0.23364335 t	AA249437_a t	EST: j3966.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5', mRNA sequence. (from Genbank)
C C C C C C C C C C C C C C C C C C C		i i		RC	A0273	EST: ze97d11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366933 3' similar to contains Alu repetitive element;, mRNA
392 Frostate	0.5086383	0.5086383 0.4345133	0.366412	0.23348135 17 at		sequence, (from Genbank)

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393	Prostate	0.5084479	0.434114	0.366371	0.23340301	AA234141_s _at	Homo sapiens katanin p80 subunit mRNA. complete cds
394	Prostate	0.507778	0.433728	0.36621	0 23328044 47		Homo conjone clone 0/E44 DNA
0			1		11070707.0	RC_AA5999	EST: ag28h10.s1 Jia bone marrow stroma Homo sapiens cDNA clone
395	395 Prostate	0.5074742		0.366182	0.2331981 91 at	91_at	1090915 3', mRNA sequence. (from Genbank)
200	riostate	0.5061113	0.4333497	0.365948	0.23315383 U42359_at	U42359_at	N33 protein form 1 (N33) gene, exon 10 and complete cds
397	397 Prostate	0.5060412	0.433254	0 365046	30040000	RC_AA6204	
				0.0000	0.23307303 40 at	46207	KecQ protein-like 4
398	Prostate	0.5058664	0.5058664 0.4329896	0.365734	0.23275709 95_at	1070	1055499 3', mRNA sequence. (from Genhank)
399	Prostate	0.5058322	0.4329538	0.365642	0.23263827	AA365742_s at	
400	400 Prostate	0.5056704	0.4327875	0.365454	RC_A 0.23244311 58 at	RC_AA1428 58 at	EST: Z40e04.s1 Soares pregnant uterus NbHPU Homo sapiens
401	401 Prostate	0.50539	0.432649	0.365414	RC_A 0.23237228 49 at	RC_AA4475 49 at	RC_AA4475 UDP-N-actey/glucosamine pyrophosphorylase 1; Sperm associated 49 at
402	402 Prostate	0.5051856	0.4325792	0.365358	0.23225614	D79601 f at	0.23225614 D79601 f at (from Genhank)
403	403 Prostate	0.5051112	0.4325317	0.365193	0.23214176.27	RC_AA4460 27_s at	Early drowth response 2 (Krov-20 (Drosophila) homology
							STOREST CONDITION TO (DIOSOPTING) HOMOLOGY)
404	404 Prostate	0.5050933	0.4323327	0.365033	RC_A 0.23185767 61_at	A5984	EST: ae48h01.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 950161 3', mRNA sequence. (from Genbank)
405	405 Prostate	0.5045458	0.432308	0.364953	0.23177072 44	_AA5991	Monein phoenhatoon torant culturit 4
406	406 Prostate	0.5045164	0	0.364724	0.23158269 U67156 at		Mitoden-activated kinase kinase kinase 5 (MADKKKS) mDNA
407	407 Prostate	0.5041468	0.4319305	0.364624	0 2314845	RC_D25718	EST: Human colon 3'directed Mbol cDNA, HUMGS04084, clone
408	408 Prostate	0.5040523	0.4319247	0.36458	1 -		Diadenosine tetraphosphatase mRNA
409	409 Prostate	0.5039243	0.4319012	0.364411	0.2313318 N42196 at		Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds
410	410 Prostate	0.5037847	0.4348748	0.00	000000000000000000000000000000000000000		EST: zc11a10.r1 Soares parathyroid tumor NbHPA Homo sapiens
411	411 Prostate	0.5033535	0.4346304	0.364484	RC_AA3947		EST: zf5zc08.s1 Soares ovary fumor NbHOT Homo sapiens cDNA
412	412 Prostate	0.5030474	0.1316.248	0.363002	100000000	מון	CONE 72390 3, MKNA Sequence. (from Genbank) EST: yw32h06.r1 Homo sapiens cDNA clone 253979 5. (from
		1100000	0.40104.0	0.303333	0.230000211	U.Z.SUGOUZ IN/ SBOS I at Genbank)	Genbank)

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Inventors: Sridhar Ramaswamy, et al. branched chain keto acid dehydrogenase complex; maple syrup urine RC_AA4960 | EST: zv72d08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: ze96g03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA P4HB Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-EST: zx96a12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA hydroxylase), beta polypeptide (protein disulfide isomerase; thyroid RC_AA4769 | EST: zu38c05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA Dihydrolipoamide branched chain transacylase (E2 component of EST: Human aorta cDNA 5'-end GEN-323G06, mRNA sequence. EST: aa51c06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone AA285284_a Homo sapiens NADP-dependent isocitrate dehydrogenase (IDH) EST: zw80h06.s1 Soares testis NHT Homo sapiens cDNA clone GCSH Glycine cleavage system protein H (aminomethyl carrier) ApM2 mRNA for GS2374 (unknown product specific to adipose H89551_s_a | EST: yw28e07.r1 Homo sapiens cDNA clone 253572 5'. (from K+ channel beta 1a subunit mRNA, alternatively spliced IMAGE;824458 3', mRNA sequence. (from Genbank) clone 759183 3', mRNA sequence. (from Genbank) clone 811582 3', mRNA sequence. (from Genbank) clone 366868 3', mRNA sequence. (from Genbank) clone 740264 3', mRNA sequence. (from Genbank) 782555 3', mRNA sequence. (from Genbank) Hepsin (transmembrane protease, serine 1) Integrin alpha 8 subunit mRNA, 3' end Secreted frizzled-related protein 1 hormone binding protein p55) KIAA0065 gene, partial cds KIAA0310 gene product mRNA, complete cds Integrin, alpha 8 (from Genbank) MAT8 protein Genbank) disease) 0.23065019|S49953_s_at|N-cym tissue) 0.23036776|X66785_i_at RC_AA4545 0.23011512 L36531 at-2 RC AA4903 RC AA0294 AF001900_a AB002308_a RC_AA4317 0.22950125 D31763 at 0.22936775 X93036_at 0.2289285 T28246 at ˈat Ħ, 0.2297981 L36531 at म 0.2280336 D45370 at 0.22837944 L39833 at 0.22967741|97_s_at 0.23076434 302783 0.23051204|D57737_. 0.2294932 18_s_at 0.22813979 D00723 0.22949994 62 at 0.22859085|22_at 0.22854143|99 at 0.23029144 37 0.22924876 0.22911148 0.22893159 0.2282243 0.363073 0.363845 0.363346 0.3639440.363671 0.362483 0.3639540.36321 0.363195 0.362946 0.362933 0.5003853 0.4307364 0.362748 0.362639 0.362483 0.362113 0.362144 0.36206 0.361745 0.361478 0.361609 0.4315063 0.4315696 0.5003974 | 0.4307732 0.5002678 | 0.4307352 0.4997987 | 0.4307112 0.431357 0.5014889 0.4309902 0,5019936 0.4313687 0.5017911 0.4312735 0.5013135 0.4309738 0.4997084 | 0.4307112 0.4314967 0.5017911 0.4312611 0.5007668 0.4309557 0.4993705 0.4306297 0.4989584 0.4302877 0.4989091 0.4299843 0.429983 0.4986846 0.4299813 0.4994963 0.4306861 0.4298061 0.5021772 0.5025252 0.5020724 0.5018032 0.4986771 0.4988997 413 Prostate 414 Prostate 415|Prostate 416|Prostate 417 Prostate 418 Prostate 419 Prostate 420 Prostate 421 Prostate 422 Prostate 425 Prostate 426 Prostate 423 Prostate 424 Prostate 427|Prostate 428 Prostate 429 Prostate 430 Prostate 431 Prostate 432 Prostate 433 Prostate 434 Prostate

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435 Prostate	0.4983941	0.4297482	0.361461	RC 0.22781888 39	_AA4777	EST: zu34a07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739860 3', mRNA sequence. (from Genbank)
436 Prostate	0.4983423	0.4296413	0.361444	0.22758767 D49387	.9387_at	NADP dependent leukotriene b4 12-hydroxydehydrogenase, partial cds
			***************************************			EST: zt28g07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 714409.3' eimilar to TD-E04407 E04407 NMADA ALAGORIA
437 Prostate		0	0.361072	RC_AA2 0.2275285 27 s at	RC_AA2924 27 s at	GLUTAMATE-BINDING SUBUNIT: ;; mRNA sequence. (from Genbank)
438 Prostate	0.4976596	0.429543	0.360954	0.22744726 U30894	0894 at	N-sulphoducosamine sulphohydrolase mRNA
439 Prostate	0.4975875	0.4292265	0.360909	RC_A 0.22733112 47 at	RC_AA4339 47_at	EST: zw52g10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773730 3', mRNA sequence (from Genhank)
440 Prostate	0.4973697	0.4291074	0.360864	RC_A 0.22722267 55_at	RC_AA4528 55_at	Human mannose-specific lectin (MR60) mRNA, complete cds
441 Prostate	0.4973115	0.4290175	0.360665	0.22711325 S62539 at		Insulin receptor substrate-1 Ihiman ekeletal miecia monin Roog nu
442 Prostate	0.497174	0.4290175	0.360505	0.2270408977 s at	479	EST: zw82e09.s1 Soares testis NHT Homo sapiens cDNA clone
443 Prostate	0.4970815	0.4289598	0.360425	0.22698799 L04270 at		LYMPHOTOXIN-BETA RECEPTOR PRECLIBADE
444 Prostate	0.4967847	0.4289326	0.360265	AA4 0.226745 t	מ	EST: zv61b01.r1 Soares testis NHT Homo sapiens cDNA clone 758089 5' mRNA sequence (from Genhank)
445 Prostate	0.496342	0.4288378	0.360156	0.22664878 04 at	A4045	EST: zw38b09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 772313.31 mRNA sequence (from Canbank)
446 Prostate	0.4960628	0.4288147	0.359983	RC_A 0.22657686 28_at	A1509	EST: zl47e06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505090 3', mRNA sequence, (from Genbank)
447 Prostate	0.4958171	0.4287976	0.359918	RC_A 0.226441 19_at	A0432	EST: zk55g09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486784 3' similar to contains Alu repetitive element; mRNA sequence (from Genhank)
448 Prostate	0.4952663	0.4287861	0.359822	RC_ 0.2263282193	A2812	EST: zt02h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712007 3' similar to SW:IPYR_BOVIN P37980 INORGANIC PYROPHOSPHATASE: mRNA sequence (from Contact)
449 Prostate	0.4952615	0.4287541	0.359787	0.22606835 63 a	A4120	EST: zu10b08.s1 Soares testis NHT Homo sapiens cDNA clone 731415 3', mRNA sequence. (from Genbank)
450 Prostate	0.4951125	0.4287541	0.359637	AA4 0.22602642 t	AA405288_a c	EST: zt37f09.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 724553 5' similar to contains Alu repetitive element; contains element LTR5 repetitive element: mRNA sequence (food Contains)
451 Prostate	0.4945203	0.4280362	0.359528	RC_A 0.22584971_at	A1364	EST: zl01e08.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491078 3', mRNA sequence. (from Genbank)

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Inventors: Sridhar Ramaswarny, et al. 0.22534484 U94831_at-2 Homo sapiens multispanning membrane protein mRNA, complete cds 0.22523685 U01833_at Nucleotide-binding protein mRNA clone 509500 3' similar to TR:G809573 G809573 GLUTAREDOXIN.;, EST: zw99e08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA AA461426 r EST: zx63h02.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: zd41b11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA DMD Dystrophin (muscular dystrophy, Duchenne and Becker types) RC_AA2932 | EST: zt28b08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA EST: Homo sapiens thymus mRNA (randomly primed, normalized), EST: zl65e03.s1 Stratagene colon (#937204) Homo sapiens cDNA sapiens cDNA clone 593840 3', mRNA sequence. (from Genbank) RC_AA4550 EST: aa04e08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 0.22450556 72_at CDNA clone 526238 3', mRNA sequence. (from Genbank) RC_AA2362 EST: zr51e07.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: Human aorta cDNA 5'-end GEN-286G10, mRNA sequence. EST: zo87a05.s1 Stratagene ovarian cancer (#937219) Homo EST: yi56e02.r1 Homo sapiens cDNA clone 143258 5'. (from cDNA clone 526238 3', mRNA sequence. (from Genbank) single-pass sequence, mRNA sequence. (from Genbank) clone 796179 5', mRNA sequence. (from Genbank) clone 785126 3', mRNA sequence. (from Genbank) clone 714423 3', mRNA sequence. (from Genbank) clone 343197 5', mRNA sequence. (from Genbank) CYP1B1 Cytochrome P450 IB1 (dioxin-inducible) 812294 3', mRNA sequence. (from Genbank) 666948 3', mRNA sequence. (from Genbank) Homo sapiens KIAA0439 mRNA, partial cds Endothelial differentiation-related factor 1 Multispanning membrane protein mRNA mRNA sequence. (from Genbank) KIAA0176 gene, partial cds 64 KD AUTOANTIGEN D1 Amplaxin (EMS1) mRNA 0.22501433|D79601_i_at | (from Genbank) Genbank) 0.22495238 W27827 at RC_AA4763 RC_AA1668 RC_AA0561 ij ਙ 0.22383511 M98343 at 0.22553377 U94831 at RC AA5987 0.2257586 D79998 at 0.2246568 X54162 at 0.22414841|R73982 at 0.22368766 U03688 at 0.22434072|L44367 at 0.22562273 W68097 0.22316931 M18533 0.22476682|93 at ä 0.2240174|52 at 0.22351626 10 at 0.2257353 66 at 0.22340499 41 at 0.22333422 25 at 0.22485581 at 0.2241661787 0.358744 0.358592 0.356950.356906 0.3590660.358661 0.358294 0.358184 0.357069 0.357045 0.359308 0.358165 0.357963 0.357693 0.357538 0.487839 0.4257926 0.357456 0.357278 0.359284 0.35891 0.357701 0.425725 0.357397 0.4943693 0.4279348 0.4891504 0.4265034 0.4277588 0.4277523 0.4929107 0.4276341 0.49254 0.4273988 0.4899189 0.4271086 0.4896146 0.4269415 0.4885833 0.4261915 0.4881712 0.4258363 0.4870743 0.4257187 0.4869723 0.4257183 0.425673 0.4929107 0.4276916 0.4879358 0.4258225 0.425725 0.4892179 0.4265257 0.4867469 0.4256854 0.4940013 0.4931679 0.4867377 0.4878324 0.4870774 456 Prostate 457 Prostate 452 Prostate 467 Prostate 453 Prostate 454 Prostate 458 Prostate 459 Prostate 461 Prostate 462 Prostate 463 Prostate 464 Prostate 465 Prostate 466 Prostate 468 Prostate 469 Prostate 470 Prostate 471 Prostate 472 Prostate 455 Prostate 460 Prostate 473 Prostate

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Inventors: Sridhar Ramaswamy, et al. Kidney mRNA for putative membrane protein with histidine rich charge RC_AA4494 | EST: zx05c11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA Eukaryotic translation elongation factor 1 delta (guanine nucleotide 666362 3' similar to contains Alu repetitive element; contains PTR7 EST: zs31b05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone RC_AA4890 EST: aa56g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone AA228148 s EST: zr58d07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone AA233231_a EST: zr69c12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zr45e02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone AA045870_a EST: zk75a04.r1 Soares pregnant uterus NbHPU Homo sapiens RC_AA1568 EST: zl20h08.s1 Soares pregnant uterus NbHPU Homo sapiens Solute carrier family 22 (organic cation transporter), member 5 Proteasome (prosome, macropain) 26S subunit, non-ATPase, cDNA clone 502527 3', mRNA sequence. (from Genbank) cDNA clone 488622 5', mRNA sequence, (from Genbank) Homo sapiens katanin p80 subunit mRNA, complete cds repetitive element;, mRNA sequence. (from Genbank) IMAGE:686769 3', mRNA sequence. (from Genbank) H.sapiens gene from PAC 295C6, similar to rat PO44 IMAGE:824990 3', mRNA sequence. (from Genbank) clone 785588 3', mRNA sequence. (from Genbank) CCAAT/enhancer binding protein (C/EBP), delta 667597 5', mRNA sequence. (from Genbank) 668662 5', mRNA sequence. (from Genbank) FACL1 Long chain fatty acid acyl-coA ligase Proteasome subunit p40 / Mov34 protein Diazepam binding inhibitor (DBI) mRNA CRAT Camitine acetyltransferase Nucleotide binding protein mRNA X BOX BINDING PROTEIN-1 ORF, Xq terminal portion exchange protein) 0.2220622|D50063_at-2|(Mov34 homolog) clusters RC_AA2556 AA046840_a AA428006_a RC_AA0246 M14200_ma AA173998_a 0.22244516 M31627 at 0.22286671 D10040 at 0.22274701|R29657_at RC AA2322 0.22216727 D50063 at 0.22195727|D82060_at 0.22142391 D16469_at 0.22124158 L04510_at at 0.2209206 X78706 0.222970417 at 0.22308686 22 at 0.22222532 91 at 0.22181395|35_at 0.22114493 73 at 0.2208542 08 at 0.2226348 1 at 0.22179504 at 0.2225681 0.22232372 0.221498 0.22165026 0.22105758 0.355532 0.356535 0.356482 0.356468 0.356427 0.356269 0.356174 0.355839 0.355604 0.355218 0.355324 0.355266 0.3550550.355301 0.4819391 0.4230056 0.354945 0.4813539 | 0.4228233 | 0.354935 0.355164 0.355023 0.354945 0.354931 0.4812442 0.4227255 0.354748 0.35473 0.4865256 0.4254746 0.4822123 0.4232519 0.4854397 | 0.4249058 0.4850763 | 0.4242047 0.4866144 | 0.4255597 0.4864205 0.4252388 0.4863043 0.4251491 0.4852038 0.4247776 0.4241798 0.4828214 | 0.4238142 0.4241585 0.4241585 0.4827728 | 0.4236276 0.4823512 0.4235345 0.4813514 | 0.422763 0.4851553 0.4243332 0.4823498 | 0.4234478 0.4818828 0.4228583 0.4812403 | 0.4225861 0.4841552 0.4831136 0.4831136 474 Prostate 482 Prostate 483 Prostate 475 Prostate 477 Prostate 479 Prostate 480 Prostate 476 Prostate 478 Prostate 481 Prostate 484 Prostate 485|Prostate 486|Prostate 187 Prostate 489|Prostate 495 Prostate 488 Prostate 492|Prostate 490 Prostate 491 Prostate 493 Prostate 494 Prostate

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EST: zs04g12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684262 3', mRNA sequence. (from Genbank)	EST: aa54d11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824757 3', mRNA sequence. (from Genbank)	EST: zq50h02.r1 Stratagene neuroepithelium (#937231) Homo		sequence. (from Genbank)	EST: zx90e04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	Gordon (1900) of Hilling A sequence: (Horil Gelloailk)	Peroxisomal biogenesis factor 11A			Placental bikinin mRNA		Homo sapiens clone 24416 mRNA sequence	EST: zw78f04.s1 Soares testis NHT Homo sapiens cDNA clone 782335.31 mRNA sequence (from Genhank)	EST: ze92c03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA	clone 366436 3', mRNA sequence. (from Genbank)	TCRG T cell receptor gamma chain	EST: zw62c11.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	AND TRANSFORMATION-DEPENDENT; mRNA sequence. (from	Genbank)	EST: zw86c05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 783848 3', mRNA sequence. (from Genbank)	EST: HUMGS0003737, Human Gene Signature, 3'-directed cDNA	sequence, mkNA sequence. (from Genbank)	CKB Creatine kinase B		Selenium binding protein 1	EST: zs90b04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704719.3' mRNA sequence (from Genhank)	Homo sapiens mRNA for GEF-2 protein
A2513	A4890		VA206983_a		A4854	RC AA4432	77_at	X61755_rna 1 s at	A4294	U78095 at	RC AA4177	61_at	A4322	A0263	-	at		A4417		A4436			CU1/82_at	M16364_s_a t	RC_AA2906	at	A2825	RC_AA4551 08_at
0.22080989 30_at	RC_A 0.22073023 09_at			0.22046477 t	RC_A	2	0.22032848 77	0.21999514	RC_A	0.21988717 178095		0.21978256 61	RC_A 0.21974431 70_at	and the same of th	0.21964496 88_at	0.2195449 M30894			0.21933801 98_at		0.21928045 76_at	70007070	0.21916084 CU1/82_at	0.21903756 t		0.21891852 79	RC_A 0.21888942 18 at	RC_A 0.21872292 08_at
0.354702	0.35467			0.354497	0.354449		0.354073	0.353912	0.353867	0.353592		0.353571	0.353392		0.353392	0.353334			0.353201		0.353141	0.0000	0.33311	0.352866		0.352788	0.352571	0.352469
0.4221488	0.4220813			0.4220557	0.421865		0.4218177	0.4217586	0.4216798	- 1		0.4216203	0.4216003	1	ı	0.4214622		,	0.4212152		0.4211292	0 404040	- 1	0.4209897		0.4208801	0.4207286	1
0.481186	0.481183			0.4811459	0.4809305		0.480412	0.4803762	0.4802926	0.4802088		0.4799088	0.4798356	The state of the s	0.4797888	0.4792092			0.4790092		0.4789818	0 4707404	0.4707104	0.4786262		0.4782155	0.4781523	0.4773699
496 Prostate	Prostate			498 Prostate	499 Prostate		500 Prostate	Prostate	502 Prostate	503 Prostate		Prostate	505 Prostate		506 Prostate	507 Prostate			508 Prostate		509 Prostate	510 Draetato	riosidie	511 Prostate		512 Prostate	513 Prostate	514 Prostate
496	497			498	499		200	501	502	503		504	505		206	207			208	(503	510	2	511		512	513	514

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors gerig giene, geren, geren, green, green, ger

Docket	i No.:	2825.2020002
Title:	Genet	ic Markers for Tumors
Invento	ors: Sri	dhar Ramaswany, et al.

515 Prostate	0.4768436		0.352194	0.21862721 D10704	10704_at	CHK Choline kinase
516 Prostate	0.4764953	- 1	0.352097	0.2185232 1.00354	00354_at	PROCHOLECYSTOKININ PRECURSOR
517 Prostate	0.4763672	0.4205153	0.352063	0.21843252 U46499	46499 <u>a</u> t	GLUTATHIONE S-TRANSFERASE, MICROSOMAL
Prostate	0.476211	0.4202813	0.351986	0.21837524 H51340 at	51340 at	EST: yo30c06.r1 Homo sapiens cDNA clone 179434 5'. (from Genhank)
			2000	T	RC AA2436	
519 Prostate	0.4761674	0.4202813	0.351861	0.2182833 95	5_at	Deoxynucleotidyltransferase, terminal
520 Prostate	0.4760428	0.4201604	0.351799	RC_A44	RC_AA4894	Dincomal protein 1 33 like
521 Prostate	0.475884	1	0.351773	0.21790563 X76057 at	76057 at	MPI Mannose phosphate isomerase
		1	100		AA482319_f	EST: ab15c03.r1 Stratagene lung (#937210) Homo sapiens cDNA
522 Prostate	0.4758772	0.4198275	0.351739	0.21784933	at	clone 840868 5', mRNA sequence. (from Genbank)
523 Prostate	0.475772	0.4198064	0.351663	0.21773437 t	R97442_s_a t	EST: yq53b01.r1 Homo sapiens cDNA clone 199465 5'. (from Genbank)
524 Prostate	0.4753561	0.4197453	0.351588	Al 0.21759991	AB004066_a t	Differentiated Embryo Chondrocyte expressed gene 1
525 Prostate	0.475234	0.4197453	0.351401	RC_A 0.21755995 74_at	A4361	EST: zv22d06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754379 3' similar to contains Alu repetitive element; contains L1.t3 L1 repetitive element;, mRNA sequence, (from Genbank)
526 Prostate	0.4750778	0.4195409	0.351396	RC_A 0.21744862 35_at	RC_AA0567 35_at	KIAA0755 gene product
527 Prostate	0.4748892	0.4194762	0.35135	A. 0.21739009 t	4173597_a	AA173597_a EST: zp03c08.r1 Stratagene ovarian cancer (#937219) Homo sapiens t
528 Prostate	0.4748345	0.4192931	0.351324	RC_A 0.21717148 81_at	A1739	EST: zp03e05.s1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595328 3', mRNA sequence. (from Genbank)
529 Prostate	0.4745788	0.4192803	0.351137	RC 0.2170594 01	RC_AA0446 01 at	EST: zk55d05.s1 Soares pregnant uterus NbHPU Homo sapiens CDNA clone 486729 3', mRNA sequence. (from Genbank)
530 Prostate	0.4744635	0.4191549	0.351101	RC_A 0.21696733 23_at	A4471	EST: zw93c01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784512 3', mRNA sequence. (from Genbank)
531 Prostate	0.4741087	0.4189834	0.351053	H(H) H(1) H(1) H(1) H(1) H(1) H(1) H(1)	HG2743- HT2846_s_a t	Caldesmon 1, Alt. Splice 4. Non-Muscle
532 Prostate	0.473874	0.4186851	0.350898	0.21673721 D87969	at	CMP-sialic acid transporter
533 Prostate	0.4734711	0.4185752	0.350805	0.21658084 X87176	at	17-beta-hydroxysteroid dehydrogenase
534 Prostate	0.4734324	0.4185299	0.350727	0.21650496 Ta	30341_s_at	0.21650496 T30341_s_at Human Chromosome 16 BAC clone CIT987SK-A-211C6
535 Prostate	0.4733933		0.350727	0.2164181 X76061	76061_at	P130 mRNA for 130K protein
536 Prostate	0.4733506	0.4183221	0.350716	0.21631354 D55696	ਬ	Cysteine protease

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HEXB Hexosaminidase B (beta polypeptide)	at Mucin (Gb:M22406)	LIMK-2	EST: zf21d10.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 377587 3' similar to contains Alu repetitive element: mRNA	sequence. (from Genbank)	EST: zo32a02.s1 Stratagene colon (#937204) Homo sapiens cDNA	clone 588554 3', mRNA sequence. (from Genbank)	Nuclear autoantigen GS2NA mRNA	TCF11 Transcription factor 11 (basic leucine zipper type)	Homo sapiens SRp46 splicing factor retropseudogene mRNA	Transforming growth factor-beta 3 (TGF-beta 3) exon 1 (and joined	CDS)	EST: zt72d01.s1 Soares testis NHT Homo sapiens cDNA clone	727873 3', mRNA sequence. (from Genbank)		IMAGE:814243 5', mRNA sequence. (from Genbank)	Translocation protein-1	NADH-CYTOCHROME B5 REDUCTASE	Polymerase (RNA) II (DNA directed) polypeptide L (7.6kD)		P2x purinoceptor mRNA	XMP mRNA	EST: zs29e03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:686620 3' similar to TR:G529430 G529430 GUANINE	NUCLEOTIDE EXCHANGE FACTOR, EIF-2B, DELTA SUBUNIT. [1]	" mRNA sequence. (from Genbank)	EST: zw70g01.s1 Soares testis NHT Homo sapiens cDNA clone	781584 3', mRNA sequence. (from Genbank)	KIAA0102 gene	EST: zl02c01.s1 Soares pregnant uterus NbHPU Homo sapiens	cDNA clone 491136 3' similar to contains element THR repetitive	element ;, mRNA sequence. (from Genbank)	EST: zr75g02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	669266 3', mRNA sequence. (from Genbank)	LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR	Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete rds	
0.2161799 M23294_at	HG1067- 0.21603681 HT1067_r_at	0.21597473 D45906_at	RC AA0558	0.2158746 29 at	RC_AA1470	0.2156876 67_at	0.21560808 U17989 at	0.21535192 X77366 at	0.21527556 N78005_at	X14885_rna	0.21525586 1_s_at	RC_AA3977	0.2151435 79_at	AA465601_a	0.21513969 t	0.21497187 D87127 at	0.21484044 M28713_at	0.21475515 D81608_at	AF000234_a	0.21462978 t	0.21451737 U52100 at			RC_AA2560	0.21440569 67_at	RC_AA4314	0.21437782 62_at	0.21433653 D14658_at		RC_AA1370	0.21426697 34_at	RC_AA2364	0.21415664 55_r_at	0.21408698 L00352_at	RC_AA4592 0.21389228.78 s. at	
0.2	0.216	0.21		0.2				0.21	0.21		0.21		0.2′		0.21		0.21	0.21		0.21	0.21				0.214		0.21	0.21			0.21		ı		0 243	
0.350697	0.350641	0.350379		0.350323		0.350138	0.350048	0.349994	0.349889		0.349677		0.349609		0.349549	0.34942	0.349251	0.349171		1	0.348495				0.348487		0.348367	0.348321		-	0.348149		9	0.34796	0.347952	1
0.4180539	0.4180054	0.4179926		0.417973		0.4179134	0.4178899	0,4175566	0.4175141		0.4174214		0.4172009		0.4171824	0.4170886	0.4168933	0.4168479		0.4167889	0.4164996				0.4163142		0.4163142	0.4163111			0.4161404		0.4161023	0.415963	0.4159472	1
0.4733381	0.4731357	0.4729984		0.4721035				0.4713742	0.4709698		0.470955		0.4708366				;	0.470028			0.4698817				0.4696866		i	0.469375			0.4687887		1	0.4681656	0.4678988	
537 Prostate	538 Prostate	539 Prostate		540 Prostate		541 Prostate	542 Prostate	543 Prostate	544 Prostate		545 Prostate		546 Prostate		547 Prostate	548 Prostate	549 Prostate	550 Prostate		551 Prostate	Prostate				553 Prostate	á	554 Prostate	555 Prostate			556 Prostate		557 Prostate	558 Prostate	559 Prostate	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
537	538	539		540	1	<u>7</u>	542	543	544		545		546		547	548	549	220		551	552			1	553		554	555			556		557	258	559	2

Docket No.: 2825.2020-002

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560 Prostate	0.4677499	0.4157948	0.347635	0.21382812	RC_AA6099 43_at	AA6099 EST: af09d11.s1 Soares testis NHT Homo sapiens cDNA clone at 1031157.31 mRNA sequence (from Genhank)
561 Prostate	0.4674173	1	0.347635	1	U07559 at	ISL1 ISL1 transcription factor, LIM/homeodomain, (islet-1)
562 Prostate	0.4672241	0.4154708	0.347622	RC_A 0.2135868 50 at	RC_AA4599 50 at	EST: zx66b03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 796397.3', mRNA sequence, (from Genbank)
		The state of the s			RC AA2274	
563 Prostate	0.4670945	0.4153872	0.347544	0.21348487 28_at	28_at	
564 Prostate	0.4670173	0.4152984	0.347289	RC_A 0.21337622 54 at	RC_AA4238 54 at	EST: zv79c03.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 759844 3', mRNA sequence, (from Genbank)
565 Prostate	0 485954	0.445282	0 347004	0.0000000	AA490758_a	
566 Prostate	0.4654475	10		0.21309635 X53331	X53331 at	No mio ror gene MGP Matrix protein gla
				-	HG4069-	
567 Prostate	0.4652272	0.415092	0 3/6017	0.2000708	HT4339_s_a	Months of the state of the stat
			10010	0.62120	ΔΔ316686 c	FST: EST188361 HCC call line (materials to lines in months) II Long
568 Prostate	0.4652084	0.4652084 0.4147359	0.346812	0.21292007		
569 Prostate	0.4648758	0.4144529	0.346496	0.2128121651	RC_AA4762	EST: zw44g01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
			W. Commonwell		_	
570 Prostate	0.4638747	0.4144386	0.346328	0.21276914 t	+	sequence. (from Genbank)
571 Prostate	0.4638384	0.4143752	0.346215	0.21261276		EXT2 Exostoses (multiple) 2
-					U33317_rna	
572 Prostate	0.4636175	- 1	0.346168	0.21258208 1_at	1_at	Defensin 6 (HD-6) gene
573 Prostate	0.463445		0.346137	0.21242008 L13391	L13391_at	REGULATOR OF G-PROTEIN SIGNALLING 2
574 Prostate	0.4633997	0.4141748	0.346122	0.2123822 D79994	D79994_at	KIAA0172 gene, partial cds
575 Prostate	0.4694637	0.440588	0 376002	RC 0 2422EEZO 22	RC_AA6210	
		-	100010	0.120001.0	RC AA4356	FST: 474a11 s1 Soares festis NHT Homo sanians cDNA clone
576 Prostate	0.4623283	0.4140204	0.345975	0.21219398 06	1 17 (728060 3', mRNA sequence. (from Genbank)
577 Prostate	0.4620402	0.4620402 0.4139726	0.345747	0.21211095	U77845 at-2	0.21211095 U77845 at-2 Human hTRIP (hTRIP) mRNA, complete cds
578 Prostate	0.4620402	0.4138997	0.345553	0.21198465 U77845	U77845_at	HTRIP (hTRIP) mRNA
579 Prostate	0.4619762	0.4619762 0.4137215	0.345544	RC_A 0.21188074 82_at	RC_AA6205 82_at	RC_AA6205 EST: ae60g01.s1 Stratagene lung carcinoma 937218 Homo sapiens 82_at cDNA clone 951312 3', mRNA sequence. (from Genbank)

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors And the plan test them the test that the test the test that the test the test that the test the test that the test the test that the test the

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	Tyrosine Phosphatase 1, Non-Receptor, Alt. Splice 3		EST: Human HL60 3'directed Mbol cDNA, HUMGS01145, clone pm2260, mRNA sequence, (from Genhank)		Phosphomannomutase 2	RC_AA0020 EST: zh85b03.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens 64 at CDNA clone 428045.31 mRNA sequence (from Contract)			EST: zr33f06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665219.31 mRNA sequence (from Genhank)	Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	V-Erba Related Ear-3 Protein	0.21072008 J02947 s at SOD3 Superoxide dismutase 3 extracellular	EST: zt51f07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725893.3' mRNA sequence (from Genhank)	EST: zv53d04.s1 Soares testis NHT Homo sapiens cDNA clone 757351 3', mRNA sequence (from Genhank)		CTNNB1 Catenin (cadherin-associated protein) heta 1 (88kh)	AA377492_a similar to ATPase, Ca2+ transporting, mRNA sequence.	Acetylserotonin N-methyltransferase-like	Semaphorin E
HG3187-	HT3366_s_a	RC_AA5214 68_at	RC_D20171 at	RC_AA4969	0.2114624 U85773 at	RC_AA0020 64 at	RC_AA4170 46 at	AA4872 at	RC_AA1956 57_at	D79276 at	HG3510- 0.2107887 HT3704_at	J02947 s at	RC_AA2923 05 s at	A4371	RC_AA1507	äţ	AA377492_a t	RC_AA4273 98_at	\B000220_a
	0.2117148t	RC 0.21170902 68	0.21155502	0.21147132 14	0.2114624	RC_A 0.21117924 64 at	RC_A 0.21116512 46_at	0.21109723 28	RC_A 0.21105784 57 at	0.21097907 D79276	0.2107887	0.21072008	RC_AA2 0.21062452 05 s at	RC_A 0.21051039 18 at	RC_A	0.21025772 X87838	0.21013573 t	0.2100736 98 at	0.20990688 t
,	0.345497	0.345438	0.345344	0.345223	0.345104	0.345036	0.34489	0.344873	0.344844	0.344698	0.344602	0.344564	0.344472	0.344441	0.344392	0.344222	0.344157	0.344134	0.344108
	0.4137022	0.4136694	0.4135719	0.413527	0	0.4133673	0.4133565	0.4132011	0.4131632	0.4131423	0.4130001	0.4129914	0.4129583	0.4129244	0.4128578	1 1	0.4128299	0.4127669	0.4127511
	0.4619107	0.461554	0.4615535	0.4612748	0.4611512	0.4607839	0.4606392	0.4605568	0.4604807	0.4602445	0.4600363	0.4597544	0.4596662	0.4591857	0.4589096	0.4586531	0.4586371	0.4586249	0.4585702 0.4127511
	580 Prostate	581 Prostate	582 Prostate	583 Prostate	584 Prostate	585 Prostate	586 Prostate	587 Prostate	588 Prostate	589 Prostate	590 Prostate	591 Prostate	592 Prostate	593 Prostate	594 Prostate	595 Prostate	596 Prostate	597 Prostate	598 Prostate
	58(58	587	583	587	58£	586	587	588	589	590	591	592	593	594	595	596	262	598

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors the deal of the found of the state of the st

Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

599 Prostate	0.4583125	5 0.412744	0.34408	0.20984566 D81932_at)81932 at	Human fetal brain cDNA 5'-end GEN-424C05, mRNA sequence. (from Genbank)
600 Prostate	0.458282	0.4127009	0.344045	0.20971763	RC_AA3465 51_at	EST: EST52717 Fetal heart II Homo sapiens cDNA 3' end, mRNA sequence. (from Genbank)
601 Prostate	0.4580848	0.4580848 0.4456424	0.000		RC_AA4875	EST: ab20h12.s1 Stratagene lung (#937210) Homo sapiens cDNA
602 Prostate	0.438033	0.4580222 0.4126451	_			clone 841415 3', mRNA sequence. (from Genbank)
603 Prostate	0.4500022	0.4123030).		J34252_at	ALDH7 Aldehyde dehydrogenase 7 (NOTE: redefinition of symbol)
ooo L losigie	0.4577188	0.45//188 0.4124649	0.343855	0,20940739 U84487	J84487_at	CX3C chemokine precursor, mRNA, alternatively spliced
						EST: zv17d09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
604 Prostate	0.4576982	0.4122647		1	A4793	753905 3' similar to contains element TAR1 TAR1 repetitive element
605 Prostate	0.4576055		اد	0.20932516 50_at		., mRNA sequence. (from Genbank)
	3000101.0		0.34300	0.20926428 076421	1/6421_at	DsRNA adenosine deaminase DRADA2b (DRADA2b) mRNA
606 Prostate	0.4574566	0.4121933	0.34	0.20905165 11 at	RC_AA4210 11 at	EST: zu09a12.s1 Soares testis NHT Homo sapiens cDNA clone
607 Prostate	0.4571891	0.4121902	0.343557	0.20899865 J04982 at	04982 at	ANT1 Adenine nucleotide translocator 1 (ekalatal musclo)
608 Prostate	0.457174	0.4420575	700	Z 0000	33	EST: zr69h06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
600 Prostate	411/04/0	- 1		0.2088/363 22 at		668699 3', mRNA sequence. (from Genbank)
ous Flusiale	0.45/0489		0.343393	0.20884766 Z50749	بع'	Sds22-like mRNA
o iu Prostate	0.4568037	0.4119704	0.343364	0.20873824 J04615	at	SNRPN Small nuclear ribonucleoprotein polypeptide N
611 Prostate	0.4564337	0.4119704	0.343306	0.20862147 Su	69272 s at	0.20862147 S69272 s at Cytoplasmic antiproteinase
			~yt			EST: ae41a12.s1 Gessler Wilms tumor Homo saniens CDNA clone
612 Prostate	0.4558826	0.4118694	0.342973	RC_A 0.20855764 02_at	A5989	898366 3' similar to contains L1.t1 L1 repetitive element; mRNA sequence. (from Genbank)
						EST 3835603 et Cocclor Wilms timer Home contraction
				<u>Ř</u>	RC_AA5985	897820 3' similar to contains Atu repetitive element: mRNA
613 Prostate	0.4553488	0.4117642	0.342719	0.20851274 71	at	sequence, (from Genbank)
614 Prostate	0.4550474	0.4445078	0.540500	<u>R</u>	-AA2582	EST: zs35g04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	- 1	0.342382	U.ZU83931b U3	at	IMAGE:687222 3', mRNA sequence. (from Genbank)
615 Prostate	0.4550388	0.4115041	0.342514	0.2082984 97	_AA4610	Human 150 kDa oxygen-regulated protein ORP150 mRNA, complete
616 Prostate	0.4549998	0.4113391	0.342509	0.2082342 M64098 at		High density lipoprofein binding profein (HBP) mRNA
617 Prostate	0.4547598	0.4112002	0 342403	R(Ю	
		- 1	0.54400			Tumor rejection antigen (gp96) 1
618 Prostate	0.4547398	0.4111493	0.342366	0.2080337184	_AA4248	EST: zw03c10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
619 Prostate	0.4546146	0.4111002	0.342353	0.20791109 M29927	at	OAT Ornithine aminotransferase (ovrate atrophy)
620 Prostate	0.4544917	0.411093	0.342257	0.20778951 D42047	at .	KIAA0089 gene, partial cds
621 Prostate	0.4543607	0.4110116	0.342201	0.20773074	15532 f at	0.20773074 T85532 f at contains Alurenotifity closure. (feed of contains the contains the contains alurenotifity closure).
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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. EST: zv65c07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: zo23g08.s1 Stratagene colon (#937204) Homo sapiens cDNA EST: zf73g10,s1 Soares pineal gland N3HPG Homo sapiens cDNA AA203501_a|EST: zx59a01.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens EST: zv08g11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone sapiens cDNA clone 594439 3', mRNA sequence. (from Genbank) EST: zs48e06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone RC_AA2561 EST: zr79a09.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zr86h05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zv59c02.s1 Soares testis NHT Homo sapiens cDNA clone Homo sapiens mRNA for villin-like protein, complete cds. (from EST: zo93d04.s1 Stratagene ovarian cancer (#937219) Homo Homo sapiens TACC2 protein (TACC2) mRNA, partial cds cDNA clone 446760 5', mRNA sequence. (from Genbank) IMAGE:700738 3', mRNA sequence. (from Genbank) clone 587774 3', mRNA sequence. (from Genbank) clone 382626 3', mRNA sequence. (from Genbank) clone 758508 3', mRNA sequence. (from Genbank) Homo sapiens mRNA for tob family, complete cds 753092 3', mRNA sequence. (from Genbank) BRAIN NEURON CYTOPLASMIC PROTEIN 1 757922 3', mRNA sequence. (from Genbank) 681880 3', mRNA sequence. (from Genbank) 682617 3', mRNA sequence. (from Genbank) Human smoothened mRNA, complete cds EPHX2 Epoxide hydrolase 2, cytoplasmic RPS4Y Ribosomal protein S4, Y-linked ATF3 Activating transcription factor 3 LDL-phospholipase A2 mRNA Nek3 mRNA for protein kinase A-kinase anchor protein 100 KIAA0382 gene, partial cds Genbank) RC_AA4365 RC_AA2851 RC_AA1349 AA133029_a AB002309_a RC_AA4367 RC AA4031 AB002380_a 0.20230192 53 i_at RC_AA2566 RC_AA1646 RC_AA0694 at RC_AA0704 0.20362942 M58459_at RC_AA4960 0.20303649|D88154_at ä 0.20263897 L19871 at 0.20236038 L05779 at ਜ਼ 0.20358667 U24577 0.20197883 M98528 0.20212989 Z29067 0.20350587 62 at 0.20343268 68 at 0.20340994 00 at 0.2033 37 at 0.20331459 68 at 0.2027383 40 at 0.203141 25 at 0.20282245 59 at 0.2022666 16 at 0.20203097 33 at 0.20304814 t 0.20259309|t 0.20248236|t 0.20308977 0.338437 0.338292 0.33794 0.338394 0.338171 0.33804 0.337833 0.337796 0.33776 0.337675 0.337619 0.337149 0.337591 0.337364 0.336729 0.336646 0.337881 0.337411 0.337104 0.336329 0.336751 0.336094 0.4451118 | 0.4069111 0.4453411 | 0.4070605 0.4463672 0.4077636 0.4462358 0.4077579 0.407492 0.4459188 | 0.4073233 0.4451298 0.4070396 0.4445111 | 0.4067781 0.4444396 | 0.4067443 0.4441059 | 0.4067166 0.406448 0.4458916 0.4072642 0.4431706 0.4063713 0.407167 0.4438286 0.4065543 0.406448 0.4450391 | 0.4068884 0.4426568 | 0.4062735 0.4061262 0.4418305 | 0.4061262 0.406093 0.4063621 0.4459783 0.4455394 0.4417298 0.4431396 0.441923 0.443666 0.4432063 665 Prostate 666 Prostate 664 Prostate 667|Prostate 668 Prostate 669 Prostate 670 Prostate 671 Prostate 672|Prostate 673 Prostate 674 Prostate 675|Prostate 676 Prostate 677 Prostate Prostate 679|Prostate 681 Prostate 682|Prostate 684 Prostate 680 Prostate Prostate 685 Prostate

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	RC_AA2560 [EST: zs29d04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 42 at IMAGE:686599 3', mRNA sequence, (from Genbank)	EST: ab09g07.s1 Stratagene lung (#937210) Homo sapiens cDNA	order of the Name of dealers, (1011) Contains)	EST: zr18h05.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 663801 3', mRNA sequence, (from Genbank)	EST: zx78f01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 809881 5', mRNA sequence, (from Genbank)	KIAA0336 gene product	Human GABA-A receptor pi subunit mRNA, complete cds	Phosphoribosypyrophosphate synthetase-associated protein 39	AA093748_a EST: cl0752.seq.F Fetal heart, Lambda ZAP Express Homo sapiens	cDNA 5', mRNA sequence. (from Genbank)	EST: zr64h01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668209 3' similar to contains Att repatitive element: mDNA	sequence. (from Genbank)	EST: yu61d04.r1 Homo sapiens cDNA clone 230599 5'. (from	Genbank)	AA209290_a cDNA clone 648384 5' similar to contains element MER22 repetitive	element ;; mRNA sequence. (from Genbank)	EST: zx88d07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 810829 3', mRNA sequence. (from Genbank)	EST: zx84f04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 810463 3', mRNA sequence. (from Genbank)	Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding	mitochondrial protein, complete cds	HPN Hepsin	EST: zx61a12.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 795934 3', mRNA sequence. (from Genbank)	EST: ze36a01.s1 Soares retina N2b4HR Homo sapiens cDNA clone	361032 3', mRNA sequence. (from Genbank)	EST: Human HL60 3'directed Mbol cDNA, HUMGS00627, clone	mm2330, mRNA sequence. (from Genbank)	EST: yg35a04.r9 Homo sapiens cDNA clone 34269 5'. (from	Genbank)	G6PD Glucose-6-phosphate dehydrogenase	GATA2 GATA-binding protein 2
	RC_AA2560 42 at	RC_AA4854	5	RC_AA2269 90_at	AA464334 s		D54358 at	U95367 at	D61391_at	AA093748_a	ب	RC AA2520	33_at		H81492_at	AA209290_a		RC_AA4588	99 <u>_</u> at	RC_AA4571	40 at	RC_AA2563	76 s at	X07732 at	RC_AA4609	16_at	RC_AA0171	61_at	-	at	1	0.1984888 R36553 at	M24470 at	0.1983133 M68891 at
1 460 400	RC 0.20005098 42	RC 0 1999700209	20010001.0	RC_A 0.19979359 90_at		0.19977663	0.1997443 D54358	0.19953504 U95367	0.19950843 D61391		0.19935721 t		0.19934022 33_at	000000000000000000000000000000000000000	0.1992//22 H81492		0.19907656		0.198971 99	000	0.19896/4 40 at		0.19895968 76 s at	0.19872452 X07732 at	1	0.1987123 16		0.19858259 61		0.19850706		0.1984888	0.19844672 M24470	0.1983133
-	0.334724	0 334685	Canto	0.334596		0.334561	0.334393	0.334277	0.33395		0.333949		0.333939	0 00004	0.333834		0.333782		0.333575	000	0.333503		0.333468	0.333194	0	0.333143		0.333015	6	0.332939		0.332861	0.332828	0.332752
	0.4044705	0.404085	1	0.404278		0.4042311	0.4041654	0.4041195	0.4040963		0.4040305		0.4039871	0.4000047	0.4039317		0.4038667		0.40376	400000	0.403583	1	0.403507	0.403507	707007	0.4032191		0.4031832		0.4031622				0.4030568
	0.4385174	0 4384335		0.4384063		0.4383704	0.4383659	0.4381131	0.4380261		0.4379628		0.4379367	7,00701,0	0,43/3017		0.4377557		0.4376873	0.4976406	0.4373420	1000	0.43/503/	0.43/4330	7007700	0.43/420/		0.43/2653	100001	0.4370687	00000	0.4369998	0.4367928	0.4367324
	707 Prostate	708 Prostate		709 Prostate		710 Prostate	711 Prostate	712 Prostate	713 Prostate		/14 Prostate		715 Prostate	Droctato	riostate		717 Prostate		/18 Prostate	710 Dractata	riostate	7	724 Prostate	171 Flosiale	Desptoto	722 Prostate		Prostate		724 Prostate		725 Prostate	726 Prostate	727 Prostate
	707	708		709		710	711	712	713	ì	/14		715	716	0		717	Ĭ	/18	740	2	7007	707	17)	700	77)	1	(73	107	124	1	427	726	121

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors with the state of the first that the state of the state o

RC_AA6214 EST: af92d09.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA AA292440_s | Homo sapiens negative growth-regulatory protein MyD118 (MYD118) AA374109_a EST: EST86231 HSC172 cells I Homo sapiens cDNA 5' end, mRNA RC_AA4592 EST: zx89b07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA AA195136_a Zr34d05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 665289 RC_AA4789 EST: zv18d03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone AA071256_a Zm73d01.r1 Stratagene neuroepithelium (#937231) Homo sapiens EST: zx99b12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zp82d10.s1 Stratagene HeLa cell s3 937216 Homo sapiens EST: zr33f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone EST: zs78d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone RC_AA2618 EST: zs18g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone RC_AA1472 EST: zo64g03.s1 Stratagene pancreas (#937208) Homo sapiens RC_AA4170 EST: zu13c03.s1 Soares testis NHT Homo sapiens cDNA clone SOAT Sterol O-acyltransferase (acyl-Coenzyme A: cholesterol EST: yi09a01.r1 Homo sapiens cDNA clone 138696 5'. (from cDNA clone 626707 3', mRNA sequence. (from Genbank) cDNA clone 531265 5', mRNA sequence. (from Genbank) cDNA clone 591700 3', mRNA sequence. (from Genbank) IMAGE:685604 3', mRNA sequence. (from Genbank) IMAGE:703593 3', mRNA sequence. (from Genbank) clone 1055249 3', mRNA sequence. (from Genbank) clone 810901 3', mRNA sequence. (from Genbank) Dnaj Homolog (Gb:X63368), Alt. Splice Form 2 753989 3', mRNA sequence. (from Genbank) Carnitine palmitoyltransferase (CPT1) mRNA 665217 3', mRNA sequence, (from Genbank) 811871 3', mRNA sequence. (from Genbank) 731716 3', mRNA sequence. (from Genbank) PTS 6-pyruvoyltetrahydropterin synthase 5', mRNA sequence. (from Genbank) CDH3 Cadherin 3 (P-cadherin) Mitogen inducible gene mig-2 sequence. (from Genbank) mRNA, complete cds acyltransferase) Genbank) HT3573_s_a RC_AA2788 RC_AA1956 RC_AA4549 RC_AA1917 0.19802769 U09646_at 0.19815956|L21934 at 0.19773218 R63545 at 0.19738871 D17400 at 0.19714217 Z24725 at 0.19673526 X63629 at HG3395 0.1979474 16 f at 0.19694628 18 s at 0.19810496 60 at 0.19789223 58 at 0.19764638 93 at 0.19737059|71 at 0.19728471 67 at 0.19753803 56 at 0.19705033 08 at 0.19701813 79 at aţ 0.19781542 t 0.19823146 0.19697765 0.19681153 0.19686767 0.3326840.332652 0.332537 0.332379 0.332416 0.332404 0.332382 0.3324670.332188 0.331975 0.331956 0.331808 0.331665 0.331573 0.331962 0.331591 0.331444 0.33139 0.331183 0.331390.33127 0.4365064 | 0.4024445 0.4362698 | 0.4023952 0.402983 0.4366095 | 0.4029703 | 0.4365448 0.4028299 0.4365364 0.4025403 0.4362235 | 0.4023664 0.4354708 0.4022616 0.4350477 | 0.4021196 0.4345098 0.4020691 0.4344536 0.4020049 0.4358467 | 0.4023311 0.4354711 | 0.4022841 0.4339835 0.4019191 0.4358108 0.4023311 0.4328035 0.4008208 0.4338846 0.4015465 0.4337904 0.4014925 0.4330917 0.4010649 0.4328548 | 0.4009121 0.4329 0.4010241 0.4366635730 Prostate
731 Prostate 728 Prostate 729 Prostate Prostate 732|Prostate 733 Prostate 734|Prostate 737 Prostate 738 Prostate 739|Prostate 740 Prostate 735 Prostate 736 Prostate 741 Prostate 742|Prostate 743 Prostate 744 Prostate 745 Prostate 747 Prostate 746 Prostate 748 Prostate

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

749 Prostate 0.4327704 0.4008161 0.331143 0.19653058 52	0.4008161 0.331143 0.19653058 52	0.4008161 0.331143 0.19653058 52	3 0.19653058 52	1/3 11	1/3 11		Homo sapiens mRNA for KIAA0293 gene, partial cds
					<u>ن</u>	RC AA0016	EST: zh82g08.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 427838 3' similar to contains Alu repetitive element; mRNA element; mRNA
750 Prostate 0,4326661 0.4008137 0.331106 0.1969	0.4008137 0.331106	0.4008137 0.331106		0.196	0.19652055 48_at		sequence. (from Genbank)
000000000000000000000000000000000000000	0000000	0000000			RC 0 400 3 70 3 7 E0	RC_AA2534	EST: zs06f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
0,4320492 0.400029 0.331030	0.4006028 0.331030	0.4006028 0.331030		0. 130	10010	03 al	MACE: 004400 0, HENN'T Sequence: (Horr Consound)
- 1	0.4003765 0.331033	0.4003765 0.331033	- 1	U. 190,	744011	0.19624431 D63486 at RC AA4634	MAAU 132 yerre
753 Prostate 0.431336 0.40024 0.331013 0.196	0.40024 0.331013	0.40024 0.331013	3	0.196	0.19617972 45 at	45 at	Homo sapiens KIAA0439 mRNA, partial cds
						A2436	sapiens cDNA clone
754 Prostate 0.4313242 0.4000148 0.33099 0.196	0.4000148 0.33099	0.4000148 0.33099		0.196	0.1961369892	92_at	668576 3', mRNA sequence. (from Genbank)
0.4312824 0.3996762 0.330718	0.3996762 0.330718	0.3996762 0.330718	8	0.196	0.19601087 t	120867_s_a	GLUD1 Glutamate dehydrogenase
						C_AA4469	Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete
756 Prostate 0.4311726 0.3996258 0.330627 0.196	0.3996258 0.330627	0.3996258 0.330627	27	0.196	0.19600748 64_at		1
					0	RC_AA2337	sapiens cDNA clone
757 Prostate 0.431136 0.3995624 0.3305/4 0.195	0.3995624 0.3305/4	0.3995624 0.3305/4		0.195	0.1959Z664 90_at	90_at	000204 3, MKNA Sequence. (Iloni Genibalik)
758 Prostate 0.4304979 0.3995085 0.33054 0.19588415 17_at	0.3995085 0.33054	0.3995085 0.33054	4.5	0.1958	8415	RC_AA4780 17_at	Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds
0 430034E3 0 30004E30 0 330E3	0.2004630	0.2004630		0.40577	0002	RC_AA4498	Human modulator recognition factor I (MRE-1) mRNA: 3' end
7000000	7000000	7000000	1	0.1001	1	RC AA4210	ne
760 Prostate 0.4301287 0.3993386 0.330486 0.19564317 50_at	0.3993386 0.330486	0.3993386 0.330486		0.1956	4317	50_at	
761 Prostate 0.430074 0.3992576 0.330481 0.1955	0.3992576 0.330481	0.3992576 0.330481		0.1955	4058	0.19554058 U62015_at	
The state of the s			1	1		AA312994_a	Homo sapiens cDNA 5' end, mRNA
0	0.3990995 0.330303 0	0.3990995 0.330303 0	0.330303 0	0	1383		sequence. (from Genbank)
0.4298206 0.3990897 0.330193	0.3990897 0.330193	0.3990897 0.330193			4222	0.1954222 D50916_at	KIAA0126 gene
						AA464029_a	
764 Prostate 0.4297597 0.3987017 0.330111 0.1953	0.3987017 0.330111	0.3987017 0.330111		0.195;	0.19539207 t	ţ	Myosin, light polypeptide 5, regulatory
	000000	000000	L	404	RC 0.4050700 94	RC_AA2876	EST: zs53f07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
765 Prostate 0.4296312 0.3960723 0.330033 0.183	0.3960723 0.330033	0.3960723 0.330033	3	0.130	0617	AA425563 a	EST: zw46e06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
766 Prostate 0.4295986 0.3986723 0.329762 0.19512317 t	0.3986723 0.329762	0.3986723 0.329762	0.329762		12317	ا ب	clone 773122 5', mRNA sequence. (from Genbank)
0.4295588 0.398567 0.329731	0.398567 0.329731	0.398567 0.329731	0.329731		49569	0.1949569 U23942 at	CYP51 Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)
			-	·	1	RC_AA6100	EST: af08h02.s1 Soares testis NHT Homo sapiens cDNA clone
768 Prostate 0.4294392 0.3983211 0.329664 0.194	0.3983211 0.329664	0.3983211 0.329664	64		0.19491450 80 at	80 at	103 109 1 3, Illinia Sequelles, (nom Centralin)
769 Prostate 0.4292552 0.3982899 0.329651 0.19	0.3982899 0.329651	0.3982899 0.329651	0.329651	0.19	0.19482696 49	RC_AA4832 49 at	Homo sapiens chromosome 19, cosmid R33729

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Docket No.:	2825.2020-002
Title: Genetic	c Markers for Tumors
Inventors: Srid	lhar Ramaswamy, et al.

770 Prostate	0.4290439	0.3981572	0.32965	0.19472744	M29037_s_a t	17 beta-hydroxysteroid dehydrogenase (17BHSDI) gene exons 1-5
771 Prostate	0.4289562	0.3981506	0.329578	0.19462134 61		EST: aa45a12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 823870 3', mRNA sequence. (from Genbank)
772 Prostate	0.4289091	0.3980968	0.329483	RC 0.1946197 31	RC_AA2926 31_at	EST: zs58g01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701712 3', mRNA sequence. (from Genbank)
773 Prostate	0.4288587	0.3979899	0.326426	0 104614 EG +	\287308_a	EST: zs52f04.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone AA287308_a IMAGE:701119 5' similar to contains Alu repetitive element;contains
774 Prostate	0.4288124	1 1	0.329365	0.1942915 U35735	35735_at	eletrient MERT repetitive element ;, mRNA sequence. (from Genbank) RACH1 (RACH1) mRNA
775 Prostate	0.428749	0.3977339	0.329342	RC 0.19428954 03	_AA1558 at	EST: zo48h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 5901613', mRNA sequence (from Genhank)
776 Prostate	0.4286153	0.3976284	0.329261	0.19423206 t-2	2620_s_a	Cytochrome P450, subfamily IVF, polypeptide 3 (leukotriene B4 omega hydroxylase)
777 Prostate	0.4286153	0.3975871	0.329198	D1 0.19412683 t	D12620_s_a t	LTB4H Leukotriene B4 omega hydroxylase (cytochrome P450, subfamily IVF)
778 Prostate	0.4284203	0.3975263	0.329153	0.19403212 66	AA1148 s at	Homo sapiens homeobox A11 (HOXA11) rene_complete.cds
779 Prostate	0.4283599	0.3974879	0.329076	0.19394909 U28249 at		MAT8 protein
780 Prostate	0.4280409	0.397439	0.329048	0.193829691	a.	EST: EST74873 Pineal gland II Homo sapiens cDNA 5' end, mRNA sequence. (from Genbank)
781 Prostate	0.4280153	0.39742	0.328819	0.19375175 t	R78838_s_a	EST: yi90d06.r1 Homo sapiens cDNA clone 146507 5' similar to
782 Prostate	0.4275732	0.:	0.328684	0.19357948 X89066 at		TRPC1 Transient receptor potential channel 1
783 Prostate	0.4273481	0.3973976	0.32857	0.19342211 X75593_at		Rab 13
784 Prostate	0.4272367	0.3973084	0.328541	0.19341566 H66367	at	EST: yu14a06.r1 Homo sapiens cDNA clone 233746 5' similar to contains Alu repetitive element;. (from Genbank)
785 Prostate	0.4271023	0.3972519	0.328424	0.19335182 54	2_AA0116	RC_AA0116 EST: zi03c05.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens 54_at cDNA clone 429704 3', mRNA sequence. (from Genbank)
786 Prostate	0.4266099	0.3971175	0.328401	RC_A 0.19332372 38_at	A4482	Homo sapiens mRNA for KIAA0915 protein, complete cds
787 Prostate	0.4264824	0.3970003	0.328393	0.19324963 D31286_at		Homo sapiens mRNA for smallest subunit of ubiquinol-cytochrome c reductase, complete cds
788 Prostate	0.4264698	0.3969697	0.328372	V015 0.1931194 1_at	12_rna	Cellular oncogene c-fos (complete sequence)
789 Prostate	0.4259252	0.3969217	0.328302	RC_A 0.19300123 67_at	A5044	HEAT SHOCK 70 KD PROTEIN 1

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700	Droototo	0.4950072		2000	4000001	-	ES1: 14e10 Human retina cDNA randomly primed sublibrary Homo
180	790 Frostate			0.328216	0.19292852 W25821	ਜ਼	sapiens cDNA, mKNA sequence. (from Genbank)
(B.	/91 Prostate	-+	\sim $ $		0.19285561 Z11793	Z11793_at	Selenoprotein P
792	792 Prostate	0.4257871	0.396773	0.32808	0.19284156 L40397	L40397_at	(clone S31i125) mRNA, 3' end of cds
793	793 Prostate	0.4256406	0.396744	0.328071	0.19274718 M28211	M28211_at	RAS-RELATED PROTEIN RAB-4A
794	794 Prostate	0.4255692	0.3967108	0.328042	HG2604	į	on o
795	795 Prostate	0.4244045 0.3967068	0.3967068	0.327961	0.19256182 T09468 at		Homo saniens TACC1 (TACC1) mRNA complete cde
						RC_AA4365	EST: zv08c11.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
962	796 Prostate	0.4242599	0.3963889	0.327955	0.19251592 53_at	53_at	753044 3', mRNA sequence. (from Genbank)
1	((RC_AA0538	EST: ze75b02.s1 Sóares fetal heart NbHH19W Homo sapiens cDNA
797	797 Prostate	0.4241512	0.4241512 0.3963723	0.327924	0.1923873 83 at	83_at	clone 364779 3', mRNA sequence. (from Genbank)
7.98	798 Prostate	0.4233569	0.4233569 0.3963343	0.327646	0.19229203 D63480	D63480_at	KIAA0146 gene, partial cds
799	799 Prostate	0.4231926 0.3962487	0.3962487	0.327592	0.1922502 L33881	L33881 at	PRKCI Protein kinase C, iota
						M13231_s_a	
8	Prostate	0.4230956	0.3962155	0.327572	0.19221573	ا ب	T-cell receptor, gamma cluster
200	0,000	77.007	7	1		D10216_s_a	POU domain, class 1, transcription factor 1 (Pit1, growth hormone
100	ou i Prostate	0.4225114	0.3961/3	0.32745	0.19207254		factor 1)
802	802 Prostate	0.4223507	0.3960989	0.327436	0.19199635 U72649	U72649_at	BTG2 (BTG2) mRNA
000	7	7007007	10000	1		D31313_s_a	EST: Human fetal-lung cDNA 5'-end sequence, mRNA sequence.
803	803 Prostate	0.4221884 0.3960874	0.3960874	0.327397	0.1919021		(from Genbank)
804	804 Prostate	0.4219862	0.3959613	0.327324	0.19179529 U35139_at	U35139_at	NECDIN related protein mRNA
805	805 Prostate	0.4219184	0.3959597	0.327321	0 10167033	139226 at.2	Munein VIII (Heber eundramo 18 fautacamal recessiva, en care
806	806 Prostate	0.4219184	0.3957888	0.327297	0.101653561130226	130226 at	0.101653561130206 at Minosin VIIA (Heldto) monta
2		0.17.10	0.0001000	0.021201	0.1910000	039220 at	Mydsiii viiA (USHIB) IIIRNA
807	807 Prostate	0.4216776	0.3955513	0.327297	0.19154319	AB000584_a t	Prostate differentiation factor mRNA
						AA228127_a	AA228127_a EST: zr58c05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone
808	808 Prostate		0.3952626	0.327146	0.19147629		667592 5', mRNA sequence. (from Genbank)
808	809 Prostate	0.4215747	0.3952517	0.327093	0.19137256 X17025	X17025 at	Homolog of yeast IPP isomerase
8	810 Prostate	0.4213993 0.3952054	0.3952054	0.327026	0.1913152 D79985	D79985_at	A cell surface protein
811	811 Prostate	0.4213829	0.3951472	0.327016	0.19127809 D13641_at	D13641_at	KIAA0016 gene
812	812 Prostate	0.4212766	0.3950817	0.326997	0.19115831	RC_AA2581 58_at	EST: zs35b02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:687147 31, mRNA sequence. (from Genbank)
						RC_AA4239	EST: zv62h04.s1 Soares testis NHT Homo sapiens cDNA clone
813	813 Prostate	0.4211496 0.3947606	0.3947606	0.326972	0.19109187 74 at	74_at	758263 3', mRNA sequence. (from Genbank)
814	814 Prostate	0.4208253 0.3946797	0.3946797	0.326918	0.19093364 D57823	D57823_at	H.sapiens mRNA for Sec23A isoform, 2748bp
815	815 Prostate	0.4208242 0.3945882	0.3945882	0.326519	0.19090173 X74331	X74331_at	PRIM2A DNA primase polypeptide 2A (58kD)
3		1		i			EST: yo13f07.r1 Homo sapiens cDNA clone 177829 5'. (from
010	816 Prostate	0.4207758	0.3945/0/	0.326519	0.190/34 H46U/4	H46074 at	Genbank)

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					H quel desp H' bed' trin		5010 1 500ECT El (from
							EST: za25b12.r1 Homo sapiens cDNA cione zassor 3. (illum
817 Prostate	tate	0.4203761	0.394561	0.326425	0.19070965 N94146	at	Genbank)
818 Prostate	tate	0.4202022	0.3945041	0.326325	0.19066928 U85193	ä,	Nuclear factor I-BZ (INFIBZ) mikina
819 Prostate	tate	0.4201458	0.394383	0.326229	0.1905944 M75126 at		HK1 Hexokinase 1
820 Prostate	tate	0.4200172	0.3943754	0.326057	0.19053781 D86960_at	Ì	KIAA0205 gene
			1		RC	44613	EST: zx65a08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cUNA
821 Prostate	state	0.4198446	0.3943699	0.326029	0.19042568 00 at	50607	cione 795310 3, Illiana Sequerice: (illuiri Octubrilia) EST: Himan fetal brain cDNA 3'-end GEN-120401, mRNA sequence.
822 Prostate	itate.	0 4198187	0.3943579	0,326026	0.19034584 at		(from Genbank)
823 Prostate	state	0.4196816		0.325899	0.19028157 M73547_at		POLYPOSIS LOCUS PROTEIN 1
824 Prostate	state	0.4195609	0.3941727	0.325899	0.19016132 t	203649_a	AA203649_a EST: zx58e12.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens t
825 Prostate	state	0.4193544		0.325716	AF 0.19008482 t		IPL (IPL) mRNA
826 Prostate	state	0.4192291	0.3940621	0.325711	RC_A 0.19001427 16_at	A4521	EST: zx15c02.s1 Soares total retus Nbzriro sw normo saprens correctione 786530 3', mRNA sequence. (from Genbank)
827 Prostate	state	0.4190343	0.3940621	0.325698	0.18993546 91	_AA1478 at	EST: zo43f05.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 589665 3', mRNA sequence. (from Genbank)
Oto to co C	o to to	0.4486043	1	L	RC_A 0 18986106 18 at	AA4313	EST: zw70d09.s1 Soares testis NHT Homo sapiens cDNA clone 781553 3', mRNA sequence. (from Genbank)
820 Prostate	state	0.4182051	4		0.189856 U02680 at	30 at	Protein tyrosine kinase mRNA
ototaga Oce	o to to	0.4184297	-		0.1897782 26	AA0763 at	Ribosomal protein L32
034 Brostate	State	0.4180297			0.18972114 51	AA2819 at	EST: zs89e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704670 3', mRNA sequence. (from Genbank)
	Joigin	0.4100201	1		R(AA0402	EST: ±105e04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
832 Prostate	state	0.4179683	3 0.3936731	0.325269	0.1890519 /0	at 454462 a	EST: zw28f11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA
833 Prostate	State	0.4176296	5 0.3935787	0.32521	0.1895263 t	i	clone 770637 5', mRNA sequence. (from Genbank)
834 Prostate	state	0.41752		0	0.1894787 S80562	30562_at	CNN3 Calponin 3, acidic
835 Prostate	state	0.4174088		<u>Ļ.</u>	0.18944083 M34192	34192_at	IVD Isovaleryl Coenzyme A dehydrogenase
936 Brochate	ototo	0.416987	1	0.325126	0.18934672 X17094 at	17094 at	PACE Paired basic amino acid cleaving enzyme (turin, mermane associated receptor protein)
037 Droctate	State	0.4169661	-		RC_A 0.18925475 14 at	RC_AA4431 14 at	EST: zx74c07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 809484 3', mRNA sequence. (from Genbank)
838 Prostate	State	0.4167318	10		0.18922225 U06631	06631_at	
	100	0.446675	1)	0.18916391	RC_AA4812 68_at	EST; aa35c04.s1 NCI_CGAP_GCB1 Homo sapiens culve doller IMAGE:815238 3; mRNA sequence. (from Genbank)
839 Prostate	Ostare	0.41001	1 0,00200	20.0	-		

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840 Prostate	ostate	0.4165961	0.3928434	0.324862	RC 0.1890887 27	RC_AA4486 27_f_at	EST: zx10a05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 786032 3' similar to contains Alu repetitive element;, mRNA sequence. (from Genbank)
841 Prostate	ostate	0.4164773	3 0.3927999	0.324827	0.18906832	AA328993_s _at	
842 Prostate	ostate	0.4157123	3 0.3927659	0.324731	0.18895558 C01833	C01833_at	EST: HUMGS0003801, Human Gene Signature, 3'-directed cDNA sequence. mRNA sequence. (from Genhank)
843 Prostate	ostate	0.4151094	0.3927232	0.32464	0.18894494	RC_AA4909 30_at	
844 Prostate	ostate	0.41506	0.3926233	0.324537	RC_A	A4501	EST: zx42e04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 789150 3' similar to TR:G641819 G641819 HHEB
845 Prostate	ostate	0.4150477	⊥	0.324401	0.18867612 92 at	RC_AA4361 92_at	EST: 2/22f01.s1 Soares NHHMPu S1 Homo sapiens cDNA clone
846 Prostate	ostate	0.4149323	0.3925212	0.324332	0.18862917 15	RC_AA2367 15_at	EST: zt29c10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 723762 3', mRNA sequence (from Ganhank)
847 Prostate	Ostate	0.4143633	0.3924784	0.324112	0.18850122 L07594	.07594 at	TGFBR3 Transforming growth factor, beta receptor III (betaglycan, 300kD))
848 Prostate	state	0.4141221	0.3924667	0.324086	0.18841319 73 at	898	EST: 2s55g07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701436 31 mRNA sequence (from Gonback)
849 Prostate	state	0.4136635		0.324082	M 0.18830906	3 ma	Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
851 Prostate	State	0.4135426		0.323952	0.18817572 L40391	at	(clone s153) mRNA fragment
852 Prostate	State	0.4132956	0.3923549	0.323952	0.18817572 M85289	at	HSPG2 Heparan sulfate proteoglycan
853 Prostate	state	0.412986	1	0.323817	0.18813461 D63477 at		KIAA0143 gene, partial cds
854 Prostate	state	0.412788		0.323808	0.18799576 R76363 at		Homo sapiens Chromosome 16 BAC closs CITO87517 44M2
855 Prostate	state	0.4126909	0.3921285	0.323808	RC_A 0.18794096 05 at	A4125	EST: zt97b09.s1 Soares testis NHT Homo sapiens cDNA clone
856 Prostate	state	0.4125964	0.391906	0.323744	0.1879026 N31668	8 at	Novel centrosomal protein RanRDM
857 Prostate	state	0.4119702	0.3918923	0.32358	RC_AA<0.18779713 44 f at	1888	EST: aa55a11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:824828 3. mRNA sequence (from Genhank)
858 Prostate		0.4117664	0.3918372	0.323479	0.18776494	 	UDP-Gal:betaGlcNAc beta 1.4- galactosyltransferase nolynentide 4
859 Prostate		0.4117362	0.391823	0.323428	RC_AA4787 0.18767688 94_at	<u> </u>	EST: zv20e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 754200 3', mRNA sequence. (from Genhank)
860 Prostate	state	0.411589	0.391754	0.323344	0.18758014 s	25786	Myosin, heavy polypeptide-like (110kD)

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	Interleukin 16 (lymphocyte chemoatractant factory	isintegrin/cysteine-rich protei		Homo sapiens mRNA for KIAA0684 protein, partial cds	EST: aa68h12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:826151 3, mRNA sequence (from Garbart)	Transcription factor AP-2 alpha (activating enhancer-binding protein 2		DCT Dopachrome fautomerase (dopachrome delta-isomerase,	otem Z)	A PRECURSOR	EST: zr56d01.r1 Soares NhHMPu S1 Homo sapiens cDNA clone	EST: zv05f04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	752767 3', mRNA sequence. (from Genbank)	EST: zo36a01.s1 Stratagene endothelial cell 937223 Homo sapiens	cDINA clone 588936 3' similar to SW:YBF7_YEAST P34222 HYPOTHETICAL 23 1 KD DDOTEIN IN STID4 CF247 HEFF CEATS	REGION.;; mRNA sequence. (from Genhank)	AFFX-BioDn-3 st (endonanous contral)	(in miles considerate)	AFFX-BioDn-3_st (miscellaneous control - 11k chins)	artial cds		EST: zk17g04.s1 Soares pregnant uterus NbHPU Homo sapiens	dion factor 4	EST: af19g10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	derice (1011) Gendank)
	0391 <u>s</u> a	U41766_s_a t	AA128724_a	1	_AA5213 _at	A4521		0.18541263 [149785 at hyrosina rolated and		0.1852362/M15169 at ADDRA Administration of the Committee of Anna Administration of the Committee of the Com	Œ	A4178		EST: zo36a01.s1	RC AA1431 HYPOTHETICAL 2	at	X-BioDn-	BioDn-				AU318	11 at	3101	234634 f
H Water State H	M9 0.18583238 t-2	56 0.18579483		62 0.185/0139	11 0.18559916 54		/6 0.18551043 08 at						74 U.18513U48 /6 at	-		59 0.18508972 90 s	AFF. 0.18505378 3 st					2 0.18465701 14 at		3 0.18448263 16 i at	
	125 0.321921	375 0.321856		0.321182	73 0.321711		076175.0	74 0.321401	ļ	1		1 0 00 0 V				14 0.321159	36 0.321052				0.320953	0.320852		5 0.320793	
	46 0.3903125	77 0.3902375	83 0 3004000	3	14 0.3901773	78 0 3001460	1	19 0.3901374	0.390047	36 0.3900428	0.3899363	0 3800017	}			2 0.3896814	2 0.3896766			7 0 3895537	- 1		3 0.3893094	3 0.3891715	
	0.408646	0.407977	0.4079583	TO TOTAL	0.4078014	0.4076878	0.101.0	0.4074649	0.4074521	0.4072436	0.4070797	0.4065349				0.4064272	0.4062292	400000	0.4062292	0.4001930	0.4001.0	0.4059938	0.4059903	0.4058068	
	883 Prostate	884 Prostate	885 Prostate		886 Prostate	887 Prostate		888 Prostate	889 Prostate	890 Prostate	891 Prostate	892 Prostate				893 Prostate	894 Prostate	ROE Droctoto	896 Prostate	897 Prostate		898 Prostate	899 Prostate	900 Prostate	004

	3) sr					ventors:	Sridl										
i rokali ruzisii ilisela tiaria taessi	Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and	CDWE9 anticon () anticon ()		KIAA0183 gene, partial cds	 	AA486511_a HYPOTHETICAL 20.9 KD PROTFIN	Genbank) EST: aa50f01,s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone	IMAGE:824377 3', mRNA sequence. (from Genbank)	TEB4 protein mRNA	Arg/Abl-interacting protein AraBP2	0.18372235 L20492 s at Gamma-dirtamytranoforms 1	RC_AA4537 EST: aa19f01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 90 at 813721.3' mRNA sequence (from Contact).	GSTT1 gene extracted from Human DNA sequence from BAC 322B1	on chromosome 22q11.2-qter contains GSTT1, GSTT2 glutathione transferases 4E-binding protein 1 pseudogene, D-dopachrome	Codonomic des pecual de la la alla polymorphic CA repeat	EST: zu43d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 740757 5' mRNa servience (from Control)	EST: aa90h11.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 838629 3' similar to contains Alu repetitive element; mRNA sequence. (from Genbank)
181. 1886	RC_AA2877		RC_AA4890 74 at	0.18411641 D80005 at	RC_AA4283 25_at		t RC_AA4897	0/_at AF009301_a	+	KC_AA1932 04_at	L20492 s at	RC_AA4537 90 at		84718_cds at	RC_AA0888		_AA4569 at
	RC 0.18434486.35	0.1842992 55	0.18420975 74	0.18411641	0.18411295 25		0.18409792	0.18399018 07 at AF000	0.18385305	0.18377991 04_at	0.18372235	0.1836577 90 at		Z; 0.18362539	0.18336846 51	0.18333037	0.18321554 81
	0.320708	0.320583	0.320499		0.320253		0.3202	2	0.32013	0.319992	0.319973	0.319967		0.319938	0.31982	0.319803	0.319733
	0.3891494	0.3891183	0	0.389085	0.3890787		0.3090400	1	0.388903	0.3887318	0.3886707	0.3885544		0.3883877	0.3883841	0.3883561	0.3883128
	0.4053121	0.405306	0.4052855	0.4052009	0.4052003	0.4051800	0.4051694	0.4043605	0.4047083	0.4042842	0.4041726	0.4040466		0.4039669	0.4039596	0.4037938	0.4037715 0.3883128
	902 Prostate	903 Prostate	904 Prostate	905 Prostate	906 Prostate	907 Prostate	908 Prostate	909 Prostata		910 Prostate	911 Prostate	912 Prostate		913 Prostate	914 Prostate	915 Prostate	916 Prostate

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047 0500	2010	0.4007000	- 1			ŧ	માતો પૈતાપા માત્રી પાલી પાલી મેળવી મેલલે સ્ટાર્ગ
	osidie	0.4037338	0.3882989	0.319/33	0.18319468 D21851_at	D21851_at	KIAA0028 gene, partial cds
918 Pre	Prostate	0.403671	0.3882406	0.349747	0.18316568 OF	RC_AA4033	
					0.10510300	PC AAAAA	Glone 725212 3; mKNA sequence. (from Genbank)
919 Pro	Prostate	0.4034759	0.3882097	0.319717	0.18312657	62_at	EST: da44c03.ST Soares NnHMPU ST Homo sapiens cDNA clone 823792 3', mRNA sequence. (from Genbank)
920 Prostate	ostate	0.4031337	0.3882001	0.319676	0.183018	0.183018 H41895 at	EST: yo07h11.r1 Homo sapiens cDNA clone 177285 5'. (from Genbank)
921 Pro	Prostate	0.402958	0.3881559	0.319644	RC_A 0.18299669 23 at	RC_AA2563 23 at	EST: zr80f05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 682017 3', mRNA sequence. (from Genhank)
1						RC AA0019	
922 Prostate	ostate	0.4026491		0.319419	0.1829485 28 at	28_at	cDNA clone 427905 3', mRNA sequence. (from Genhank)
923 Prostate	ostate	0.4026029	0.3881457	0.319412	0.18285854 D50927_at	D50927_at	KIAA0137 gene
924 Prostate	ostate	0.4025732	0.3881173	0.31927	RC 0.18276237 97	RC_AA2512 97_at	EST: zs10a10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684762 3. mRNA sequence (from Genhank)
925 Prostate	state	0.4025597	0 3880583	0.240460	1 40000000	AA216094_s	EST: hp0453.seq.F Fetal heart, Lambda ZAP Express Homo sapiens
926 Prostate	state	0.4024883		0.319148		at M88163 at	
927 Prostate	state	0.4024381	0	0.319134	RC_AA4 0.1825456 68_s_at	RC_AA4868 68_s_at	Slit (Drosophila) homolog 2
028 Droctato	40	0.4000640	0000000			RC_AA4427	Homo sapiens inner mitochondrial membrane translocase Tim23 (TIM23) mRNA, nuclear gene encoding mitochondrial protein,
929 Prostate	state	0.4021527		0.318983	0.18242222 68 i at	68 i at M33680 at	Complete cds
930 Prostate	state	0.4020408		0.318944	RC_A 0.1822983210_at	3 4	EST: zu37a08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
034 Droctoto	40	000000000000000000000000000000000000000	1			4A011479_a	AA011479_a EST: zi01b10.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
301110	Sidie	0.4019333	0.3875953	0.318822	0.18218704 t		cDNA clone 429499 5', mRNA sequence. (from Genbank)
932 Prostate	state	0.4014008	0.3875688	0.318811	0.1821415 U69114	at-	c.s.i. numan Down syndrome region, YAC 152F7, mRNA sequence. (from Genbank)
933 Prostate	state	0.4012037	0.387523	0.318685	RC_A 0.18209605 25_at	A1590	EST: zo57h03.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 591029 3', mRNA sequence, (from Genhank)
934 Prostate	state	0.4008134	0.3875125	0.318656	RC 0 18197335 05	_AA4912	Company of the Action of the A
935 Prostate	state	0.4007025		0.318547	0.18193193 D80009	at	KIAA0187 gene
936 Prostate	state	0.4003674	0.3873945	0.318527	0.18185376 IL4 at		No info for gene
937 Prostate	state	0.4000988	0.3873667	0.318484	0.18174767 X79888 at		AUH mRNA
938 Prostate	state	0.3998589	0.3873302	0.318458	U 0.18161681	U47025_s_a	PYGB Glycogen phosphorylase B (brain form)

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939 Prostate	9 0.3993242	0.3873293	0.318361	0.18161076 42_at	Etoposide-induced mRNA
940 Prostate	0.3990546	0.3873209	0.318225	RC_AA1803 0.18154973.21 at	Homo canions (clone \$164) wDNIA 21 and of ada
941 Prostate			0.318175		Cell surface protein HCAR mRNA
942 Prostate		0.3871708	0.318057	0.1813474 U72507 at	0.1813474 U72507 at-2 Human 40871 mRNA nartial seguence (from Genhank)
943 Prostate	9 0.3985443	0.3871149	0.318019	0.18131801 U72507_at	40871 mRNA partial sequence
944 Prostate	9 0.3984186	0.3871095	0.317891	RC_AA4192	
945 Prostate		0.3870637	0.317826	0.1812315 H66279 at	V72b07 r1 Homo saniens cDNA clone 210805 5' (from Conhant)
946 Prostate	0.3979961	0.3869908	0.317794	AA410565 0.1810997 t	AA410565_a EST: zv23d06.r1 Soares NhHMPu S1 Homo sapiens cDNA clone to 754475 5', mRNA sequence (from Genhank)
947 Prostate	0.3979238	0.3868783	0.347704	RC_AA2533	
948 Prostate			0.317695	0.1810318 Y09858 at	Homo sapiens clone 24659 mRNA sequence Unknown protein
949 Prostate	0.3979104	0.3868431	0.317675	0.18094458 Y09858 at-	0.18094458 Y09858 at-2 H sapiens mRNA for unknown profein (from Cenhank)
950 Prostate	0.3977601	0.3868421	0.317573	0.18091044 M25077 at	60-kdal ribonucleoprotein (Ro) mRNA
054 Droctoto				58057	
952 Prostate	0.3977344	0.3868181	0.31/535	0.1807694 at	Periplakin
953 Prostate	\dagger	- 1	0.017300	0.16073004 A70476 at	COALOMER BEIA'SUBUNII
	-	i	0.011.092	0.100023191.43964 at	PSENZ Presentlin 2 (Alzheimer disease 4)
L C				RC_AA2810	EST: zt01f01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711865 3' similar to contains Alu repetitive element;, mRNA
954 Prostate			0.317239	0.18061261 92_at	sequence. (from Genbank)
955 Prostate	0.3973098	0.3865537	0.317235	0.18055633 U77396 at	LPS-Induced TNF-Alpha Factor (LITAF) mRNA
956 Prostate	0.3970723	0.386523	0.317171	AA017469_a 0.18048686 t	BEST: ze38f11.r1 Soares retina N2b4HR Homo sapiens cDNA clone 361293 5', mRNA sequence, (from Genbank)
957 Prostate	0.3967476	0.3864747	0.317098	D58019_s_a	
958 Prostate	0.3966605	0.3861831	0.317047	0.1804609 V00594 s	0.1804609 V00594 s at Metallothionein isoform 2
959 Prostate	0.3966207	0.3861783	0.31697	0.18037982 80 at	EST: zr51f08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666951 3', mRNA sequence, (from Genbank)
960 Prostate	0.3965805	0.3861576	0.316922	RC_AA0183 0.18022922 46 at	
961 Prostate	0.3965654	0.3861554	0.31688	D31161_s_a	

				13" that that if there dente		then from the small state that the transfer that the
962 Prostate	0.3962975	5 0.3861492	0.316859	0.18015334	RC_AA3427 80_at	EST: EST48360 Fetal spleen Homo sapiens cDNA 3' end, mRNA sequence, (from Genhank)
963 Prostate	0.3962705	5 0.386134	0.316828	0.180098581152522	152522 at	Arfantin 2 mitation towards
964 Prostate	0.3960956	3 0.3861249			11 1	Homo sapiens clone 24629 mRNA seminars
965 Prostate			0.316647	0.18001218	H49499_s_a t	Homo canians chromosomo 10
966 Prostate	0.3960558	3 0.3859657	0.316636		716350 at	SA mRNA for SA gene product
967 Prostate	0.3957903	0.3859039	0.316556	0.17980534	AA091278_a t	
968 Prostate	0.3956522	0.3857664	0.316549	RC_A 0.17979702 62_at	RC_AA2590 62_at	
969 Prostate	0.3956273	0.3857104	0.316481	0.179696521	AA402121_a t	
970 Prostate	0.3955916	0.3857104	0.316414	HG2810 0.17964965 HT2921	HG2810- HT2921 at	Homeofic Profein DIO
971 Prostate	0.3952883	0.3856884	0.316407	0.17957145 86 at	\\ _\	EST: zo66c01.s1 Stratagene pancreas (#937208) Homo sapiens
972 Prostate	0.3952823	0.3856613	0.316385	0.1794639121	RC_AA3985 21 at	EST: z447d09.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
9/3 Prostate	0.3951265	,	0.316295	0.17944537 L41816	41816 at	Cam kinase I mRNA
974 Prostate	0.3949496	0.3854027	0.316245	0.17941353 U72515	172515 at	G3f mRNA
975 Prostate	0.3942614	0.3853829	0.316106	RC_A 0:1793347 13 at	A1570	EST: zl21b03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502541.3' mRNA sariianga (from Carbail)
976 Prostate	0.3942431	0.3852371	0.316089	RC 0.17925505 42	_AA2522 at	EST: zr64g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668214.31 mRNA sequence (from Conhock)
977 Prostate	0.394226	0.3851859	0.315979	0.17925505 at	27176_s_	EST: 23c2 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence (from Cenhank)
978 Prostate	0.3940985	0.385127	0.315818	X 0.179226651	X89986_s_a t	NBK anonfolic indured protoin
979 Prostate	0.3933957	0.3850906	0.315818		A442274_a	AA442274_a EST: zv54a06.r1 Soares testis NHT Homo sapiens cDNA clone
980 Prostate	0.3933111	0.3850804	0.315774	0.17896011 R06629 at		Adducin 2 (hote)
981 Prostate	0.3930253	0.3850281	0.315638	0.17887908 X56807 at-2		Desmocollin 2
902 F10State	0.3930253	0.3850281	0.315581	0.17879327 X56807		DESMOCOLLIN 2A/BB PRECIJRSOR
983 Prostate	0.3929346	0.3849988	0.31558	R. 0.17875476	RC_D59894 at	EST: Human fetal brain cDNA 3'-end GEN-073B05, mRNA sequence.
984 Prostate	0.3928745	0.3849641	0.315552	11-1	T	(clone 35.3) DRAL mRNA
985 Prostate	0.39284	0.3849206	0.315516	RC_A 0.17862254 43_at	A2530	EST: zr52b12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667007 3', mRNA sequence. (from Genhank)

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Homo sapiens hHa4 gene, complete CDS	RC_AA2532 EST: zr53g12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone	RTS beta protein	RC_AA4062 EST: zu65e08.s1 Soares testis NHT Homo sapiens cDNA clone 742886 3' mRNA sequence (from Genhank)		0.17821486 S62539 s at Insulin recentor substrate 1	KIAA0005 gene	AA150333_a Homo sapiens thyroid hormone receptor activator molecule (TRAM-1) t	Clone 350/2 melanoma ubiquitous mutated protein (MUM-1) gene, partial cds	EST: 37f9 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA mRNA sequence (from Genhank)	Chromosome segregation gene homolog CAS mRNA	Deleted in split hand/split foot 1 (DSS1) mRNA	Homo sapiens mRNA for KIAA0776 protein, partial cds		RC_AA2806 EST: zs95h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 87_at IMAGE:705279 3', mRNA sequence. (from Genbank)
AA340065_s .98 at	RC_AA2532	0.17835936 X67098 at	RC_AA4062 0.17830187 18 at	RC_AA0529 0.17825313 47 i at	86 S62539 s at	0.17804605 D13630 at		0.17793225 U20908_at		1	1	188035_s_a	RC_AA2338 0.1775948 41 at	RC_AA2806 93 87_at
0.17860498	0 178390	0.178359	0.178301	0.178253	0.178214	0.178046	0.17794557	0.177932	0.17789	0.17788	0.177765	0.17763752 t	0.17759	RC_A 0.17753293 87_at
0.315384	0.315343	0.315255	0.315244	0.315241	0.315209	0.315163	0.315051	0.314991	0.31493	0.314855	0.314802	0.314783	0.31465	0.31465
0.392768 0.3848803	0.384696	0.384696	0.3846896	0.3845063	0.3844245	0.384361	0.3843182	0.3842264	0.3841692	0.3840391	0.3839263	0.3838315	0.3838297	0.3837899
0.392768	0.3927505	0.3922151	0.392006	0.3914417	0.3914041	0.3913986	0.3913282	0.3912189	0.3911457	-	0.3908841	0.3904275	0.3904215	0.3903119
986 Prostate	987 Prostate	988 Prostate	989 Prostate	990 Prostate	991 Prostate	992 Prostate	993 Prostate	994 Prostate	995 Prostate	996 Prostate	997 Prostate	998 Prostate	999 Prostate	1000 Prostate
986	987	988	989	990	991	992	993	994	995	966	997	966	666	1000

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FIG. 12V2

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O. O.	-Sullouransterase mKNA	Paxillin mRNA	RC_AA4342 EST: zw24q05.s1 Soares ovany firmor NIVHOT Home confidence	Informe 77/0964 31 month against the comment of the	Gold of the sequence. (from Genbank)		HG NET gene exon 1	ARSB Anden Popular	Taken Manual and Manua	D13897 rna Peptide YY precursor gene extracted from Human DNA for	AN DEPTHE		Seven in absentia (Droscottila) kamala a	0.383634781 0E444 - POLY 10 DOS 10 DO	COCCOST 19 144 at POSPHOENOIDY TUVATE CARDOXY Kinase 1 (solution)	EMO4 Flori	CENTAL CONTROL OF THE PROPERTY	U.3/54/505 M31994 at AI DH1 Aldehyde dehydrococc 1 -1.1.1	Translate delight of the soluble
0.623652 0.469475851186036 of C. 16-4	organización de la contraction del contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction de la contraction d	0.579002 0.43806225 U14588 at Paxillin mRNA	RC AA4342	0.557459 0.42065385 45 r at	15	0.542078 0.410309631 24	0.4 1000000 B	0.533008 0.40186924 M32373 at ARSB Aryle Uffeton B	5	D13897_ma	0.39495236	1	0.388/8/8 R25253 at	0 383634781 0E444 at	0.000004/ 0 LOJ 144 BL	0.37931246 M64082 at	מינו מטוביה ומטינטים	0.375475051M31994 at	
0.623652	100001	0.579002		0.557459		0.54207B	200	0.533008			0.524504	0 540040	01.081.0.0	0.514072	1	0.509061	0 504440	0.304413	
0.7189214	0 00700	7006/00.0		0.6428464		0.6222867		0.6137351			0.6054473	0 5074044	40140	0.5927476	0.0000	0.5899819	0 5835107	0.0000121	
0.7236232 0.7189214	0 74 42036	0.1142330 0.00/905/	1	0.7051538 0.6428464		0.6645773 0.6222867	21, 010	0.659478 0.6137351		1	0.6550589 0.6054473	0 6428370 0 5074044	0.00210.0	0.6412759 0.5927476	7200000	0.032971 0.5899819	0 6270231 0 5835127	0.021.0201	
1 Kenal	2 Renal	5	0	o Kerial		4 Renal	Denne	o renal		0000	חארוס	7 Renal		8 Kenal	9 Benal	्राखा	10 Renal		

FIG. 13A

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11 Renal	0.6124989	0.5762743	0.500571	0.37189296 7	U/316/_cds 7 at	H LUCA14.6 gene extracted from Human cosmid LUCA14
12 Renal	0.6097494	1		0.3688056 M27318	127318 f	at INTERFERON ALPHA4 PRECURSOR
13 Renal	0.6088486	0.6088486 0.5700821	0.493593	0.3654079[1]92015	192015 at	Clone 143789 defective mariner transnoon Lemar? mDMA common
14 Renal	0.6077709	0.6077709 0.5665063]	0.36294618 U31384		G protein gamma-11 subunit mRNA
15 Renal	0.6037929	0.5646834	0.487563	0.36004543 D42039 at	742039 at	KIAA0081 gene, partial cds
16 Renal	0.6037357	0.5617836	0.485499	0.3574315	AA452353_i	Protein phosphatase 2 (formerly 2A), regulatory subunit B" (PR 72), alpha isoform and (PR 130), hata isoform
17 Renal	0.6029763	1		0.3552889 X66436	K66436 at	POSSIBLE GTP-BINDING PROTFIN HSR1
18 Renal	0.5986047	0.5530478	0.481411	0.35289082 U32114		Caveolin-2 mRNA
19 Renal	0.5976415	0.5524086	0.47945	0.35053915 M28439	M28439_at	CYTOSKELETAL 17
20 Renal	0.5975566	0.5500898	0.476969	0.34884948 t	X99393_s_a t	
21 Renal	0.5973349	0 5/18/755	0.475949	J 247460	100207_rna2	a) extracted from Human leukocyte
22 Renal	0.5884828	0.5460057	0.479500	0.047 100		Ilpna-a gene
5	0.0001020		0.473502	0.3450/2512 U86962	Joegoz at	
23 Renal	0.5817567	0.5451021	0.471977	0.3431942 \$81916	381916_at	Phosphoglycerate kinase {alternatively spliced} [human, properties of muscl, properties of mu
24 Renal	0.5785691	0.5442907	0.469703	0.34171772	J03735_f_at	0.3417172 U03735_f_at MAGE-3 antigen (MAGE-3) gene
7	0 5704 40		70000			ERASE 2B7 PRECURSOR,
20 Reliai	0.5/8142	2	0.468094	0.340043 J05428 at	105428 at	
Z6 Kenal	0.5774897	0.540307	0.46676	0.3384387 M31659_at	//31659_at	GT mitochondrial solute carrier protein homologue mRNA
27 Renal	0.577166	0.5386123	0.465425	Z 0.33695215	Z80345_ma 1_s_at	SCAD gene, exon 1 and joining features
					AA314587_a	
28 Renal	0.5763867	0.5368555	0.463865	0.33575952 t		cDNA 5' end, mRNA sequence. (from Genbank)
29 Renal	0.5733975	0 5360127	0.462335	RC 0 33460178 64	_AA4573	
			2001	1	HG3998-	מומנוים מינים אומנוים מינים אומנים או
30 Renal	0.5733829		0.461339	0.3333448 HT4268	1T4268_at	L-Glycerol-3-Phosphate:Nad+ Oxidoreductase
31 Renal	0.5712965	0.5323939	0.459847	0.33201018 M96944	//96944_at	PAIRED BOX PROTEIN PAX-5
32 Renal	0.5710069	0.5318915	0.458679	RC_A 0.33062482 83_s	RC_AA4565 83 s at	Human PL6 protein (PL6) mRNA. complete cds
33 Renal	0.5704181	0.5305039	0.457928	0.32922646 L07590 at	.07590 at	PPP2R3 Protein phosphatase 2 (formerly 2A), regulatory subunit B" (PR 72), albha isoform and (PR 130), beta isoform
34 Renal	0.5699427	0.5284476	0.45722	0 32758245 1 36644	36644 of	Docontor protoin tracing kings (UEI/7) mDN/A of and

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EST: yd23a06.r1 Homo sapiens cDNA clone 109042 5', (from Genbank)	MYH3 Myosin, heavy polypeptide 3, skeletal muscle, embryonic	CALCR Calcifornia recentor	Tax helper protein 1	OR17-40 gene extracted from Human olfactory receptor gene cluster on chromosome 17, OR17-228 and OR17-40, and OR17-24 and	Storoidogosic footos 4 monta	HE6 Tm7 recentor	CYP2C18 Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polymentide 18	Rat HREV107-like protein	Zinc Finger Protein Znf155	GPI anchored molecule like protein	EST: zu62c02.s1 Soares testis NHT Homo sapiens cDNA clone	Small mains sigh motion ()	THYROXINE-BINDING GLOBULIN PRECURSOR	FATTY ACID-BINDING PROTEIN HEART	VCAM1 Vascular cell adhasion molecula 4	GSTA1 Glutathione S-transferase A2	WT1 Wilms tumor 1	Facioscapulohumeral muscular dystrophy (FSHD) gene region, D4Z4	Pay8 mPNA	TISSUE FACTOR PATHWAY INHIBITOR PRECIIESOR	SLC2A2 Solute carrier family 2 (facilitated glucose transporter), member 2		KENIN PRECURSOR, RENAL	C-erb-A mKNA for thyroid hormone receptor	COND1 Cyclin D1 (PRAD1; parathyroid adenomatosis 1)
T80685_at	X13100_s_a t	X69920_s_a	D14827 at	375	D88155_s_a	X81892 at	M61853 at	X92814 at	HG4243- HT4513 at	84290	RC_AA4013	M21530 21	M14091 at	U57623_s_a t	M30257_s_a	M16594 at		038024 at		M59499 at	J03810 at	M26901_s_a		X50708 at	108180 at
0.32679015 T80685_at	0.32595423	0.32484365	0.32380253 D14827	U586 0.32258534.2. at	0.32169798	0.32051897 X81892	0.31971857 M61853 at	0.3185993 X92814	HG4243-0.31764483 HT4513	0.31692484 t	0.31592748.41	0.31505772 M21530	0.31407627 M14091	0.3132262	0.3125271	0.31178474 M16594	0.31079242 M60614	0.3103334 D38024	0.30965507 X69699	0.30897507 M59499	0.3083576 J03810 at	10000	0.307894	0.306856 X04707	0.30023032
0.455012	0.454189	0.4534	0.452031	0.45112	0.450483	0.450309	0.448726	0.44789	0.44739	0.446623	0 445734	0.444671	0.44371	0.442931	0.442024	0.441733	0.440548	0.439719	0.439292	0.438973	0.438347	0.43764.0	0.43/010	0.436354	1.00004-0
0.527718	0.5256051	0.5253213	0.5245482	0.5219296	0.5213687	0.5206158	0.5196485	0.5173948	0.5159215	0.5158634	0.5152429	0.5147941	0.5136164	0.5132961	0.5128887	0.511822	0.5104736	0.5100777	0.5093127	0.5092225	0.5086933	0 5075974	0.5070452	0.5065996	0.000000
0.5692905	0.5681835	0.5666657	0.5633689	0.5615135	0.5604476	0.5596337	0.5582625	0.5569618	0.5561226	0.5551963	0.5529269	0.5519459 0.5147941	0.5514525	0.5510593	0.5503163	0.5473999	0.5459741	0.5439452 0.5100777	0.5437236 0.5093127	0.5421976	0.5420483	0 5417493	0.5415649	1	
35 Renal	36 Renal	37 Renal	38 Renal	39 Renal	40 Renal	41 Renal	42 Renal	43 Renal	44 Renal	45 Renal	46 Renal	47 Renal	48 Renal	49 Renal	50 Renal	51 Renal	52 Renal	53 Renal	54 Renal	55 Renal	56 Renal	57 Renal	58 Renal	59 Renal	

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Inventors: Sridhar Ramaswamy, et al. EST: zx11g04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA TTPA Tocopherol (alpha) transfer protein (ataxia (Friedreich-like) with RC_AA4043 | EST: zw37a04.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA EST: ae48b06.s1 Stratagene lung carcinoma 937218 Homo sapiens brakepoint: orf1/unknown 43 amino acid transcript...orf3/unknown 50 Growth hormone-releasing hormone receptor form b gene extracted Description: orf3 gene extracted from region centromeric to t(12;17) U17579_ma |from Human growth hormone-releasing hormone receptor gene, amino acid transcript [human, testis, acampomelic campomelic dysplasia and sex reversal patient, Genomic, 3 genes, 3414 nt] cDNA clone 950099 3', mRNA sequence. (from Genbank) Exon 1 from Human prolactin gene 5' region./ntype=DNA SLC10A1 Na/taurocholate cotransporting polypeptide clone 786198 3', mRNA sequence. (from Genbank) clone 772206 3', mRNA sequence. (from Genbank) IGF2 Insulin-like growth factor 2 (somatomedin A) alternatively spliced forms a, b, and c, partial cds Calmitine Calcium-Binding Protein, Mitochondrial Fas, Apo-1 gene (promoter and exon I) Na,K-ATPase gamma subunit mRNA Hepatocyte nuclear factor 4, gamma Retinoid X receptor-gamma mRNA Blue Cone Photoreceptor Pigment Interferon alpha gene IFN-alpha 6 Insulin-Like Growth Factor 2 Homeotic Protein Hox5.4 KIAA0735 gene product CRP C-reactive protein vitamin E deficiency) /annot=mRNA ZNF183 gene HT3593_s_a RC_AA5984 RC_AA4486 X82279_s_a M17863_s_a 0.29714543 W26257 at S83366 cds 0.30419895 D49488 at X00368_xpt 0.30180454 U50743_at 0.30080283|HT3696_at 0.29922056 HT5197_at 0.30020672 U38480_at 0.29866818 L21893_at 0.29830635 X56692 at 0.2959705 HT3739 at 0.29952967 Z49826 at 0.2955634 X02958 at 0.29503918 X98253_at HG3502-HG4749-HG3412-HG3543-0.29654333|81 f at 0.30566636 10_at 0.30474308|88 at 0.30271451 at 0.29457882 2 at 0.29426545|3_at 0.30332038|t 0.3012688 0.29758814 0.435823 0.435343 0.43365 0.432658 0.434117 0.42844 0.426675 0.431951 0.430822 0.430411 0.429907 0.427667 0.5293385 0.5004296 0.427014 0.424726 0.5268567 0.4975213 0.423614 0.5267267 0.4973052 0.422879 0.422853 0.422436 0.429471 0.425717 0.5275608 | 0.4978543 | 0.424352 0.5284635 0.5002533 0.5364182 0.5054519 0.5355861 0.5035169 0.5369051 | 0.5057533 | 0.5350391 0.5032614 0.5347237 0.5031233 0.5024473 0.5336061 0.5020564 0.5312939 0.5009093 0.505252 0.5038647 0.5021753 0.5330759 0.5019126 0.5253429 0.4958387 0.4990851 0.4960711 0.499681 0.5360441 0.5345752 0.5363359 0.5284146 0.5266106 0.534575 0.5280957 64 Renal 65 Renal Renal Renal Rena Renal 66 Renal 67 Renal 68 Renal 69 Renal 70 Renal 72 Renal 71 Renal Renal Renal 73 Renal 75 Renal 76 Renal 74 Renal 77 Renal 80 Renal 61 62 63 6/

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81 Renal	0.5251769	0.4950556	0.421732	0.2938592	HG1071- 0.2938592 HT1071 at	Bone Morphogenetic Protein 3
82 Renal	0.524478	0.4940273	0.421019	0.29338193 X98307	X98307 at	UV-B repressed sequence, HUR 7
83 Renal	0.524478	0.4936573	0.420435	0.2928866 X98307	X98307_at-2	H.sapiens mRNA for UV-B repressed sequence, HUR 7
84 Renal	0.5228156	0.4934258	0.419967	0.29243842 S81294	S81294 at	DCC=deleted in colorectal cancer (alternatively spliced, exon 1A) Ihuman, brain tumor, tumor no. 245, mRNA Partial, 216 ntl
85 Renal	0.5226573	0.493371	0.41961	0.2919467	X07618 s a t-2	Human mRNA for cytochrome P450 db1 variant a. (from Genbank)
86 Renal	0.5226573	0.4932461	0.419199	0.29154822	X07618_s_a t	Cytochrome P450 db1 variant a
87 Renal	0.5217367	0.4930835	0.418993	0.29116666	HG3638- HT3993_s_a t	Amvloid Beta (A4) Precursor Protein, Alt. Splice 4
88 Renal	0.5215014		0.418571	0.29069647 M36634	M36634_at	VIP Vasoactive intestinal peptide
89 Renal	0.5208378	0.4921912	0.418088	0.29025248 M24248_at	M24248_at	MYL3 Myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
90 Renal	0.5200136	0.4905491	0.417268	0.28987566	M62628_s_a t	Alpha-1 lg germline C-region membrane-coding region, 3' end
91 Renal	0.519979	0.4903485	0.416472	0.289555 M13207	M13207 at	CSF2 Colony-stimulating factor 2 (GM-CSF)
92 Renal	0.5192758	0.4902283	0.416108	HG3231- 0.28915972 HT3408 at	HG3231- HT3408 at	Protease Receptor-1, Effector Cell
93 Renal	0.5173352	0.4888274	0.415593	0.2886322	RC_AA4466 50 at	EST: zw89g02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
S C C C	0.011000		0,41000	0.2000322		dollo 104110 o'i mistro seddence. (non ochodins)
			-		HG2841- HT2968_s_a	
94 Renal	0.5172132	0.487926	0.414892	0.28830683	+-	Albumin, Alt. Splice 1
95 Renal	0.5166175	0.4877747	0.414549	0.28777137 S77812	S77812 at	FLT1 Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
					HG3432-	
96 Renal	0.5148366		0.414251	0.28745458 HT3621	HT3621_at	Fibroblast Growth Factor Receptor K-Sam, Alt. Splice 4, K-Sam Iv
97 Renal	0.5138602		0.414004	0.28705877 S67798	S67798_at	HYALURONIDASE PRECURSOR
98 Renal	0.5122757	0.4865042	0.413662	0.2865816 U64197	U64197_at	CC chemokine LARC precursor
99 Renal	0.5120382	0.486361	0.412998	0.2861182 U14910	U14910_at	RPE-retinal G protein-coupled receptor (rgr) mRNA
100 Renal	0.5119239	0.4852832	0.412591	0.28576726 D17357	D17357_at	Activin beta-A gene, regulatory sequence of 5'upstream region
101 Renal	0.510655	0.4849925	0.411791	0.28543746 M15169	M15169_at	ADRB2 Adrenergic, beta-2-, receptor, surface
102 Renal	0.5106257	0.4846978	0.41168	HG3987 0.2851244 HT4257	HG3987- HT4257_at	Cpg-Enriched Dna, Clone E06
103 Renal	0.5101805	0.4842634	0.411618	0.2848569	HG3236- 0.2848569 HT3413 f at	at Neurofibromatosis 2 Tumor Suppressor (Gb:L27065)
			-			

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U11870_rna Interleukin-8 receptor type A (IL8RBA) gene, promoter and complete	UDP-GLUCURONOSYLTRANSFERASE 2B10 PRECURSOR, MICROSOMAL	ApM2 mRNA for GS2374 (unknown product specific to adipose tissue)	0.28329715 M28585 f at IENA16 Interform clubs 16	CD4 CD4 antinen (n55)	(pp21) mRNA	0.2822789 M31667 f at CYTOCHROME P450 IA2	Regulator of G-protein signalling 5	HB9 homeobox gene	Crystallin. Aloha A	CTLA8 Cytotoxic T lymphocyte-associated serine esterase 8	Ifp35 gene extracted from Human BRCA1, Rho7 and vatl genes, and inf35 gene partial ode	Antisense mRNA for RCMA nentirle	Goldi complex autoantiden goldin-97 mRNA	EST: zv90g12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767110 5' mRNA sequence (from Genhank)	GS2 mRNA	RC_AA2335 EST: zr30g08.s1 Stratagene NT2 neuronal precursor 937230 Homo 32_at sapiens cDNA clone 664958 3', mRNA sequence. (from Genbank)	CD40LG CD40 antigen ligand (hyper lgM syndrome)	RPS11 Ribosomal protein S11	HG2148-	Zinc finger protein (SRE-ZRP) mRNA 3' and	RC_AA4560 EST: aa17d05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 813513.3' mRNA sequence (from Genhank)	Cadherin-6	Zq87g01.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 649008 5', mRNA sequence. (from Genbank)
U11870_rna 1_at	X63359 at	D45370_at	M28585 f at	S79267 at		M31667 f at	RC_AA3484 66_s_at	U07664 at	HG3286- HT3463 at	U32659 at	L78833_cds 4_at	0.2800195 Z29572 at	U51587 at	AA4243 at		RC_AA2335 32_at	D31797 at	M32598_at	HG2148- HT2248 f at	M88579 at	RC_AA4560 93_at	D31784 at	AA211295_a t
0.28438586	0.28411022 X63359	0.283777 D45370			0	0.2822789	0		HG3286 0.2810928 HT3463	0.28074247 U32659	L788 0.28037712 4 at	0.2800195	0.2796258 U51587	0.27941263	0.27907494 U03886	RC_A 0.278763 32_at	0.278476 D31797	0.27805278 M32598	0.97781078	0.27753037 M88579	RC_A 0.2771931 93 at	0.27684647 D31784	0.27646902 t
0.410856	0.410673	0.410462	0.410143	0.409853	0.409403	0.409152	0.409056	0.408348	0.407952	0.407486	0.407066	0.406901	0.406511	0.405941	0.405546	0.405395	0.404732	0.404579	0.40429	0.403718	0.40342	0.4032	0.402843
0.4840603	0.48401	0.483975	0.4836609		0.4825053	0.4816677	0.4814259	0.4805757	0.4800084	0.4790703	0.4786463	0.4783976	0.478174	0.4776675	0.4772277		0.4769793	0.4766741	0.4763677		0.4758397	0.4758215	0.4758109
0.5096447	0.5091612	0.5086218	0.5078191	0.5074842	0.5063532	0.505725	0.5055621	0.5054359	0.5022615	0.5005578	0.5004692	0.4999971	0.4996918	0.4984784	0.4980153	0.4972384	0.4966165	0.4963382	0.4961634	0.4960195	0.4957403	0.4946911	0.4938916
104 Renal	105 Renal	106 Renal	107 Renal	108 Renal	109 Renal	110 Renal	111 Renal	112 Renal	113 Renal	114 Renal	115 Renal	116 Renal	117 Renal	118 Renal	119 Renal	120 Renal	121 Renal	122 Renal	123 Renal	124 Renal	125 Renal	126 Renal	127 Renal

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Neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds	MYL4 Myosin, light polypeptide 4, alkali; atrial, embryonic	EST: zb65a09.r1 Soares fetal lung NbHL19W Homo sapiens cDNA	clone 308440 5' similar to contains Alu repetitive element;, mRNA	sequence. (from Genbank)	MACH-alpha-2 protein			CD86 CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)	EST: zq69c06.s1 Stratagene neuroepithelium (#937231) Homo	sapiens cDNA clone 646858 3', mRNA sequence. (from Genbank)	Alpha satellite and satellite 3 junction DNA sequence	Tresis lises	DOUBLE DOUGHER DOUGHER STREET THE STREET STR	CGMP-DEPENDENT DROTEN KINASE BETA ISOZVAR	OTC Ornithine carbamovitransferase		Nuclear Factor 1, Variant Hepatic	Mitogen-responsive phosphoprofein (DOC-2) mRNA	5-HT2AR=serotonin 5-HT2A receptor {promoter} [human, Genomic,	10/0 IIIJ	77/7/ A Bris Major nistocompatibility complex, class II, DQ beta 1	ZAKI-4 MKNA in numan skin fibroblast	Surfactant protein A mRNA	EST: 2o52g12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 590566 3' mRNA segmence (from Genhank)	(All Dallock Control C	C6 gene, exon 1	GCP-2 gene (granulocyte chemotactic protein-2) extracted from		chemotactic protein-2 (GCP-2) gene	Cone transducin alpha subunit gene extracted from H.sapiens gene for cone transducin alpha enhant	Pl Gl Plasminoren-like profein	DNA sequence from PAC 453A3 contains FST and STS	CD104 protein
5 L07615_at	0.27563456 X52005_at			0 WZ4962 at	X98176_at	1	0.27302114 1895/1_t_at	004343 at	RC_AA2057		M21305 at	112440 24			K02100 at	HG2339-	0.27209738 HT2435 at	0.2718957 U53446 at	S78723_ma	Modaed at		1 40422 =+	0.27 003213 L 10123 at	KC_AA1557 63 at	X72177 rna	1_at		U83303_cds	2 at	218859_ma	M93143 at	10	Y10505 at
	0.27563456		302723200	0.27 3517 US W 24962	0.27533743 X98176	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	0.27 302114	0.27474076 004343		0.27437055 24 at	0.27387922 M21305	0.273407131112440	0.2731371 X82324	0.2728986 Y07512	0.2725721 K02100		0.27209738	0.2718957	S787	0.27126011M24364	-0.2710308 D82407	0.27085246	0.27000215	RC_A 0.27050576 63 at		0.2702475 1_at		700070	0.2700812	0.2697378411	0.26947364 M93143	0.26922822 Z83745	0.26905018 Y10505 at
	0.402161				0.401269	0.404060	202104.0	0.400817	001001	0.400700	0.40020	0.399609	0.399065	0.398813	0.398434		0.398313	0.39818	0.398002	0.397754	0.397521	0.397186	001 166.0	0.396955		0.396744		0.308852	0.030002	0.396368	0.39619	0.395694	0.395353
0.4752962	0.4746762		0.4742230	0.414623	0.474179	0.4730048		0.4734312	0.4720004	0.4730640			1	0.4721566	0.471933		0.4716626	0.4714976	0.4704	0.4702396	0.4701102	0 4695216	0.70001.0	0.4694558	,	0.4691881		0 4689745	0.10001	0.4687249	0.4681715	0.4679957	0.48205 0.4678475
0.4935767	0.4933341		0.4032557	0.4004004	0.4931884	0.4930548	0.4020240	700006450	778660000	0.4922017	0.4918339	0.4911411	0.4910342	0.4902448	0.4898108		0.4891868	0.4874343	0.4870393	0.4862061	0.4859688	0.4858132	70000	0.4856626		0.4854891		0.4845726	21	0.4840626		0.482527	0.48205
128 Renal	129 Kenal		130 Renal	434 Donal	131 Keriai	132 Renal	133 Donal	100 100	134 Renal	135 Renal	136 Renal	137 Renal	138 Renal	139 Renal	140 Renal		141 Kenal	142 Kenal	143 Renal	144 Renal	145 Renal	146 Renal		147 Renal	- 1	148 Renal		149 Renal		150 Renal	151 Renal	152 Renal	153 Renal

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)X	X90579 s a	6.3 0.23
154	Renal	0.4817508	0.4676682	0.395116	0.2687374 t	1	H.sapiens DNA for cyp related pseudogene
į	-	1				X56411_rna	
155	155 Kenal	0.4805055	2	0.395016	0.26840362 1	at	ADH4 gene for class II alcohol dehydrogenase (pi subunit), exon 1
156	156 Renal	0.4797793	0.466339	0.394861	0.26822448 U40215	40215_at	SYN2 Synapsin IIb
					Č	1	
157	157 Renal	777700777	0.4661244	0.20444	K 76360736 0	RC_AAZZ/5	EST: Zr18dU9.S1 Stratagene N I 2 neuronal precursor 937230 Homo
1017	Nona Dena	0.47.30477		0.33441	0.20793337 13	ا ا	sapiens cunA cione bb3/b1 3, mKNA sequence. (from Genbank)
1001	150 Kenal	0.479015	0.4653074	0.394147	0.26775378 U03270	03270_at	Centrin mRNA
RC I	159 Kenal	0.4789934	0.4789934 0.4651112	0.394025	0.26745495 U66083	66083_at	MAGE-9 antigen (MAGE9) gene
160	160 Renal	0.4776748	0.4776748 0.4649223	0.39387	0.2671558 X52479	52479_at	PRKCA Protein kinase C, alpha
161	161 Renal	0.477149	0.477149 0.4646435	0.393353	0.2669536 t	U16799_s_a t	Na.K-ATPase beta-1 subunit mRNA
					Ī	HG2987-	
					Ĭ	HT3136 s a	
162	162 Renal	0.4769938	0.4644854	0.39316	0.2666773 t		Vasoactive Intestinal Peptide
1631	163 Renal	0.4764756	0.4643896	0.393009	0.26648134 J03242		s at IGF2 Insulin-like growth factor 2 (somatomedin A)
164	164 Renal	0.476325	0.4641056	0.392718	0.2662302 R11267		Homo sapiens chromosome 19. cosmid F22329
1651	165 Renal	0.4760614	0.4640841	0.392558	0.26598355 M76180	at	DDC Dopa decarboxylase (aromatic L-amino acid decarboxylase)
1661	166 Renal	0.4758192		0.392183	0.26575044 L27080	₩	Melanocortin 5 receptor (MC5R) gene
167	167 Renal	0.4753879	0.4639266	0.392036	0.2654998 M94065 at	T	DHODH Dihydroorotate dehydrogenase
168	168 Renal	0.4740228		0.391747	0.26535887 U08049	at	Peripheral myelin protein-22 (PMP22) gene, non-coding exon 1A
1691	169 Renal	0.4738825	0.4638733	0.391343	0.26506042 U04520 at	at	COL4A5 Collagen, type IV, alpha 5 (Alport syndrome)
1701	170 Renal	0.4738723		0.391133	0.26482716 H93249	at	Angiotensin receptor-like 2
1711	171 Renal	0.4736692	0.4637421	0.391007	0.26447693 Z17240	ä	HMG2 High-mobility group (nonhistone chromosomal) profein 2
1721	172 Renal	0.4730158		0.390675	0.26419505 L18877	f at	MELANOMA-ASSOCIATED ANTIGEN 12
173 [173 Renal	0.4729687	0.4633065	0.390658	0.26389384 X96969	ä	Urea transporter
174	174 Renal	0.4726276	0.463132	0.390375	0.26356116 U21936	at	Peptide transporter (HPEPT1) mRNA
175	175 Renal	0.4725176	0.4725176 0.4621524	0.389689	0.26341596 M25322 at		SELP Selectin P (granule membrane protein 140k) antigen CD69)
176 F	176 Renal	0.4725164	0.4725164 0.4618957	0.389681	0.2630577 U43030	T	Cardiotrophin-1 (CTF1) mRNA
1771 F	177 Renal	0.4723269	0.4615095	0.389289	0.26285127 U62438 at	T	CHRNB3 Cholineraic receptor, nicotinic, beta polynentide 3
178 F	178 Renal	0.4723269	0.461395	0.389223	0.26256073 UK	32438 at-2	0.26256073 U62438 at-2 Cholineraic recentor. nicotinic. heta nolynentide 3
179 F	179 Renal	0.4716551	0.461187	0.388704	U6 0.26238436	88902_cds _f_at	U88902_cds Integrase gene extracted from Human endogenous retrovirus H clone
180 F	180 Renal	0.4711404	0.4609575	0.388277	0.261977 U02019_at		Heterogeneous nuclear ribonucleoprotein D (hnRNP D), partial cds, clone cDx4

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184 Donal	0 4708646	V 4600664	700000	0.000474700		
400 DOLO	0.470010	L	0.00027	0.20174700 A99142	- 1	Half Keratin, nHbb
182 Kenal	0.4704123	0.4605589	0.387993	0.2615/203 U51334	51334_at	Putative RNA binding protein (RBP56) mRNA
						ACAT1 Acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl
183 Renal	0.470077	- 1	0.387886	0.26128706 D10511	10511_at	Coenzyme A thiolase)
184 Renal	0.4691925	0.4604487	0.387271	0.26097825 M13485_at	13485_at	Metallothionein I-B gene
185 Renal	0.468209	0.460412	0.386938	0.26090252 U00930	0930 at	Clone CE29 8.1 (CAC)n/(GTG)n repeat-containing mRNA
186 Renal	0.4673617	0.4604045	0.386815	0.2605903 X04571)4571 at	EGF Epidermal growth factor
187 Renal	0.4670265	0.4597874	0.386445	0.26031488 K01900 at	11900 at	IFNA8 Interferon, alpha 8
188 Renal	0.4668361	0.4597704	0.386286	0.26004514 U59914	39914 at	Chromosome 15 Mad homolog Smad6 mRNA
189 Renal	0.4663277	0.4596564	0.386261	0.25991943 U58130_at	58130_at	Bumetanide-sensitive Na-K-2Cl cotransporter (NKCC2) mRNA
	4				And the second s	
190 Renal	0.4659388		0.386247	0.2596626 D45371	15371_at	ApM1 mRNA for GS3109 (novel adipose specific collagen-like factor)
191 Renal	0.4647116	0.4594835	0.385977	0.2593686 U13220	13220_at	Forkhead protein FREAC-2 mRNA, partial cds
100 Donol	0.4646940	700000	0000	3X	X99886_s_a	
192 Nellal	0.4046249		0.383722	0.259763777		MCP-2 gene
190 Kellal	0.4037511	0.4592623	0.385384	0.25895628 Y11897 at	1897 <u>a</u> t	Brx gene 3'UTR
194 Kenal	0.4636717	0.4588284	0.385218	0.2586058 M13149_at	13149_at	HRG Histidine-rich glycoprotein
r C		1	1		D87002_cds	POM121-like 1 gene extracted from Human (lambda) DNA for
195 Kenai	0.4631/3	0.458656	0.385097	0.2582481 2_at	at	immunoglobin light chain
196 Renal	0.4616602	0.4576354	0.384807	0.2580935 U09609 at)9609 at	NFKB2 Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100)
7				M	M27533_s_a	
197 Kenal	0.4615954		0.384481	0.257960861		lg rearranged B7 protein mRNA VC1-region
198 Renal	0.4605679	0.4575374	0.3844	0.25768372 D25248	.5248_at	Randomly sequenced mRNA
199 Renal	0.4594386	0.4571116	0.384316	0.25741625 U38276_at	88276_at	Semaphorin III family homolog mRNA
200 Renal	0.459354	0.4568678	0.383994	RC_A 0.25720614 35_at	RC_AA4179 35_at	EST: zv94c08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 767438 3' mRNA sequence (from Genhank)
201 Renal	0.4591454	0.4567329	0.383674	0.25699124 X89960	9960 at	Mitochondrial capsule selenoprotein
202 Renal	0.4585022	0.4565887	0.383325	0.256783071	U83598_s_a	Death domain recentor 3 colubba form (DDR3) mDNA martial ode
203 Renal	0.4584846	0.4563644	0.383208	0.25673687 X83127	3127 at	K+ channel beta 1a subunit mRNA, alternatively spliced
204 Renal	0.4579437	0.4561909	0.38304	0.2564286611	1238 s at	0.25642866111238 s. at GP5 Glycoprotein V (nistalet)
205 Renal	0.457156		0.382502	0.25621232\Y08417	8417 c at	s af CHRNB3 Cholineraic recentor prouting hote polymontide 3
206 Renal	0.456969		0.382427	0.25609115 D90359		TRANSCRIPTION INITIATION FACTOR THIN 250 KD SUBLINIT
207 Renal	0.4561397	0.4556257	0.382219	0.25586584 U79242	9242_at	Clone 23560 mRNA sequence
208 Renal	0.4558845	0.4553845	0.382173	0.25558877 D1	6626 at-2	0.25558877 D16626 at-2 Histidine ammonia-lyase
209 Renal	0.4558845	0.4547038	0.381992	0.25537455 D16626 at	6626_at	HAL Histidine ammonia-lyase

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237 Denal		0.4462224		0.07	000000000000000000000000000000000000000		EST: K5685F Fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K5685 5' similar to EST(Y103A03.R1), mRNA sequence. (from
707		0.4402324	0.4407939	0.375657	0.24962375 N88827	N8882/_at	Genbank)
238 Renal	<u> a </u>	0.446096	0.4466362	0.375339	0.24951465 L12760_s	L12760_s_at	PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC
239 Rena		0.4450003	0.4485057	0 9764 50	1000000	HG2460-	
2001001	İ	0.4403000	- 1	0.375159	0.24928167 H12556 at	H12556_at	Integrin Beta 1 (Gb:M34189)
240 Rena		0.4457481	0.4464997	0.375086	0.24917136	Z29077_xpt1 _at	Z29077_xpt1 Un-named-transcript-1 from H.sapiens cdc25 gene promoterat region./ntype=DNA /annot=mRNA
241 Renal		0.4453765	0.4457137	0.374688	0.248915	0 248915 M84349 at	CD59 CD59 antigen p18-20 (antigen identified by monoclonal antihodies 16 3 A E E 146 E 130 E 130 C 130
242 Rena		0.4446758	0.445549	0.374284	0.24878845 U78793	U78793 at	Folate receptor alpha (hFR) mRNA, partial cds
						HG4113-	
243 Rena		0.4446306	0.4455332	0.373955	0.24855393	HT4383_s_a t	Offactory Receptor Or17-201
			l			HG2290-	
244 Renal		0.4430218	0.4450903	0.373909	0,24838038 HT2386	HT2386_at	Calcitonin
245 Renal		0.4428053	0 4440075	772577		M54914_s_a	
246 Don		3.4420033	0.10844.0	0.373313	0.24816780	1	FOLLITROPIN BETA CHAIN PRECURSOR
240 Keria		0.4424292	0.4448434	0.373394	0.24782759 X79888_at	X79888_at	AUH mRNA
247 Renal		0.4423468	0.4446103	0.373283	0.24764816	X86401_s_a t	L-arginine:dlycine amidinotransferase
248 Ranal		O AAA7EGE	0 4 4 11 4 11 0	00000		X16609_s_a	
240		0007144.0		0.37.3200	0.24753550		ANK1 Ankyrin 1, erythrocytic
249 Kenal		0.4414078	0.4444898	0.373042	0.24740592 D49490 at	D49490_at	Protein disulfide isomerase-related protein (PDIR)
250 Renal		0.4410874	0.4444415	0.372689	0.24716543 U47334 at		Gamma aminobutyric acid receptor beta4 subunit-like mRNA, partial cds
251 Renal		0.4409656	0.4442276	0.372679	RC_A 0.24701273 14 at	A0355	EST: zk26b02.s1 Soares pregnant uterus NbHPU Homo sapiens
[]							(Nilphi) Gallage Canality of Total Calling IX
252 Kena		0.4408604	0.444168	0.372377	0.24694474 HT3769	₩,	Zinc Finger Protein (Gb:M88359)
253 Renal		0.4405067	0.4438285	0.37236	0.24664462	X65962_s_a t	CYP2C17 Cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 17
254 Renal		0.4402601	0.4433534	0.37222	0.2464867 U52154	at to	Clone KGP G-protein coupled inwardly rectifying potassium channel mRNA
255 Rena		0.4401465	0.4432873	0.371862	0.24632388 M16801	at	MLR Mineralocorticoid recentor (aldosterone recentor)
256 Renal	<u>a</u>	0.439692	0.4428797	0.371646	0.2462302 X83543	at	APXL Apical protein (Xenopus laevis-like)
257 Renal		0.4391957	0.4428474	0.371526	0.24606343 X13444	at	T-CELL SURFACE GLYCOPROTEIN CD8 BETA.3 CHAIN PRECURSOR
258 Renal		0.4390288	0.44274	0.371439	0.24586882 M65085	at	FSHR Follicle stimulating hormone receptor

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0.24084386|S81419_at

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0.4304842 0.4376725

287 Renal

0.24070808|X01059_at 0.24051054 X78687_at

0.366822

0.4374535

0.4299807 0.4298089

288 Renal 289 Renal

0.366627

0.4372046

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		Dystrophin, dystrophin (Purkinje promoter, alternatively spiliced)	
တ	S81419_at	Intringity, control brain and control of the contro	
×	X01059 at	hormone)	
$\cdot \mid \times$	T	G9 gene encoding sialidase	
		Unknown gene extracted from Human HLA class III region containing	
		NOTCH4 gene, partial sequence, homeobox PBXZ (HPBX) gene,	
	389336 cds	U89336 cds receptor for advanced glycosylation end products (KAGE) gene, and o	
	18 at	unidentified cds, complete sequence	
1	J02888 at	NMOR2 Quinone oxidoreductase (NQO2)	
15.4-	3C AA4475	RC AA4475 EST: zw90h07.s1 Soares total fetus Nb2HF8 9w Homo sapiens conva	
	504 at	clone 784285 3', mRNA sequence. (from Genbank)	
-	M59911 at	ITGA3 Integrin alpha-3 subunit	Tit
-	1 S77415 at	Melanocortin-4 receptor [human, Genomic, 16/1 nt]	le:
 	11178556 at	Cisplatin resistance associated alpha protein (hCRA alpha) mRNA	et N Go
- 1	715005 at	CENPE Centromere protein E (312kD)	ene
1100	5 M31651 at	SHBG Sex hormone-binding globulin	etic
m	3 M88163 at	SNF2L1 SNF2 (sucrose nonfermenting, yeast, homolog)-like 1	
+		KCNA6 Potassium voltage-gated channel, shaker-related sublannly,	arl
=	1 X17622 at	member 6	kei
la	8 M20530_at	SPINK1 Serine protease inhibitor, Kazal type 1	s f
0	8 U53442 at	P38Beta MAP kinase mRNA	or
ī	HG4332-		Τι
_	1 HT4602 at	Zinc Finger Protein Znfpt1	
		ELAV-like neuronal protein 1 isotorm Hel-NZ (Hel-NT) IIIRNA, Parual	
5	15 U13706_at	cds	
1	RC_D58185	RC_D58185 EST: Human aorta cDNA 3'-end GEN-354C01, IIIRNA sequence:	_
₫	4 at	(from Genbank)	_

0.23977031 M59911_at

0.24000885 04_at

0.3659890.365905

0.4370709 0.436872

0.428873 0.4286834

292|Renal

293 Renal 294 Renal

0.23964794 S77415_at

0.365789

0.4286338 0.4367907

0.2391816 M31651_at

0,365487 0.365361

0.4284764 0.4366091 0.4280776 0.4365664

0.4285545 0.4366997

295|Renal 296 Renal 297 Renal

0.4277073 0.4364947

298 Rena

0.23901333 M88163_at

0.2393702 Z15005_at

0.23956911 U78556_at

0.365686 0.365596 0.23875788 M20530_at 0.23849778 U53442_at

0.2388741 X17622_at

0.36528

0.4276336 0.4361454

299 Renal 300 Renal 301 Renal

0.365017

0.23837191 HT4602_at

0.364775

0.434961

0.4274338

302 Renal

0.364873

0.4275243 0.4354979

0.4276045 0.4359124

0.24016605 J02888 at

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290 Renal 291 Renal

0.4289232 0.4370761

0.2403425 8 at

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WNT5A Wingless-type MMTV integration site 5A, human homolog EST: EST17092 Aorta endothelial cells, TNF alpha-treated Homo

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0.23763552 | L20861

0.363352

0.434591

0.4254589

307 Renal

HMGCL 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase

(from Genbank)

0.23794194 at

0.364484

0.4268817 | 0.4347154

304 Renal

0.2381095|U13706_at

0.364641

0.4270585 0.4347154

303 Renal

(hydroxymethylglutaricaciduria)

No info for gene

/EL024w/RI

0.2376996 P1 at

0.36361

0.4265924 0.4346966

306 Renal

0.23784144 L07033_at

0.364295

0.434706

0.4268105

305 Renal

RC_AA3043 |sapiens cDNA 3' end similar to EST containing Alu repeat, mRNA

sequence. (from Genbank)

0.23741938 44 f at

0.363341

0.4253571 0.4344069

308 Renal

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DBT Dihydrolipoamide branched chain transacylase (E2 component a of branched chain keto acid dehydrogenase complex; maple syrup urine disease)	EST: xx05h06.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 785627 3', mRNA sequence. (from Genbank)	HBRAVO/Nr-CAM precursor (hBRAVO/Nr-CAM) gene	CYB5 Cytochrome b-5	Gag 2 protein from Human endogenous retrovirus HERV-	K10./ntype≕DNA /annot=CDS	FGFR3 Fibroblast growth factor receptor 3 (achondroplasia,	thanatophoric dwarfism)	Putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds		HTR2C 5-hydroxytryptamine (serotonin) receptor 2C	lleal lipid binding protein mRNA	RIEG Rieger syndrome (solurshin)	0.23584041 U69961_at-2 Paired-like homeodomain transcription factor 2	Frataxin (FRDA) gene, promoter region and	DNA binding protein for surfactant protein B mRNA	M5 muscarinic acetylcholine receptor gene	MULTIDRUG RESISTANCE PROTEIN 1	EST: zh91h05.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens	cDNA clone 428697 3' similar to contains Alu repetitive element;,	mRNA sequence. (from Genbank)	RLBP1 Cellular retinaldehyde-binding protein	A28-RGS14p mRNA	CGM7 Carcinoembryonic antigen gene family member 7	Histidyl-tRNA synthetase homolog (HO3) mRNA	MAP KINASE-ACTIVATED PROTEIN KINASE 2	DNA sequence from clone RP1-151B14 on chromosome 22 Contains	Solika (sumatostatu) receptor 3) gene, pseudogene similar to	ribosomal protein L39, KACZ (ras-related C3 botulinum toxin	substrate 2 (rho family, small GTP binding protein Rac2)) gene, ESTs,	STSs, GSSs and CpG islands, complete sequence	ORPHAN RECEPTOR TR2	LU gene for Lutheran blood group glycoprotein	Extracellular matrix protein collagen type XIV, C-terminus
M27093_s_t	RC_AA4503	73_at	U55258 at	M22976 at	M14123_xpt	3_at		M64347_at	L16782_at	X80763_s_a	1	0.2360774 X90908 at	0.23597923 U69961_at	U69961_at-2	U43753_cds 2_at	L10405 at	M80333 at	M14758_at		RC_AA0043	53_at	L34219_at	U70426_at	0.23454165 D90276_at	0.2343712 U18937_at	U12779_at				1	0.2340767 Z86000_at	0.23394343 M21985_at	X83425_at	Y11710_ma 1_at
0.23732324		0.23717207 73	0.23701248 U55258	0.23687395 M22976		0.23675115 3_at		0.23656695 M64347	0.23628488 L16782		0.23621109	0.2360774	0.23597923	0.23584041	0.23560219 2 at	0.23545852 L10405	0.23534898 M80333	0.23514846 M14758			0.23489729 53 at	0.23475614 L34219	0.2346112 U70426	0.23454165	0.2343712	0.23418541 U12779					0.2340767	0.23394343	0.23368876 X83425	0.2336179
0.363115		0.363114	0.363113	0.362572		0.362406		0.36237	0.362171		0.36205	0.36205	0.361773	0.361736	0.361535	0.36138	0.361026	0.36101			0.360883	0.360712	0.360665	0.360289	0.360201	0.360027				1	0.359976	0.359802	0.359756	0.359537
0.4342575		0.4340541	0.4339815	0.4338114		0.4337421		0.4334933	0.4334756				0.4322593	0.4322593	0.4319465	0.4317624	0.4317512	0.4316221			0.4314864	0.4313865	0.431221	0.4308143	0.4302467	0.4301441				70000	0.4300801	0.4300267	0.4299301	0.4298415
0.425243		0.4251254	0.4249124	0.4238513		0.4237619		0.4236083	0.4231577	1	0.422/03/	0.4225365	0.422017	0.422017	0.4216357	0.4216345	0.4213863	0.4213459		(0.4212861	0.4208609	0.4204913	0.4203819	0.4200121 0.4302467	0.4200087				0000	0.4200085	0.4199946 0.4300267	0.4199186	0.4196365
309 Renal	MAN and a second	310 Renal	311 Renal	312 Renal		313 Renal		314 Renal	315 Renal	-	310 Kenal	317 Kenal	318 Renal	319 Renal	320 Renal	321 Renal	322 Renal	323 Renal			324 Kenal	325 Renal	326 Renal	327 Renal	328 Renal	329 Renal				_	330 Kenal	331 Renal	332 Renal	333 Renal
309		310	311	312		313		314	315		310	31	318	319	320	321	322	323		Ö	324	325	326	327	328	329				Ċ	3	331	332	333

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors giori, gerit, gant, pann pann, men, pann,

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334	Renal	0.4196039	0.4297887	0.359489	0.2332813	RC_AA4521 30_at	EST: zx15d05.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 786537 3', mRNA sequence. (from Genbank)
335	335 Renal	0.4194522	0.4297887	0.359278	RC_A 0.23314606 70_at	RC_AA0071 70_at	EST: 13cDNA84-3.seq Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone HY30-cDNA12 3', mRNA sequence. (from Genbank)
336	336 Renal	0.4190468	0.4295895	0.359164	0.23300155 049974	U49974 f at	f at Mariner? transnosable element complete consensus comments
337	337 Renal	0.4188597	0.4295651	0.358991	0.23291014	M26393_s_a t	Acyl-Coenzyme A dehydrogenase
338	338 Renal	0.4188416	0.4295132	0.358707	0 23282695	U12387_s_a	TDMT Thionimp C and the state of the state o
339	339 Renal	0.4185665	ì		0.2325892 1144848	U44848 at	Niclear receivatory factor 4 (NIDE 4) and an inter-
340	340 Renal	0.418561		0.358562	0.2325325 U13666 at	U13666 at	G protein-colinled recentor (GPD4) good
341	341 Renal	0.4181312		0.358489	0.23242423 L02950 at	_02950_at	CRYM Crystallin Mu
342	342 Renal	0.4179115	0.4291949	0.358279	0.23222579 M25164	M25164 at	THYROTROPIN BETA CHAIN PRECIIRSOR
3/13	3/13/ Dono!	170404	7	1	_		
37.5	344 Ponel	0.4170101	0.4291683	0.358178	0.23215204 HT4822	at	Colony-Stimulating Factor 1, Macrophage, Alt. Splice 3
5	אפושו	0.4173727	0.4290789	0.358082	0.2320245 D86519_at		Truncated pancreatic polypeptide receptor PP2 mRNA
345	345 Renal	0.4169045	0.4287652	0.357736	0.23181531±	A182909_a	EST: zp51d08.r1 Stratagene HeLa cell s3 937216 Homo sapiens
346	Renal	0.4166946	0.4287064	0.357673	0.23169628 783336 at	783336 at	HADRIA GENERAL STREET SECTION SECTION SECTIONS SECTIONS SECTION SECTIONS SECTION SECTI
347	347 Renal	0.4162298	0.4286731	0.357449	0.23159422 L40933 at	Т	Phosphorlincomitase related grotain (DOMER)
						T	Homo sanians phosphorthromations related and the contractions and the contractions and the contractions and the contractions and the contractions and the contractions and the contractions and the contractions are contracted and the contractions are contracted and the contractions are contracted and the contractions are contracted and the contractions are contracted and the contractions are contracted and the
348	348 Renal	0.4162298	0.4286258	0.357166	0.23140834 L40933 at-2		complete cds
349	349 Renal	0.4159051	0.4285968	0.357012	0.23129977	M18391_s_a	TVBOSINIE BEOTETINI VINIA 1911 100 TOTAL 100 T
							INCOMMENTAL FINANCIAL RECEPTOR EPH PRECURSOR
350	350 Renal	0.4155744 0.4280471	0.4280471	0.356817	0.23117651 U11872 at		interteuktir-s receptor type B (IL8RB) mRNA, splice variant IL8RB1, partial cds
100	351 Kenal	0.4150478	0.4150478 0.4280306	0.356727	0.23110898 X52011	äŧ	MYF6 Muscle determination factor
205	352 Kenal	0.41491	0.41491 0.4279622	0.356569	0.23094295 D87024	at	Immunoglobulin lambda gene locus DNA clone-02H4
000	Sool Kenai		0.4275723	0.356394	0.23081186 U19906		VASOPRESSIN V1A RECEPTOR
955	354 Kenal		0.4274197	0.356307	0.23066366 M24900 at		V-ERBA RELATED PROTFIN FAR-1
350	355 Renai	- 1	0.4273355	0.356286	0.23052967 J00212	+-	IFNA21 Interferon, alpha 21
0000	Kenal	0.4140909	0.4273262	0.356144	0.23035994 U09411	at	ZNF132 Zinc finger protein 132 (clone pHZ-12)
357	357 Renal	0.4140842	0.4272097	0.355899	0.23021741 722548	to	SERINE/THREONINE-PROTEIN KINASE RECEPTOR R2
358	358 Renal	0.4138938	0.4272065	0.355806	0.230090571182303	, t	Inknown profes mBNA medic ad-
329	359 Renal	0.4138169	0.4270621	0.355705	0.22998436 M76482 at	at to	DSG3 Desmoolein 3 (nemohigus vulgaris antigan)
360 F	360 Renal	0.4136464 0.4269424	0.4269424	0.355531	X 0.22983654 t	Œ	PTGER3 Prostaglandin E receptor 3 (subtype EP3) (alternative
					1 100000		J. DUUU (3)

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361 Renal	0.4131471	0.426882	0.355399	0.22960745 U28055_at	MST1 Macrophage stimulating 1 (hepatocyte growth factor-like)
362 Renal	0.4130569	0.426745	0.355382	0.2294616 X86570_at	Acidic hair keratin 1
363 Renal	0.4122247	0.4264519	0.355283	0.22931892 X68994 at	CREB gene, exon Y
364 Renal	0.4117986		0.355227	0.22924946 X70340_at	TGFA Transforming growth factor, alpha
365 Renal	0.4116842	0.4116842 0.4261806	0.355068	0.22905804 J03027_at	HLA-G MHC class I protein HLA-G
366 Renal	0.4111903	0.4111903 0.4250974	0.354908	0.22893767 M85164_at	ELK4 SRF accessory protein 1B (SAP-1)
367 Renal	0.4110927	0.4110927 0.4260954	0.354781	0.2287951 X69115_at	ZNF37A Zinc finger protein 37a (KOX 21)
				U31903_s_a	i
368 Renal	0.4109768	0.4109768 0.4259909		0.2286218 t	CREB-RP (creb-rp) mRNA
369 Renal	0.4108892	0.4256344	0.354498	0.2285062 X80878_at	R kappa B mRNA
370 Renal	0.410046	0.4254816	0.354367	0.22839436 U25128_at	PTH2 parathyroid hormone receptor mRNA
371 Renal	0.4099722	0.4252266	0.354271	0.2282706 S68805 at	L-arginine:glycine amidinotransferase [human, kidney carcinoma cells, mRNA, 2330 nt]
		1		X59	
372 Renal	0.4098469	0.4249915	0.354164	0.22818829 1_s_at	PBX2 mRNA
C C C C C C C C C C C C C C C C C C C	0022000		7	HG3355-	(040004-10/
373 Kenal	0.4097795	0.4249467	0.354005	0.2280433 H13532 at	Peroxisome Proliferator Activated Receptor (90.230972)
3/4 Kenal	0.4086/86	0.4086/86 0.424/629	0.353919	- 11	CDH5 Cadherin 5, VE-cadherin (Vascular epithellum)
375 Renal	0.4084653	0.4084653 0.4246295	0.353761	21	Zinc finger protein mRNA, 3' end
376 Renal	0.4082082	0.4082082 0.4242346	0.353406	0.22760104 M59829_at	MHC class III HSP70-HOM gene (HLA)
770	000		1	000000000000000000000000000000000000000	NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL
orr Reilal	0.408042	0.4240703	0.333157		LINKED ISOPORMI PRECURSOR
378 Kenal	0.40/94/9	0.40/94/9 0.4240014	0.353138	0.22731654 M13666 at	MYB Proto-oncogene c-myb {alternative products}
379 Renal	0.4079266	0.4079266 0.4238806	0.353114	0.22708957 U82310_at	Unknown protein mRNA, partial cds
					Description: orf1 gene extracted from region centromeric to t(12;17) brakepoint; orf1/unknown 43 amino acid transcriptorf3/unknown 50
				S83366_cds	
380 Renal	0.4073801	0.4235334	0.352954	0.22704422 1_at	
381 Rana	0.4080284	0.4933476	0.352025	RC_AA2628	EST: zs26b02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
382 Renal	0.4065624		0.35283	0.225070515100 at	Drofocadherin 42 mRNA for abhreviated PC42
	- Automatical Control of the Control			M14158_cds	
383 Renal	0.406537		0.352664	0.22662409 4_at	receptor germline beta-chain D1.1 and J1.1 to J1.6 genes
384 Renal	0.4060856	0.4232099	0.352574	0.22644052 U67614_at	No description available for U67614
385 Renal	0.4054925	0.4231928	0.352543	0.22626273 U10690_f_e	0.22626273 U10690_f_at MAGE-5a antigen (MAGE5a) gene
386 Renal	0.405372	0.422649	0.352249	0.22613432 M16405_at	MUSCARINIC ACETYLCHOLINE RECEPTOR M4
387 Renal	0.4052052	0.4052052 0.4226379	0.352114	0.22608586 104093_s_s	UDP-GLUCURONOSYLTRANSFERASE 1F PRECURSOR, at MICROSOMAL

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Bear 0.4050798 0.4225664 0.352014 0.22589439 H79230 at Genbank) Fragile X locus h						ir tung tung II. tunk tunk	war, www.	from
0.4048739 0.4222553 0.351855 0.22570261 M16282_at 0.404346 0.4222593 0.351659 0.22557326 S77582_at 0.404346 0.4222593 0.351659 0.22557326 S77582_at 0.4036214 0.4220168 0.351659 0.22550912 J05556_at 0.4036282 0.421757 0.351478 0.22530912 J05556_at 0.4036282 0.421757 0.351478 0.22530912 J05556_at 0.4036282 0.421757 0.351478 0.22530912 J05556_at 0.4033422 0.4217446 0.350926 0.22494872 S68874_s_at 0.4031481 0.421746 0.350926 0.22499554t 0.4226393 0.4213373 0.35076 0.22499554t 0.4226393 0.4213535 0.35076 0.22499554t 0.4226393 0.4213535 0.35076 0.224924271 Z48511_at 0.4024642 0.4209718 0.350675 0.22435418 M37245_at 0.4024642 0.4209718 0.350675 0.224035418 M37165_at 0.4073873 0.4209531 0.360273 0.22403641 0.31176_at 0.401373 0.4203495 0.350730 0.22435418 M31165_at 0.4013373 0.4203495 0.350730 0.2235946 M99473_at 0.4012114 0.4202897 0.349586 0.22359416 M99473_at 0.4009431 0.4198688 0.349798 0.22359426 t 0.22359416 0.22359416 0.2235948 0.2223698 0.22223698 0.2223698 0.22			0.4050798	0.4225664	0.352014	0.22589439	at	EST; yu27e05.r1 Homo sapiens curve done 2000 io come Genbank)
0.4048739	22 22 23 24 24 24 24 24 24 24 24 24 24 24 24 24	nai	0.4030130	0.4220004				Fragile X locus M2C containing an unidentified open leading france, 5
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	411	Renal	0.399385	55 0.419492				I NINIZ 110b011111 (Sweleder 1903)

तार्थन तुम्पन तुम्पन प्राण्य प्राप्त तुम्पन सम्पन्न तुम्पन तुम्पन तुम्पन तुम्पन तुम्पन तुम्पन तुम्पन तुम्पन तु स्र में तिन्त्री सिन्त्री सिन्त्री सिन्त्री सिन्त्री सुन्त्री सुन्त्री सिन्त्री

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Renal	0.3990949	0.419488	0.348942	AA134488_a 0.22274947 t	AA134488_a Zo26f12.r1 Stratagene colon (#937204) Homo sapiens cDNA clone t 588047 5', mRNA sequence. (from Genbank)
Renal	0.3990306	0.4194454	0.348771	0.22257294 D88613 at	НGСМа
414 Renal	0.3990282	0.4192733	0.348708	0.22248846 X81333 at	PPH beta subunit protein
415 Renal	0.3989536	0.41924	0.348601	0.22240154 U10686_at	MAGE-11 antigen (MAGE11) gene
416 Renal	0.3987506	0.4192145	0.348564	0.22224782 M73489 at	Heat-stable enterotoxin receptor mRNA
					VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1
417 Renal	0.3986234	0.419084	0.34844	0.22213174 X51602_at	PRECURSOR
					Ccr2 gene (ccr2a) extracted from Homo sapiens ccr2b (ccr2), ccr2a
-	0.0000	0.4400440	070070		(ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, and lactoferrin (lactoferrin)
Kenal	0.3984112	0.4190419	0.348378		gene, partial cds, complete sequence
Renal	0.3981755		0.348166		Kallistatin. Protease Inhibitor 4
420 Renal	0.3977778	0.4188449	0.348134	0.22188286 X91348 at	Predicted non coding cDNA (DGCR5)
421 Renal	0.3977778	0.4186541	0.348104	0.2218123 X91348_at-2	0.2218123 X91348_at-2 H.sapiens predicted non coding cDNA (DGCR5)
422 Renal	0.3976371	0.4185515	0.348092	0.22175573 U87972_at	NAD+-isocitrate dehydrogenase mRNA, partial cds
423 Renal	0.3974625	0.418485	0.348022	0.22165784 M26880_at	UBA52 Ubiquitin A-52 residue ribosomal protein fusion product 1
424 Renal	0.3973343	0.418357	0.347952	0.22149038 U19142_at	GAGE1 G antigen 1 (GAGE-1)
425 Renal	0.3970754	0.418179	0.347765	0.22124243 M23668_at	ADRENODOXIN PRECURSOR
Renal	0.3970079		0.347519	0.22119683 Z11559_at	IREB1 Iron-responsive element binding protein 1
Renal	0.3961533	0	0.347417	0.22104162 U66578_at	Purinergic receptor P2Y9 mRNA
Renal	0.396008		0.347395	0.22084461 U50929_at	Betaine:homocysteine methyltransferase mRNA
Renal	0.3958074	0.41749	0.347223	0.22071193 U72209_at	YY1-associated factor 2 (YAF2) mRNA
430 Renal	0.3956077	0.417376	0.347085	0.22063436 M10943_at	Metallothionein-If gene (hMT-If)
431 Renal	0.3954826	0.4173618	0.346899	0.2205449 X99141_at	Hair keratin, hHb3
Renal	0.3954071	0.4172122	0.346863	0.2203038 U87964_at	Putative G-protein (GP-1) mRNA
Renal	0.3953168	0.4169845	0.346603	0.22025992 M74297_at	HOXA4 Homeo box A4
434 Renal	0.3952664	0.4167714	0.346601	0.22015975 U13395_at	Oxidoreductase (HHCMA56) mRNA
				RC AA0554	EST: zl74e11.s1 Stratagene colon (#937z04) Homo sapiens cDNA clone 510380 3' similar to contains Alu repetitive element;, mRNA
435 Renal	0.3952	0.4165319	0.346198	0.22009698 04 f at	sequence, (from Genbank)
436 Renal	0.3949601	0.4164842	0.346186	0.21993133 S80905 f at	0.21993133 S80905 f at PRB2 locus salivary proline-rich protein mRNA, clone cP7
					U30998 Homo sapiens 530 melanoma Homo sapiens cDNA clone
437 Renal	0.394329	0.4163989	0.346137	0.21981794 U30998_at	nmd, mRNA sequence
438 Renal	0.3941328	0.4163486	0.345869	0.219783 Z29678_at	MitF mRNA
			ĺ	X02176_s_a	
Renal	0.3938225	0.4163345	- 1	0.21968207 t	C9 Complement component C9
Renal	0.3936858	0.4162787	0.345615	0.21949068 U28281 at	SCTR Secretin receptor
	412 Renal 414 Renal 415 Renal 415 Renal 416 Renal 417 Renal 420 Renal 421 Renal 421 Renal 421 Renal 422 Renal 424 Renal 425 Renal 426 Renal 427 Renal 427 Renal 427 Renal 437 Renal 437 Renal 437 Renal 437 Renal 438 Renal 439 Renal 439 Renal 439 Renal 439 Renal		0.3990949 0.3990306 0.3990282 0.3980536 0.3987506 0.39877778 0.3977778 0.3977778 0.3977778 0.397079 0.3970754 0.3970774 0.3970779 0.396008 0.3954071 0.3954071 0.3954071 0.3954071 0.3954071 0.3954071 0.3954071 0.3954071 0.3954071 0.3954071	0.3990949 0.419488 0.3990949 0.3990306 0.4194454 0.3990282 0.4192733 0.3980536 0.4192445 0.3987506 0.4192145 0.3987506 0.4190844 0.39877778 0.4189785 0.3977778 0.4186541 0.3977778 0.4186541 0.3977778 0.4186541 0.3976371 0.4185515 0.3976371 0.4185515 0.3976079 0.4180574 0.395008 0.417601 0.3954071 0.4172122 0.3954071 0.4163845 0.3952664 0.4163389 0.3952664 0.4163345 0.3938225 0.4163345 0.3938225 0.4163345 0.39388225 0.4163345 0.3938828 0.4163345	0.3990949 0.419488 0.348942 0.22274947 0.3990306 0.4194454 0.348771 0.22257294 0.3990282 0.4192733 0.348708 0.222440154 0.3987506 0.41924 0.348601 0.222440154 0.3987506 0.419244 0.348604 0.222440154 0.3987606 0.419244 0.348564 0.222440154 0.39877778 0.4180449 0.34816 0.2218123 0.3977778 0.418649 0.348134 0.221828286 0.3977778 0.4186541 0.348134 0.221828286 0.3977778 0.4186541 0.348104 0.2214573 0.3977778 0.4186541 0.348092 0.2214243 0.3977778 0.4186541 0.348092 0.2214243 0.3977778 0.4186541 0.347662 0.2214243 0.3976625 0.418674 0.347662 0.2214443 0.3976754 0.418674 0.34787 0.2214466 0.3956007 0.41760 0.34680 0.2204461 0.395

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FIG. 13R

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M81780_cds SMPD1 gene (acid sphingomyelinase) extracted from Homo sapiens EST: zx87e06.r1 Soares ovary turnor NbHOT Homo sapiens cDNA BMP-5=bone morphogenic protein-5 (promoter) [human, Genomic, M15517_cds TTR gene extracted from Human mutant prealburnin gene directly EST: zr44f10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone Adrenoleukodystrophy related protein (hALDR) gene, partial cds RC_AA4355 EST: zt85g06.s1 Soares testis NHT Homo sapiens cDNA clone DKFZphsnu1_1b16, 5' read, mRNA sequence. (from Genbank) EST: Homo sapiens mRNA; expressed sequence tag; clone UQCRB Ubiquinol-cytochrome c reductase binding protein CRARF C4/C2 activating component of Ra-reactive factor STAT4 Signal transducer and activator of transcription 4 acid sphingomyelinase (SMPD1) gene, ORF's 1-3's clone 810754 5', mRNA sequence. (from Genbank) linked to familial amyloidotic polyneuropathy (FAP) Cell division cycle 42 (GTP-binding protein, 25kD) Orphan receptor GPR9 (GPR9) gene, partial cds Flg-2 gene for fibroblast growth factor receptor 666283 3', mRNA sequence. (from Genbank) 729178 3', mRNA sequence. (from Genbank) HMOX1 Heme oxygenase (decycling) OIAS (2'-5') oligoadenylate synthetase Tumour suppressor protein, HUGL EDA Ectodermal dysplasia protein Transcription Factor (Gb:L32162) LDHC Lactate dehydrogenase C Olfactory receptor-like gene Interleukin 3 (IL-3) mRNA 0.21659662|U13680_at-2|Lactate dehydrogenase C Putative chloride channel Unknown 14kDa protein CD39 CD39 antigen 1116 nt AA480838 s M22348_s_a U32674_s_a 0.21818678 M20137_at X02875_s_a X86371_s_a RC_AA2338 RC_AA4880 0.21789522 HT4241_at 0.21633242 X83378 at 0.2177407 U59228_at 0.21900862 S73813 at 0.21846297 X06985 at 0.21735369 X95384 at 0.21643445 U13680 at 0.21693847 U28150 at 0.21670319 D17525 at ä 0.21916859|S81957_at 0.21877442 L78440 at 0.2180325 X58255 at 0.21713173 L35475 at HG3971-0.21929209 | 298497 0.21831895 3 s at 0.2188385|97 at 0.21723846 74 at 0.21621221|07 at 0.21746671 5 at ä 0.21854855 0.21812798 0.21757255 0.2168348 0.21940257 0.344835 0.34556 0.345526 0.3929899 0.4158582 0.345264 0.345205 0.344716 0.34456 0.344512 0.343849 0.343503 0.342516 0,345563 0.345099 0.344114 0.343984 0.343429 0.34323 0.343146 0.342896 0.342699 0.342612 0.344261 0.3909785 0.4145568 0.343888 0.343497 0.343285 0.343381 0.3931437 0.4159394 0.3927434 0.4156061 0.3922619 0.4155586 0.3913983 0.4148741 0.3919278 0.4150119 0.3909106 0.4145226 0.3908465 0.4143627 0.39021 0.4141249 0.3897939 0.4127775 0.3894637, 0.4126578 0.392935 0.4158127 0.391211 0.4145787 0.3903177 0.4142064 0.3934735 0.4162787 0.3920944 0.4155054 0.41533 0.4160348 0.3922592 0.4155227 0.390837 0.4143391 0.3901584 0.4140622 0.3900426 0.4140292 0.3898647 0.4135601 0.41327 0.3897955 0.4128727 0.3933882 0.3920615 0.3897955Renal Renal Renal 443 Renal 445 Renal 446 Renal Renal 441 Renal 444 Renal 447 Renal 448 Renal 449 Renal 450 Renal 455 Renal 458 Renal 454 Renal 456 Renal 457 Renal 459 Renal 460 Renal 461 Renal 462 Renal 463|Renal 464 Renal 465 Renal 466 Renal 453 451 452

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467	467 Renal	0.3892597	0.4124726	0.342467	0.21608788 Y08136_at		ASM-like phosphodiesterase 3a
468	468 Renal	0.3887051	0.4124129	0.342407	0.21601352 D14686 at		AMT Glycine cleavage system protein T (aminomethyltransferase)
1691	ARO Denal	0.3886017	0.4123450	0.342203	0.24586327 D50024 at	T	KIDA0134 gene
1001	120 Denoi	0.000001	- 1	0.07774	0.94579464 M29749 at		NAND CVTOCHDOME BE BENICTASE
4,01	בוומו	0.3002032		0.342171	0.21372431 191	T	
471	471 Renal	0.3873729	0.4121672	0.342129	0.21560512 X52889	ä	MYH7 Myosin, heavy polypeptide /, cardiac muscle, beta
							EST: ze74h03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA
					α.	_AA0253	clone 364757 3' similar to contains OFR.t1 OFR repetitive element ;,
472	472 Renal	0.3871222	0.4120859	0.342051	0.21549097 51	at	mRNA sequence. (from Genbank)
							Hs-TBX2=T-box gene {T-box region} [human, fetal kidney, mRNA
473	473 Renal	0.386937	0.4119662	0.341679	0.21544583 S81264	s at	at Partial, 283 nt]
474	474 Renal	0.3868803	0.411963	0.341484	0.21535738 U01120	at	G6PT Glucose-6-phosphatase
1	- T	1000		00777			
4/3	4/3 Kerial	0.3608523		0.341468	0.21522906 097018 at		Echinoderm microtubule-associated protein noriolog flueway IIIRNA
476	476 Renal	0.3867081	0.4116475	0.341433	0.2150264 Y00264_at		APP Amyloid A4 protein of Alzheimer's disease
					2	RC_D59362	EST: Human fetal brain cDNA 3'-end GEN-023A02, mRNA sequence.
477	477 Renal	0.3866564	0.4116346	0.34143	0.21497259	at	(from Genbank)
478	478 Renal	0.3864065	0.4115213	0.341306	0.21489744 U58658 at		Unknown protein mRNA within the p53 intron 1
479	479 Renal	0.3859122	0.4114434	0.341269	0.21479595 L19314	at	HRY gene
480	480 Renal	0.3855977	0.4113829	0.341213	0.2146994 X02956 at		IFNA5 Interferon, alpha 5
481	481 Renal	0.3855954	0.4113756	0.34112	0.21459176 U12622 at		Beaded intermediate filament protein CP115 mRNA, partial cds
482	482 Renal	0.3855891	0.4112196	0.340794	0.21441936 U08989	भ	Glutamate transporter mRNA
483	483 Renal	0.3854718	0.4111506	0.340542	0.21434422 U70867	äţ	Prostaglandin transporter hPGT mRNA
	The state of the s						
					~	AA0051	EST: zh95g08.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens
484	484 Renal	0.3852766	0.4110371	0.340518	0.21418306 96	5_at	cDNA clone 429086 3', mRNA sequence. (from Genbank)
485	485 Renal	0.3844384	0.41083	0.340421	U 0.21406052 t	U29943_s_a t	ELAV-like neuronal protein-2 Hel-N2 mRNA
486	486 Renal	0.3844263	0.4106331	0.34037	0.21391034 D31765 at		KIAA0061 gene, partial cds
487	487 Renal	0.3842909	0.4105851	0.340358	0.21389607 U16282 at		ELL mRNA
700	1000	0 00 4074.0		0.000	00000		(clone cD24-1) Huntington's disease candidate region mRNA
462	488 Kenal	0.3842713	- 1	0.34032	0.21368133 L3/199	ä.	iragment
489	489 Renal	0.3838697	0.4104933	0.340307	0.21358728 M74096	at	ACADL Acyl-Coenzyme A dehydrogenase, long chain
490 1	490 Renal	0.3837603	0.4102729	0.340248	HG3454 0.21342765 HT3647	- at	Zinc Finger Protein 20
							ATP7A ATPase, Cu++ transporting, alpha polypeptide (Menkes
491	Renal	0.3835089	0.4102442	0.340127	0.21334514 L06133	at	syndrome)
492	492 Renal	0.383429	0.4101942	0.340005	X 0.21326189 t	X83492_s_a t	Fas/Apo-1 (clone pCRTM11-Fasdelta(4,7))
493	493 Renal	0.3833537		0.339902	0.2131191 U31248	31248 at	ZNF174 Zinc finger protein 174

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AOA! Ranal	0 2821015	710160X	230066	1 24207070 X63747 24	DA DONINGS (AP) 1-11 ANTION 1
495 Renal	0.3831752		0.339764		FCER1A High affinity ldE receptor alpha-subunit (FCERI)
	0.3829342	0.4101422	0.339427		Clone rasi-1 matrix metalloproteinase RASI-1 mRNA
	0.3828145	0.3828145 0.4096177	0.339375	0.21265146 U20350_at	CMKRL1 Chemokine receptor-like 1
	0.38241	0.38241 0.4094276	0.33919	0.2125849 X67697_at	SPERM ANTIGEN HEZ PRECURSOR
	0.3823005	0.4092183	0.339052	0.21245904 U76010_at	Putative zinc transporter ZnT-3 (ZnT-3) mRNA
	0.3808028	0.4091129	0.338987	0.21238157 Y08976_at	FEV protein
501 Renal	0.3807296	0.4091128	0.338931	0.21220458 t	a SMA5 mRNA
502 Renal	0.3806546	0.4090794	0.338908	0.212103 U31501 at	Fragile X mental retardation syndrome related protein (FXR2) mRNA
	000000000000000000000000000000000000000			AA437346_	EST: zw30c06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770794 5' similar to TR:G406738 G406738 SHB MRNA. ;,
503 Kenal	0.3804053	0.409059	0.338764	0.212069121	mRNA sequence. (from Genbank)
Renal	0.3799121	0.4090375	0.338764	0.21188968 M61855_at	CYP2C9 Cytochrome P450, subtamily IIC (mephenytoin 4-hydroxylase), polypeptide 9
Renal	0.3799048	0.408982	0.33865	0.21184519 U39905_at	SLC18A1 Solute carrier family 18 (vesicular monoamine), member 1
506 Renal	0.3793142	0.4089387	0.338636	L13761_ma1 0.21175718_at	Dihydrolipoamide dehydrogenase gene, exon 14
507 Renal	0 3780361	0.4088456	0 338/17	0.24464208 1137443	CYP2J2 Cytochrome P450, subfamily IIJ (arachidonic acid
	0.378836		0.33839		Glutamate recentor (GLUS5) mRNA
	0.3786276		0.338269		SDH2 Succinate dehydrogenase 2, flavoprotein (Fp) subunit
	0.378587	0.4086427	0.338169	0.21127494 D16294_at	3-KETOACYL-COA THIOLASE MITOCHONDRIAL
		The state of the s	The second secon		
	0070070		700004	RC_AA4958	
512 Renal	0.3780057	0.4083075	0.338	0.21098797 D63483 at	Sequence, (non Gendank) KJAA0149 gene
513 Renal	0.3778997		0.337888	0.21088673 M15881 at	UMOD Uromodulin (uromucoid, Tamm-Horsfall glycoprotein)
_	0.3776736		0.337844	0.21080297 U77975_at	Hepatocyte nuclear factor 6 (HNF-6) mRNA, partial cds
				HG721- HT4827 s	ष
515 Renal	0.3773	0.4081832	0.337798	0.21076393 t	Placental Protein 14, Endometrial Alpha 2 Globulin, Alt. Splice 2
516 Renal	0.3771043	0.4081209	0.337629	0.21066396 X16105_at	RD Radin blood group
517 Renal	0.3770738		0.337605	0.21060382 M64934_at	XK Kell blood group precursor (McLeod phenotype)
	0.3769071		0.337517	0.2105385 X97671_at	EPOR Erythropoletin receptor
519 Renal	0.3768947	0.4077682	0.337399		
520 Renal	0.3766561	- 1	0.33738		
521 Renal	0.3765176	0.4074901	0.337306	0.21029882 D31815 at	SMP-30 (senescence marker protein-30)

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				HG2850-	150-	
				HT48	s a	
543 Renal	0.3721954	0.4051834	0.334832	0.20824865 t		Biliary Glycoprotein, Alt. Splice 5, A
544 Renal	0,3721655	0.405041	0.334695	0,20811312 L49054_at		T(3;5)(q25.1;p34) fusion gene NPM-MLF1 mRNA
545 Renal	0.3720413	0.4050139	0.33458	0.20791422 Y09615_at		Mitochondrial transcription termination factor
				RC /	A1516	
546 Renal	0.3717674		0.334506	0.2078663 /4 at		Carbonic annydrase XII
547 Renal	0.3713738	\circ	0,334488	0.20780845 U34877	ja,	Biliverdin-IXalpha reductase mKNA
548 Renal	0.3713234	0.404668	0.334399	0.2076894 L77213	, or	Phosphomevalonate kinase mRNA
549 Renal	0.3712392	0.4043476	0.334339	0.2076744 D63877	ੜ	KIAA0241 gene, partial cds
						EST: yb96h08.r1 Homo sapiens cDNA clone 79071 5'. (from
550 Renal	0.3712028	0.4042949	0.334237	0.2074576 T61992 at		Genbank)
551 Renal	0.3711499	0.3711499 0.4038581	0.334102	0.20738308 M83088 at		PGM1 Phosphoglucomutase 1
552 Renal	0.3711476	0.3711476 0.4036543	0.334087	0.20734066 D38535_at		PK-120
				U893	U89335_cds	NOTCH4 gene (notch4) extracted from Human HLA class III region
553 Renal	0.370813	0.4035873	0.333797	0.20717373 2_at		containing notch4 (NOTCH4) gene, complete sequence
554 Renal	0.3705376	0.4034331	0.333756	0,20711143 L42354	म	(clone 48ES4) mRNA fragment
555 Renal	0.3704077	0.4033913	0,333635	0.20697162 L02932	, at	PPARA Peroxisome proliferative activated receptor, alpha
				HG2264-		
556 Renal	0.3704044	0.4032013	0,333611	0.20676987 HT2360	at,	Atpase, Ca2+ Transporting, Plasma Membrane 1, Alt. Splice 6
557 Renal	0.3703476	0.4029535	0.333584	0.20668733 X61615	at.	LIFR Leukemia inhibitory factor receptor
EE0 Donol	0.9700002	0.4007500	0 323 456	0.20658544 1100002	÷	M. methyl. D. sensertate recentor modulatory surjust 24 (hNB2A) mBNA
330 NEI IAI	0.010095	- 1	0.335+30	0.20036344 QUEC	1	וארווכנוון אירטים איני וכיכלינט וווסמנומנטן אמממווני בי לוווי בי לי איני איני איני איני איני איני איני
559 Renal	0.3693424	0.4023378	0.333217	0.20655525 U15172_at		Nip1 (NIP1) mRNA
0	7770000		0 000 447	X625	X62515_s_a	IIONA Danday of the second COUST
Sou Reliai	0.3092714	0.4022200	0.333147	0.200433231		Not well expenses associated macrospace protein 1 (might include
700	0.0000046	0 4004050	0 000 7	TKU_A	AZ814	Natural resistance-associated macrophage protein i (migni include
30 1 Nellal	0,30002.10		0.333113	0.2003 133 1 20 a		SERINE/THREONINE, PROTEIN KINASE RECEDITOR R3
562 Renal	0.3684205	0.402086	0 333045	0.206221491117075	te.	at PRECIUSOR
563 Renal	0.3674965		0.333025	0.20611528,103133	∤ત્ત	SP1 Sn1 transcription factor
		_i		HG3492-	1 0	
564 Kenal	0.3672717	0.4019609	0.332862	0.2059/196 H13686	386 at	Uncoupling Protein Ucp
7 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	0.3660784	0.4049544	0.335548	HGZ320-	320-	Integrin Data 3 Cutumit
303 155 101	0.000000	0.4013341	0,335,310	0.2003300031112	10 01	miegimi, pera o odbumi For or 10 10
				RC,	A0131	EST: 2e35e10.51 Soares retina NZD4rtK nomo sapiens CDNA cione 361002 3' similar to contains Alu repetitive element, mRNA
566 Renal	0.3668887	- 1	0.332428	0.20581642 60_at		sequence. (from Genbank)
567 Renal	0.3667753	0.4017219	0.332379	0.2056499 X14766	766_at	GABRA1 Gamma-aminobutyric acid (GABA) A receptor, alpha 1

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FIG. 13W

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568 Renal 569 Renal 570 Renal 571 Renal 572 Renal 573 Renal 575 Renal 576 Renal 577 Renal 578 Renal 580 Renal 582 Renal 583 Renal 586 Renal 587 Renal 588 Renal 588 Renal 588 Renal 589 Renal	0.3666224 0.3661323 0.3661323 0.365499 0.3656006 0.3656009 0.36560929 0.36560929 0.3638237 0.3638237 0.3634948 0.3634948 0.3634397 0.3634992 0.3624992 0.3621294	0.3666224 0.4016691 0.3661323 0.4016309 0.365006 0.4015688 0.3655006 0.4015681 0.3655006 0.401306 0.3655009 0.401306 0.3638237 0.4011016 0.3638237 0.4011016 0.3638237 0.40101267 0.3638237 0.4010126 0.3634367 0.4007189 0.3634397 0.4007189 0.3634397 0.40074182 0.3634992 0.4003435 0.3621728 0.4003039 0.3621294 0.3999643	0.332295 0.332198 0.332139 0.332136 0.33154 0.33154 0.331589 0.331589 0.331589 0.330962 0.330962 0.330614	0.20557608 1.s. at	S a at at at at at at at at at at at at a	
590 Renal	0.3604267	0.3995867	0.330514	0.20367342 M87860 at	U/6369_at M87860_at	Cationic amino acid transporter-28 (ATRC2) mRNA, partial cds GALECTIN-2
591 Renal	0.3602555		0.330468	0.2035/342 M8/860 0.20353624 U01160		GALECTIN-2 Transmembrane 4 superfamily protein (SAS) mRNA
592 Renal 593 Renal	0.3593847	0.399408	0.330393	0.20342363 L43366 at 0.20338346 X89426 at	L43366 at	(clone jj1b) cadherin mRNA fragment
594 Renal	0.3591742		0.33023	0.20327507 M55150 at	A05420 at M55150 at	ENM-1 protein FAH Fumarylacetoacetate
595 Renal	0.3590226	0.3989284	0.330119	0.2031748 U44059	U44059_at	Thyrotroph embryonic factor (TEF) mRNA

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HISTATIN 3 PRECURSOR	Hydroxyindole-O-methyltransferase promoter B-derived (HIOMT) mRNA	FIBRINOGEN BETA CHAIN PRECURSOR	PROS1 Plasma protein S	Evi-1	GYS1 Glycogen synthase 1 (muscle)	GGTB2 Glycoprotein-4-beta-galactosyltransferase 2	MESI3/15=extracellular matrix induced gene [human, endometrial	adenocarcinoma cells HEC1B(L), mRNA Partial, 453 nt]	CGMP phosphodiesterase alpha subunit (CGPR-A) mRNA		Homo sapiens mRNA for KIAA0664 protein, partial cds	FLT4 Fms-related tyrosine kinase 4	Butyrophilin (BTF2) mRNA	0.20193954 U90550_at-2 Human butyrophilin (BTF2) mRNA, complete cds	Insulin-like growth factor II {intron 7} [human, Genomic, 1702 nt]	AA446139_a EST: zw64a03.r1 Soares testis NHT Homo sapiens cDNA clone t	MYL5 Myosin, light polypeptide 5, regulatory		AFFX-CreX-3_at (miscellaneous control - 11k chips)	AFEX-Crex-3 at (endocenous control)		STRESS-ACTIVATED PROTEIN KINASE JNK1	GOT1 Glutamic-oxaloacetic transaminase 1, soluble (aspartate	aminotransferase 1)	POU2F2 POU domain, class 2, transcription factor 2	a EST: zv09a02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753098 5', mRNA sequence. (from Genbank)		Fibrinogen, A Alpha Polypeptide, Alt. Splice 2, E	MAOB Monoamine oxidase B	B-cell receptor associated protein (hBAP) alternatively spliced mRNA, partial 3'UTR
M26665_at	U11090 at	J00129 at	M14338 at	S82592_at	J04501_at	X14085_s_a t		S81893_at	M26061_at	RC_AA4772	52_at	X69878_at	U90550_at	U90550_at-2	S73149_at		L03785 at	AFFX-CreX-	3_at-2	AFFX-CreX-	U35005_s_a	-	1- 007 2014		M30033_s_a t	VA478688	HG2730- HT2827 s a	1	M69177_at	U72512_at
0.20298326 M26665_at	0.20275915 U11090	0.20271072 J00129 at	0.20266162 M14338	0.20251815 \$82592	0.20250145 J04501	0.20243107		0.20233926 S81893	0.20233478 M26061		0.2022664 52_at	0.20220138 X69878	0.20209628 U90550	0.20193954	0.20190722 S73149_at	0.20171547	0.20157892 L03785 at		0.201376233_at-2	AFF) 0.201328593 at		0.20124388 t	7000	0.20110995 M37400 at	0.20114276	0.201048281		0.20096345 t	0.2006801 M69177	0.20059875 U72512
0.33008	0.329961	0.329933	0.329891	0.329794	0.329775	0.329743		0.329671	0.329643		0.329609	0.329528	0.329367	0.3293	0.329231	0.329148	0.32911		0.329077	0.328872		0.32868	22000	0.32000	0.32866	0.328526		0.328512	0.328417	0,328382
0.3989023	0.3988683	0.3987047	0.3986954	0.3984921	0.3983944	0.3981897		0.3980464	0.397913		0.3977703	0.3976313	0.3976313	0.3975459	0.3974564	0.3972337	0.3972125		0.3971468	0.3969357		0.396918	73373060	0.3307007	0.396655	0.3965512			0.3963827	0.3963134
0.3588903	0.3588768	0.3588289	0.358696	0.3586696	0.3581415	0.3580428		0.3580149	0.3579947		0.3577042	0.3576125	0.3574897	0.3574897	0.3573702	0.3572469	0.3571375	i i	0.35/1369	0.3571369		0.3570361	0.3560407	0.0003427	0.3568608	0.3567165		0.3565405	0.3564823	0.3563189
597 Renal	598 Renal	599 Renal	600 Renal	601 Renal	602 Renal	603 Renal		604 Renal	605 Renal		606 Renal	607 Renal	608 Renal	609 Renal	610 Renal	611 Renal	612 Renal	-	old Kenai	614 Renal		615 Renal	616 Donal	01011611	617 Renal	618 Renal		619 Renal	620 Renal	621 Renal

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648 Renal 0.35	0.3516439 (0.3945081	0.325657	DC 0.19848417t	D00408_s_a	CYP3A7 Cytochrome P450 IIIA7 (P450-HFLa)
						The Hilling Holland from Hilman HI A class III region containing
						NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene,
-		76277000	0.325448	0 1984292 4 at	39c_cds	receptor for advanced glycosylation end products (RAGE) gene, and o unidentified cds, complete sequence
		0.0344131	0.323440	0 10823736 \$65921	ta	Anti-colorectal carcinoma light chain
650 Renai 0.35	0.3505/2/	0.3944271	0.32344	0.19023130	Ta	
651 Renal 0.35	0.3505555	0.3943587	0.325403	0.19818567 1_at	ł	Spermidine synthase gene
		0.3941846	0.325397	0.1981264 M55420_at	;ਡਂ	IgE chain, last 2 exons
		0.3940334	0.325159	0.19806585 U29615		Chitotriosidase precursor mRNA
		0,3939528	0.325133	0.19791447 N		Endogenous retrovirus envelope region mKNA (PL1)
				X	യ.	A TOWATE NI ICI EAB EACTOR 4
655 Renal 0.34		0.3938099	0.325121	0.197812081		HEFALOCYTE NOCLERIC ACTORY
656 Renal 0.	.34924	0.3938069	0.324741	0.19773096 X		CALCE Calcito milital and and and
657 Renal 0.34	189599	0.3936937	0.324658	0.19767737 J	, a	Alpha-cardiac actilityetie, or italin and
658 Renal 0.3		0.3936736	0.324583	0.19754806 N		FCGRZA FC fragment of 196, low anning ha, receptor for (55.55)
	186592	0.3935997	0.324583	U 0.19740452 t	164315_s_a	XPF Xeroderma pigmentosum, complementation group F
	486265	i	0.324502	0.19737563 N	196789_at	GJA4 Gap junction protein, alpha 4, 3/KD (connexin 3/)
			770700	1 7020007070	10 4697 24	EST: yj49f04.r1 Homo saplens cDNA dolle 192039 5 : (1971) Gonhank)
Renal 0.3	348592	- 1	0.324341	0.19722337	104021 at	Od hadrin)
	483137	0.3933162	0.324341	0.19712573	(61755_ma s_at	HOX3D gene for homeoprotein HOX3D
						Zh63b01.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens CDINA
						clone 416713 5' similar to SW:ENV1_HUMAN P10267 KE I KOVIKOS- REI ATED ENV POLYPROTEIN. [1] ;contains Alu repetitive element;,
	348135		0.324278	0.19699985	N86690_at	mRNA sequence. (from Genbank)
0	481256		0.324255	0.1969025	K81637 at	CLTB Clathrin, light polypeptide (Lcb)
					1A422123 i	EST: zv26h12.r1 Soares NhHMPu S1 Homo sapteris covidence
	481196		0.324244	0.19680189	at	sequence. (from Genbank)
	477797		0.32423	0.1967391	M55268_at	CSNK2A2 Casein kinase 2, alpha prime polypeptide
	476794		0.324112	0.19671062	_12060_s_at	0.19671062 L12060 s_at RARG Retinoic acid receptor, gamma 1
	07070	1		0.19660585	AA095600_2	AA095600 a L5079.seq.F Fetal heart, Lambda ZAP Express Homo sapleris curvate 5: mRNA sequence. (from Genbank)
	7174140	- 1		200000		ITGA2B Integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex,
669 Renal 0.3	3472509	0.3928621			J02963 at	antigen CD41B)
			0.3498043 0.3498043 0.3489599 0.3489599 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.3486265 0.34876794	0.3497235 0.3938099 0 0.3497235 0.3938099 0 0.34824 0.3938069 0 0.3489599 0.3936937 0 0.3486592 0.3935937 0 1 0.3486592 0.3935937 0 1 0.348135 0.3932594 0 1 0.3481196 0.3932548 0 1 0.3477797 0.3928819 0 1 0.347272 0.3928819 0	0.3498043 0.3939528 0.325133 0.19791447 M	0.3498043 0.3939528 0.325133 0.19791447 M

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					and their wife their time that their
	0.3425638	0.390189	0.321645	0.19407158 U88898 at	Endogenous retroviral H protease/integrase-derived ORF1 mRNA, and nitative envelope protein mDNA martial and
	0.3425187	0.3900869	0		G-profein complete profession in the partial cas
	0.3424706	0.3899632	0		
	0.3424706	0.3898534	10	0.193787111 40904 at	
	0.3423106	0.3898434	0	0.1936889 S67156 at	ASPA Aspartnantiase (aminocalone C reductase core protein ii
	0.3417245	0.3898053	0.321422	0.19365892 D13634 at	KIAA0009 gene
	0.3416438	0.3897854	0.321419	0.193561171105568 at	SLC6A4 Solute carrier family 6 (neurotransmitter transporter,
					Phosphatidylinositel (4.5)hisnbosnhata 5-nhosnhatasa hemelee
	0.3415645		0.321329	0.19342928 U45975 at	mRNA, partial cds
	0.341493		0.321254	0.19333288 U28049 at	TBX2 (TXB2) mRNA
ĺ	0.3414096	0.3896388	0.321122	0.19331224 Z34897 at	HRH1 Histamine receptor H1
	0.3410736	0.3895244	0.32105	X96924 rna 0.19311282 1_at	Gene encoding mitochondrial citrate transport protein
	0.3408606	0.3893557	0.321008	RC_AA4103	EST: zv16e01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
	0.3408184	1	0.321000	0.19501995 57 dt	733810 3, mKNA sequence. (from Genbank)
	0.3406851	1	0.320891		NACA N-acetyigalactosaminidase, alpha- High-sulphur keratin
	0.3405662	0.3889072	0.320834		Bone marrow serine protease gene (medullasin) (leukocyte neutrophil
				000000	EST: zs57g01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
	0.3405135	0.3887257	0.320752	AAZ9Z609_a 0.19265833 t	AAZ9Z609_a IMAGE:701616 5' similar to contains L1.t1 L1 repetitive element ;,
	0.3403084	0.3885924	0.320702	0.19255373 U94332 at	Osteoprotegerin (OPG) mRNA
	0.3401754	0.3884881	0.320585	13	DNA for endodenous retroviral like element
	0.3401473	0.3883623	0.320577	0.19236046 L41268 f at Nkat2b mRNA	Nkat2b mRNA
	0.3396228	0.3882358	0.320564	0.19235238 M19888_at	SPRR1B Small proline-rich protein 1B (cornifin)
	0.3394282	0.3882287	0.320545	M82967_s_a	Agranamal variations and the second s
	0.3394173		0.32052	0.19221435,104982 at	ANT1 Admins angledide to the first of the fi
	0.3392756	0.3881142	0.32047	0.192042631132376 at	Channel associated and discounting (Skeletal muscle)
	0.3392274	0	0.32047	0.19199556 L02867 at	62 kDa parangonlastic antigen mDNA 21 and
	0.3391443	0.387876	0.320259	0.19194852 U02310 at	EKHR Homolog 1 of Discophila forthood (thought
	0.3390824	0.3877849	0.320218	0.19181135 R74226 at	Homo sapiens mRNA for ATP synthase subunit e complete of
	0.3389169	0.3877172	0.320203	0.1917885D37931 at	RNS4 Riboni clases 4 (2' 5' oliopisco dominato e materiale de la constante de
	0.3385291	0.3875441	0.320132	12	ADORA1 Adenosine receptor A1
	0.3384832	0.3875274	0.320112	at	GCK Glucokinase (hexokinase 4, maturity onset diabetes of the young 2)

725 Renal	0.3381861	0.387516	0.320109	0.19156706	M31776_s_a t	BRAIN NATRIURETIC PEPTIDE PRECURSOR
726 Renal	0.3381411	0.387474	0.319641	0.19149089 D50495	J50495 at	Transcription elongation factor S-II, hS-II-T1
727 Renal	0.3376066	0.3873493	0.319621	0.19142161)	<00540 at	PRL Prolactin
728 Renal	0.3375934	0.3872063	0.319383	0.1913378 D30036_at)30036_at	PHOSPHATIDYLINOSITOL
799 Renal	0.337/308	0 3874664	0.240278	A 40420066 +	AA170806_a	EST: ATH322 HTCDL1 Homo sapiens cDNA 5/3', mRNA sequence.
730 Renal	0.3373368		0.319210	0.151250001		(Holli delibatik)
200	0000		0.0 1929	0.191202331	Mossor at	CAL Calibratic alliguiase I
731 Renal	0.3370994	0.3370994 0.3871062	0.319255	0.19114996 HT987 at	15967 - 17987 at	Mac25
732 Renal	0.3368902	0.3368902 0.3869556	0.319213	0.19104853 Y10936 at	/10936 at	Hypothetical protein downstream of DMPK and DMAHP
733 Renal	0.336607	0.3868908	0.319066	0.19091788 M60828 at	460828 at	FGF7 Fibroblast growth factor 7 (keratinocyte growth factor)
734 Renal	0.3363716	0.3868537	0.31895	A 19084176	AJ000099_s	I venenmal hvaluronidasa
735 Renal	0.3363614	4	0.318748	11-1	387464 at	KIAA0274 gene
736 Renal	0.3363575	0.3868076	0.318737	0.19065401 U79275 at	J79275 at	Clone 23947 mRNA, partial cds
737 Renal	0.3362269	0.3362269 0.3866982	0.318688	0.19051167 D28532 at)28532 at	Renal Na+-dependent phosphate cotransporter
738 Renal	0.3362221	0.3866249	0.318597	0.19044842 Z18954 at	718954 at	S100A5 S100 calcium-binding protein A5 (formerly S100D)
						EST: 14c3 Human retina cDNA randomly primed sublibrary Homo
739 Renal	0.3361335		0.318548	0.19039601 W25869	N25869_at	sapiens cDNA, mRNA sequence. (from Genbank)
740 Renal	0.3359634	[0.318464	0.1903145 M37190_at	//37190_at	Ras inhibitor mRNA, 3' end
741 Renal	0.3357193		0.318395	0.19029394 M13903	413903_at	Involucrin gene, exon 2
742 Renal	0.335545	3	0.318357	0.19005889 X98311_at	(98311_at	Carcinoembryonic antigen family member 2, CGM2
743 Renal	0.3354717	0.3862266	0.318192	0.19000942 M91217	491217_at	EST: HUMRTPGEB Homo sapiens cDNA. (from Genbank)
744 Renal	0.3353689	0.3861983	0.318034	0.18990159 M21064	//21064_at	S100A9 S100 calcium-binding protein A9 (calgranulin B)
745 Donol	0.0050000		7007700	1	RC_AA4179	EST: zv94a08.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
/ 45 Keriai	0.3353222	0.3861059	0.31/884	0.18987103 15_at	5 at	767414 3', mRNA sequence. (from Genbank)
746 Renal	0.3352031		0.317837	0.18973076 M83186	//83186 at	COX7A1 Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle)
747 Renal	0.3351668		0.317822	0.18961442 U03056	J03056_at	Hyaluronoglucosaminidase 1 (HYAL1) mRNA
748 Renal	0.3350747	0.3858386	0.317774	0.1895815 C16652	316652_at	KIAA0575 gene product
749 Renal	0.3348722	0.3857617	0.317663	0.18946299 U21049 at	J21049 at	DD96 mRNA
750 Renal	0.334522	0.3857487	0.317626	0.18937667 L13278 at	.13278 at	CRYZ Crystallin zeta (quinone reductase)
751 Renal	0.3344249	0.38567	0.317616	0.18932723 D85939_at)85939_at	P97 homologous protein
752 Renal	0.3343292	0.3852831	0.317545	0.18931971	83513 s at	0.18931971 S83513 s at ADCYAP1 Adenviate exclase activating polyneptide 1 (pituitary)
753 Renal	0.3338736	0.3852434	0.317515	0.18918636 M15990	//15990 at	C-ves-1 mRNA
754 Renal	0.333722	0.3851345	0.317512	0.18913867 X52520_at		TAT Tyrosine aminotransferase
755 Renal	0.3336839	0 3850/34	0 317/108	0.1800185 1405540	7	SLC5A2 Solute carrier family 5 (sodium/glucose cotransporter),
/ 50 1/51 Iai	0.000000		0.317430	0.109010011	, 9.	Member 2

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	_			
0.38498		0.317462	X66894_s_a 0.18888022 t	FACC Fanconi anemia complementation group C
0.3848212		0.317398	0.1888451 M74525_at	UBE2B Ubiquitin-conjugating enzyme E2B (RAD6 homolog)
0.3847713		0,317358	0.18872614 M55422 at	Krueppel-related zinc finger protein (H-plk) mRNA
0.3846266		0.317264	0.18866096 X91249_at	WHITE PROTEIN HOMOLOG
0.3845261		0.317235	0.18854165 W28252 at	EST: 44b5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genbank)
			X17360_rna	
0.3845105		0.317066	0.18840943 1_at	HOX 5.1 gene for HOX 5.1 protein
			RC_AA0246	
0.3842048	-	0.316985	0.18836315 22_at	Solute carrier family 22 (organic cation transporter), member 5
			HG4185-	
0.3841692	_	0.316884	0.18835384 HT4455_at	Estrogen Sulfotransferase, Ste
	_	0.316813	0.18828923 L43576_at	(clone EST02946) mRNA
0.3840097	_	0.316785	0.18804356 U13616_at	ANK3 Ankyrin G
0.38:9233	_	0.316779	0.1880141 M13955_at	Mesothelial keratin K7 (type II) mRNA, 3' end
0.3837909	_	0.316596	0.18791753 Y13153_at	Kynurenine 3-monooxygenase
0.3837041	~	0.316586	RC_AA2566	BEST: zr82h02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
			200000000000000000000000000000000000000	
0.3835922		0.316562	C AA1214 0.1877799 33_s_at	Axin
			U61276_s_	8
		0.316531	0.18770248 t	Transmembrane protein Jagged 1 (HJ1) mRNA
			0.1876624 X13930 f a	0.1876624 X13930_f_at CYTOCHROME P450 IIA6
	_	0.316367	0.18760407 Z11793_at	Selenoprotein P
	_	0.316266	0.18745396 U08316_at	Insulin-stimulated protein kinase 1 (ISPK-1) mRNA
	_	0.316254	0.18742038 U83461_at	Putative copper uptake protein (hCTR2) mRNA
0.382894	-	0.316215	0.18730733 D78367_at	K12 keratin
0.382755	-	0.316039	0.18724056 L20826_at	I-plastin mRNA
			RC_AA0457	
	-	0.315968	0.18714735 75 at	cDNA clone 488675 3', mRNA sequence. (from Genbank)
0.3826714	_	0.315744	0.18708047 U05861_at	DDH1 Dihydrodiol dehydrogenase
0.3825672		0.315628	0.18703298 X74764 at	Receptor protein tyrosine kinase
			X87344 cds	DMA gene extracted from H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14
0.3825566		0.315586	0.18696555 10_r_at	
0.3825398		0.315556	0.18686375 R66239 at	EST: yi34d06.r1 Homo sapiens cDNA clone 141131 5'. (from Genbank)
0.382411	_	0.315533	0.1867733 X52332 at	Homo sapiens mRNA for zinc finger protein 10

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815 Renal	Renal	0.3250527	0.37.90092	0.010012	RC_AA2588	-	EST: zs3zf05.s1 NCI_CGAP_GCB1 Homo sapiens culve civile
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							receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2,
							TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A11,
							TCRBV7S1A1N2T, TCRBV5S1A11, ICRBV1353, ICRBV3511,
							TCRBV/S3AZ1, 10RBV13SZA11, 10RBV6S5A1N1, 10RBV7S2A1N1, 10RBV6S5A1N1,
							TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1,
							TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A11,
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817	817 Renal	0.3248884	0.379554	0.313481	0.184185617_at	7 at	013)
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818	818 Renal	0.3245713	0.3/9505	0.313302	0.1040010	RC AA4002	EST: zu63f03.s1 Soares testis NHT Homo sapiens cDNA clone
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820	820 Renal	0.3244972	0.3244972 0.3793703	0.010294		X98178 s a	-
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						AA129547_e	AA129547 a EST: zn83f01.r1 Stratagene lung carcinoma 937218 Homo saplens
822	822 Renal	0.32402;	0.324023 0.3792115	0.31314	0.183862951	HG721-	CDIVA GIOTE 3041 30 5, 111 41 50 50
						HT4828_s_a	a Chaptrill Alpha Calabitin Alt Splice 3
823	823 Renal	0.323960	0.3239605 0.3791415	0.313056	0.18378769 t	9.1	Placental Protein 14, Elludine In Aprila 2 Committee TELATED
827	824 Renal	0.3239071	1 0.3791073	0.312905		6 U17418 at	PARATHYROID HORMONE/PARATH INCOLORS FOR PEPTIDE RECEPTOR PRECURSOR
87.	825 Renal	0.3238674		0.312847	7 0.18365976 U66048	6 U66048 at	Clone 161455 Dreast expressed minary and a second s
				0 240804	KC_A 0 18360248 65 at	KC_AA2347 8 65 at	Homo sapiens mRNA for KIAA0779 protein, partial cds
82(826 Renal	0.323765	0.37 68433	į	\perp	M57506 m	M57506 rna SCYA1 gene (secreted protein I-309) extracted from Human secreted
82.	827 Renal	0.323732	0.3237325 0.3788541	1 0.312772	2 0.18353726 1_at	61 at	protein (I-309) gene

And Artifaction of the Control of th

828 Renal 829 Renal	0.3235096	L	0.31276	0.18346485 S52028 s 0.18336569 J04168 at	52028 s at 14168 at	0.18336569 J04168 at SPN Sialophorin (gpL115, leukosialin, CD43)
830 Kenal	0.3234051	- 1	0.312723	0.18331559 U66559 at	66559_at	NPM1 Nucleophosmin (nucleolar phosphoprotein B23, numatrin)
०२। एसावा	0.3231022	0.3786236	0.312607	0.18322831 M80482_at	80482_at	PACE4 Paired basic amino acid cleaving system 4
832 Renal	0.3231017	0.3782547	0.31234	RC_A 0.18317835/42_at	RC_AA2438 42_at	EST: zr68a03.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 688524.3° mRNA certience (from Genhank)
833 Renal	0.3230941	L 1	0.312329	0.183041 U68233	38233 at	Farnesol receptor HRR-1 (HRR-1) mRNA
834 Renal	0.323053	0.3779843	0.312322	0.18300988 M16961	E	AHSG Alpha-2-HS-glycoprotein alpha and beta chain
83# 0000	00000		(Ĭ	HG4234.	
836 Renal	0.3230498	0.3777760	0.3123	0.18290968 HT4504	T4504_at	Methylenetetrahydrofolate Reductase
	0.022000	0.0111100	4077100	0.16260931 X16665 at	0	HOXB2 Homeo box B2
837 Renal	0.3228123	0.3776012	0.312187	0.1826765 09	at	C31.2103g03.51 Sodies Infilitive S1 Homo sapiens con clone 668120 3. mRNA semience (from Genhank)
838 Renal	0.3224518	. 1	0.311937	0.18263504 Y10512	0512 at	CD282 protein
839 Renal	0.3223818	0.3775608	0.311927	0.18255305 L27476	7476_at	X104 mRNA
						PSG11 gene (pregnancy-specific beta-1-glycoprotein 11 C-A domain)
				-	1130E ade	extracted from Human pregnancy-specific beta-1-glycoprotein
840 Renal	0.3223707	0.3774489	0.311881	0.1825066 3	3 at	ancinatively spliced C-K, C-S, C-B, and C-A domains (PSG11) gene, partial cds
841 Renal	0.3221953	0.3773829	0.311878	0.18247168 L31573	1573 at	Sulfite oxidase mRNA
0.70		,		<u>D</u> 7	D79206_s_a	
842 Kenal	0.3220803	0.3773496	0.311782	0.18232067 t		SDC4 Syndecan 4 (amphiglycan, ryudocan)
o43 Kenal	0.3220578	0.3772926	0.311689	0.18225133 Z24680	at	Garp gene mRNA
844 Renal	0.3220269	0.3771383	0.311517	0.18218234 1	U82010_ma 1_at	- I farnosv/ltransforms (ΛΟΟΛ)
845 Renal	0.3220007	0.3769856	0.311471	0.18209842 M80783 at	1	R12 profein mRNA
846 Renal		0.3768717	0.311434	0.18203145 L25119		OPRM1 Opioid recentor mu 1
847 Renal	0.3216748	0.3768414	0.31141	0.18196511 J05008 at		EDN1 Endothelin 1 {alternative products}
848 Renal	0.3216395	0.3768202	0.311403	M6 0.18189396 t	M60450_s_a	a KCNA4 Potassium voltage-gated channel, shaker-related subfamily, member 4
849 Renal	0.3215899	0.3768117	0.311391	0.18177405 J05500	at	SPTB Spectrin, beta, erythrocytic (includes sperocytosis, clinical type I)
850 Renal	0.3215417	0.3767574	0.311389	0.18174458 M22632	at	GOT2 Glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
851 Renal	0.3215307	0.3767109	0.311351	0.18164527 U90545	<u></u>	Himan codiim chacabate transporter (NDTA) m DNA
852 Renal	0.321485	0.3767016	0.31127	0.18156762 H42106 at	at	Integrin, alpha 6
853 Renal	0.32148	0.3765091	0.311136	0.18152207 T39897	s at	EST: ya13a11.r1 Homo sapiens cDNA clone 61340 5'. (from at Genbank)

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CCKAR Cholecystokinin A receptor	Hepatocyte Growth Factor Receptor	Beta-2 integrin alphaD subunit (ITGAD) gene, exons 25-30, and	partial cds	Caurelli-13	PIG-B	GS1 PROJEIN	Adrenardio Docutor Data 4	Myosin-IC mRNA	(done PK2J) CDC2-related protein kinase (PISSI RF) mRNA	EST: ab40g02.s1 Stratagene HeLa cell s3 937216 Homo sapiens	cDNA clone 843314 3' similar to SW:SOH1_YEAST P38633 SOH1	PROTEIN. [1];, mRNA sequence. (from Genbank)	GSTalpha locus gene (glutathione S-transferase) extracted from Hisaniens GSTalnha gene for distaltione S-transferase even 2	RC_AA4468 EST: zw90a07.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA	clone 784212 3', mRNA sequence. (from Genbank)	Lysyl oxidase-related protein (WS9-14) mRNA	Rod photoreceptor protein	KIAA0685 gene product	Butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-	butyrobetaine hydroxylase)	EST: ze58g08.s1 Soares retina N2b4HR Homo sapiens cDNA clone 363230 3', mRNA sequence, (from Genbank)	EST: zw66d10.s1 Soares testis NHT Homo sapiens cDNA clone	781171 3', mRNA sequence. (from Genbank)	OS-9 precurosor mRNA	PAH Phenylalanine hydroxylase	G-protein beta-3 subunit alternatively spliced form mRNA sequence			Tumor Necrosis Factor Receptor 2 Associated Protein Trap3	SP2 Sp2 transcription factor	HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR	KIAA0277 gene
U23430_s_a	HG4272- 0.18131775 HT4542_at	0.404047001140020	0.10121792 040279 at	- 31		0.18101196 M86934 at	HG/59- 0 1809933 HT759 s at	0.18090326 U14391 at	0.18078479 X78342 at		RC_AA4859	0.100/ /04 45 at	X65/2/_cds 0.180642 2 s at	RC_AA4468	0.18062116 64 at	0.18054211 U89942 at	0.18050478 D63813 at	_	A4559		0.18025285 77_at	AA4462		_at	0.18005013 L47726 at	0.17992719 U47931 at	1	HT5108_s_a		at	at	· 0.17972697 D87467 at
0.311073	0.310871	0.340844	0.310834	0.310234	0.310723	0.310012	0.310594	0.310562	0.310536		0 310300	0.0 10092	0.310318		0.310294	0.310293	0.31022	0.310181	0 040004	0.310064	0.31005		0.310019	0.309877	0.309848	0.309787		1	0.309735	0.309705	- 1	0.309553
0.376478	0.3764677	0.3206912 0.3763970	0.3206495 0.3763746	0.376322	19		0.37609	0.3760622	0.376054		0.3760118		0.3759757	1	0.3757326	0.3756543	0.3756371	0.3755995	0.3755749	0.57.007.45	0.3755262	1	0.3/53666	0.3752924	0.3751264	0.3750943		1	0.3749907	0.3749606	0.3749298	0.3748428
0.3213351	0.3207556	0.3206912	0.3206495	0.3206473	0.3204515	0.02020.0	0.3203024	0.3200921	0.3197577		0.3195469	2010	0.3195258		0.319335	0.3192502	0.3190333 0.3756371	0.3187402 0.3755995	0 3487480	6017016.0	0.3186964	0000			0.3181113	0.3180274		77	-			0.3173252
854 Renal	855 Renal	856 Renal	857 Renal	858 Renal	859 Renal		860 Renal	861 Renal	862 Renal		863 Renal		864 Renal		865 Renal	866 Renal	86/ Kenal	868 Renal	869 Renal	1000	870 Renal	074 Dane	0/ I Kellal	012 Kenai	8/3 Kenal	874 Renal		0.20	8/5 Kenal	8/6 Kenal	87/ Kenal	8/8 Kenal

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors The party party party program and party party party party of the party party of the party party of the party party of the party part

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KIAA0735 gene product	Rab 13	HRX-like protein	SP-10=intra-acrosomal protein {alternatively spliced} [human, liver, Genomic 2330 nt 4 segments]	GAGE4 C antions 6 (CAGE 6)	Putative envelope protein; orf similar to env of Type A and Type B	retroviruses and to class II HERVs gene extracted from Human	Cookers cus endogenous retrovirus HERV-K(HML6) proviral clone HML6.17 2_at putative polymerase and envelope genes, partial cds, and 3'! TR	EST: zu67c08.r1 Soares testis NHT Homo sapiens cDNA clone	Actin-like peptide mRNA, partial ods) bottom on	Protein kinase mitogen- activated 13	Enhancer of filamentation (HEF1) mRNA	Weningloma-expressed antigen 6 (MEA6) mRNA	FST: 2655h02 21 Community and All Libert Source Gene	362859 3', mRNA sequence. (from Genbank)	SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC	X123 MRNA 3' and	CCKRP Chologophinis B compa	ALDR1 Aldehyde reductase 1 (low Km aldose reductase)	0.17839879 Y10514_s_at CD152 protein	RC_AA4781 EST: zt89d04.s1 Soares testis NHT Homo sapiens cDNA clone 09 at 729511.3' mRNA sequence (from Genhank)	EST: zt74c07,s1 Soares testis NHT Homo sapiens cDNA clone 728076 3' mRNA sequence (from Genhank)	EST: zu27d04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 739207 3', mRNA sequence, (from Genbank)	0.17811115 S81243 s. at Mitogen inclined minlear ormban recentor (MINIOD) would	ITGA7 Integrin, alpha 7B	ACY1 Aminoacylase 1
RC_AA0197 12_at	X75593_at	Y08836_at	S65583_rna 1 at	U19147_s_a		1160260 242	Cookson cus	96083_a	0.1791224 U20582 at	AF004709_a			П	10			T	Т		Y10514_s_at	RC_AA4781 09 at	A3986	A4213	S81243 s at 1	X74295_at	
RC 0.17957157 12	0.17953223 X75593_at	0.17948665 Y08836	S65E 0.17935655 1 at	0.17929961			0.17923063 2_at	0.17915723	0.1791224	001001100	0.17904094	0.17893082 L43821 at	0 17881872 1120700 at	7,0100	0.17870833 28 at	0.17860527 M29550 at	0.17856164127479 at	0.17851286 D13305 at	0.17843656 X15414_at	0.17839879	RC_A 0.17832921 09 at	0.1782679117 at	RC_A 0.17817846 28_at	0.17811115	0.17804714 X74295_at	0.17800939 L07548 at
		0.309452	0.3094	0.309376			0.309313	0.309042	0.309029	000000	0.309026	0.308974	0.308877		0.308862	0.308773	0.30861	0.308551	0.308387	0.308318	0.308138	0.308056	0.308001	0.307969	0.307931	0.307893
0.3746559	0.317229 0.3745456	0.3745335	0.3744883	0.3744513			0.3744192	0.3743021	0.3742907	0.9749464	- 1	0.3740406	0.3739548		0.3739328	0.3739106	0.3737858	0.3737568	0.3737403	0.3737167	0.3736674	0.3734426	0.3734426	0.3731026	0.3730821	0.3728358
0.3172932	0.317229	0.3170421	0.3167754	0.3167454			0.3165341	0.316432	0.3163941	0.3163636	0.3160904	0.3157753	0.3157056		0.3156739	0.3156673	0.3156299	0.3156226	0.3155973	0.3154658	0.31527	0.3147596	0.3147498	0.3146823	1 1	0.3145042
879 Renal	680 Renai	881 Kenal	882 Renal	883 Renal			884 Renal	885 Renal	886 Renal	887 Renal	888 Renal	889 Renal	890 Renal		891 Renal	892 Renal	893 Renal	894 Renal	895 Renal	896 Renal	897 Renal	898 Renal	899 Renal	900 Renal	901 Renal	902 Kenal

E=h

904 Renal

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. AA486144_a | EST: ab14c10,r1 Stratagene lung (#937210) Homo sapiens cDNA MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR Fatty acids omega-hydroxylase (cytochrome P-450HKV) PLASMA RETINOL-BINDING PROTEIN PRECURSOR Skeletal muscle alternate 5'end of gene Kir4.2 5'UTR Platelet-derived growth factor (PDGFA) A chain gene Synuclein, gamma (breast cancer-specific protein 1) clone 840786 5', mRNA sequence. (from Genbank) AGOUTI SWITCH PROTEIN PRECURSOR TYROSINE-PROTEIN KINASE ITK/TSK ZNF8 Zinc finger protein 8 (clone HF.18) PIGF Phosphatidylinositol glycan, class MCC Mutated in colorectal cancers 40S RIBOSOMAL PROTEIN S17 GHR Growth hormone receptor Adrenergic Receptor, Alpha 1b Tyrosine kinase (Tnk1) mRNA Clone 14.9B mRNA sequence Alpha(1,2)fucosyltransferase KIAA0033 gene, partial cds Atpase, Cu2+ Transporting Mdm2-E (mdm2) mRNA Serotonin receptor gene 0.1762679 D25278_at-2 KIAA0036 gene product Homeotic Protein P12 0.17618574 D25278 at KIAA0036 gene KIAA0384 gene P0071 protein HT4369_s_a AB002382 a HT3281_s_a AF010126 a U33203_s_a D13720_s_a M19989 cds D13705_s_a 0.1773265 HT2921_at 0.17775387 D13644 at 0.17767093 M62397 at 0.17701097 U82321_at 0.17700393 D13435 at 0.17689146 M29581 at 0.1767205 U12775 at 0.17787024 U43408_at 0.17681238 U17894 at 0.17661725 M83181 at 0.17631018 D26067 at 0.17770758 X06562 at 0.17746572 X81889 at 0.17647257 Y13896 at 0.17741957 X00129 at 0.1765033 L11066 at HG2810-HG4099-HG3105-0.1776357 1 at 0.17685159|t0.17641173 0.17706026 0.17725606 0.17715439 0.1771518 0.17796813 0.17737001 0,306515 0.306986 0.306776 0.30662 0.30776 0.307536 0.307505 0.307432 0.307384 0.307282 0.307193 0.307193 0.307193 0.307105 0.307095 0.307017 0.307014 0.306944 0.3116399 0.3714059 0.306935 0.306906 0.306854 0.306793 0.306665 0.307692 0.307468 0.307709 0.307577 0.3116437 0.3715609 0.3120605 0.3715673 0.311444 0.3712415 0.3109215 0.3709673 0.3109215 0.3708851 0.3708255 0.3129149 0.3719544 0.3123357 0.3716208 0.3116071 0.3713586 0.3107315 0.3708629 0.3134645 0.3721453 0.3131843 0.3720278 0.3131683 0.3719966 0.3128205 0.3718598 0.3126757 0.3716984 0.3712336 0.372343 0.3136922 0.3722629 0.3135428 0.3721944 0.3124899 0.3716931 0.3141209 0.3724626 0.3722902 0.3144387 0.3727079 0.3143961 0.3726792 0.3142912 0.3726561 0.3722901 0.3107315 0.3137688 0.3138284 0.3137447 0,3111227 920 Renal 921 Renal Renal Renal Renal Renal 926 Renal 927 Renal 928 Renal 929 Renal 905 Renal 906 Renal 907 Renal 910 Renal Renal 913 Renal 914 Renal 915 Renal 916 Renal 917 Renal 918 Renal 919 Renal 922 Renal 923 Renal 924 Renal

Docket No.:

2825.2020-002

Docket No.:	2825.2020-002
Title: Gene	tic Markers for Tumors
Inventors: Sr	ridhar Ramaswamy, et al.

930 Renal		0.3105735	0.3707206	0.306423	L	0.17611796 M29194 at	IPC I mage hanatic
931 Renal		0.3105734	0.3707047	0.306356		0.17603756 M68840 at	MAOA Monoamine oxidase A
932 Renal		0.3105623	0.3706407	0.306172	RC 0.17597857 35	RC_AA0051 35_at	EST: zh95e02.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429050 3' similar to contains MER10.t3 MER10 repetitive element;, mRNA sequence. (from Genbank)
933 Renal		0.3104093	0.3705502	0.306064	HG908- 0.17592363 HT908	HG908- HT908_at	Mg61 Protein (Gb:L08239)
934 Renal		0.3103851	0.3704681	0.306034	0.175889514	L44140_cds 4_s_at	DNL1L gene extracted from Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase
935 Renal		0.3103216	1 1	0.305884		L28957 at	CHOLINEPHOSPHATE CYTINYI YI TRANSEEDASE
936 Rena		0.3101899		0.30585	0		PDK4 Pyruyate dehydrodenase kinase isoenzyme 4
93/ Kena		0.3101041	0.3702519	0.305746	0.17555682 M14764	M14764 at	NGFR Nerve growth factor recentor
						HG4535-	
938 Renal		0.3098607	0.3701085	0.305717	0.17551242	HT4940_s_a t	Dematin
939 Renal		0.3098414	0.3700652	0.305688	0.1754223 X07876	X07876_at	WNT2 Wingless-type MMTV integration site 2, human homolog
940 Renal		0.3095872	0.3700644	0.305665	0.17539027 X69111	X69111_at	ID3 Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
941 Renal		0.3093972	0.3700363	0.305595	0.17534581 W25607	W25607 at	EST: zc64c06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 327082 51 mRNA sequence (from Goobset)
942 Renal		0.3093758	0.3700361	0.305508	0.4753404	jj ,	Yj03b09.r1 Homo sapiens cDNA clone 147641 5' similar to gb:X54156 ma1 CELLULAR TUMOR ANTIGEN P53
0.40		1			1000	ואואון	EST: 39e2 Human retina cDNA randomly primed sublibrary Homo
943 Kena		0.3091755	0.3699523	0.30549	0.17527272 W27857_at	W27857_at	sapiens cDNA, mRNA sequence. (from Genbank)
944 Renal		0.3090769	0.3698397	0.305422	RC_A 0.17520563 75 at	RC_AA2438 75 at	EST: zr65f01.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 668281 3' mRNA sequence (from Ganhank)
945 Renal		0.3089404	0.369783	0.305378	0.17514792 U75968	U75968 at	CHL1 protein
946 Renal		0.3088788	0.3696925	0.305351	0.17510456	X55005_rna 1_at	C-erbA-1 mRNA for thyroid hormone recentor alnha
947 Renal		0.3087453	0.3696863	0.305342	0.17500173	M10051_s_a t	INSR Insulin receptor
948 Renal		0.3086598	0.3695467	0.305278	0.17494278 L37036 s	.37036 s_at	at NEUTROPHIL ACTIVATING PROTEIN ENA-78 PRECLIRSOR
949 Renal		35495	0.3085495 0.3694697	0.305209	0.17488225 U40990 at	J40990 at	Putative voltage-gated potassium channel (KVLQT1) mRNA, partial cds
950 Renal		0.3085351	0.3693803	0.30509	0.17485693 U03851	T	Capping protein alpha mRNA. nartial cds
951 Renal		0.3084908	0.3693143	0.304915	RC 0.17478639 47	AA4195 at	EST: zv04a05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 752624 3', mRNA sequence. (from Genbank)

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SOZ Kella	2	0.3082287	0.3092446	0.304905	0.17471132 M21494 at	M21494_at	CKM Creatine kinase, muscle
953 Rena		0.307682	0.3691434	0.304856	0.1746515 L77563	L77563_at	DGS-F partial mRNA
954 Renal		0.3076604	0 3601105	0.304664	0 47467594	AA481218_a	
955 Rena		76124		0.304021	0.174573511	1 115782 at	COTES Clouded etimilation factor 21 no DNA withink 2 77/0
		1	01100000	0.00	0,11104100		COLL S CIERARDE SUITINIANON FACION, S PIE-KINA, SUDUIN S, LIKD
956 Renal		0.3072784	0.3690038	0.304543	RC 0.1744418.00		EST: zr49c02.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 666722 3' similar to TR:G469478 G469478 SM-20.; mRNA
957 Rena		0 3074842		0.004040	0.1744410		sequerice. (irom Genbank)
		20	0.3000 10	0.304300	U. 1744U3U7 U47U54	04/054 at	Putative mono-ADP-ribosyltransferase (htMART) mRNA
958 Renal		0.3068606	0.3687052	0.304354	0.17432237 X58288	X58288_at	PTPRM Protein tyrosine phosphatase, receptor type, mu polypeptide
959 Renal		0.3066514	0.3686282	0.304293	0.17432237 U27699	U27699_at	SODIUM- AND CHLORIDE-DEPENDENT BETAINE TRANSPORTER
960 Renal		0.3065192	0.3684268	0.304155	0.1742837	M14777_s_a t	
961 Rena		0.306422	0.3683979	0.304003	0.17423628 D29963	D29963 at	Platelet-endothelial tetraspan antigen 3 mRNA
962 Renal		0.3063225	0.3683672	0.303971	0.174094661	U64573_s_a t	
062 Donal		97308060	0 0000	7.000	01007 1170		EST: yo79e01.r1 Homo sapiens cDNA clone 184152 5'. (from
964 Rena		0.3002330		0.303843	0.1740339 H30778		Genbank)
		07000	0.500050	418606.0	0.17400722 023338	725559 at	NIAAUU4U gene
965 Renal		0.3058895	0.3680263	0.303869	0.173884691.34820	34820 at	NAD+-dependent succinate-semialdehyde dehydrogenase (SSADH)
						11 -	Tronomyosin Alpha Muscla Alt Salica 2 Skalatal Muscla
966 Renal)58102	0.3058102 0.3679665	0.303842	0.17375073 HT2538	TZ538_at	(Fibroblast)
967 Renal		0.3057534	0.3677768	0.303838	0.17372268 U31986	J31986_at	Cartilage-specific homeodomain protein Cart-1 mRNA
968 Renal		0 305674	0.357780	7778080	0.47969664	X91196_s_a	4 A T
969 Renal	0	0.3056506	0.367559	0.303699	0.17356342 X13067	X13967 at	E 14 aliu A-1 pluellis I E 1 aukamia inhihitan fadar (Abaliaaria differentiation fadar)
970 Renal			0.3675534	0,30344	0.17350143 D90084	- 11	PDHA1 Pyriwate dehydrogense (linoamide) alaha 1
971 Renal				0.303412	0.17344938 X66417	It.	KAPPA CASEIN PRECURSOR
972 Rena				0.303397	0.17336708 U17714 at	J17714 at	Putative tumor suppressor (SNC6) mRNA
973 Rena		0.3051603	0.3673614	0.303223	0.17330551 M35198 at	M35198 at	Integrin B-6 mRNA
1						RC_AA3581	EST: EST66987 Fetal lung III Homo sapiens cDNA 3' end, mRNA
974 Renal		0.3050692	0.3672248	0.303078	0.17319436 47	47_at	sequence. (from Genbank)
975 Renal		50264	0.3050264 0.3672186	0.303039	0.17315984 D13969	J13969_at	DNA-BINDING PROTEIN MEL-18
976 Renal			0.3671365	0.302964	0.17313407 X79439	K79439_at	Notch 3 DNA sequence
977 Renal		0.3049178	0.3669319	0.302936	0.1730334 M25629_at	//25629_at	Kallikrein mRNA, clone clone phKK25
978 Renal		0.3049066	0.366839	0.302917	0.17294593	J04809_ma1 _at	Cytosolic adenylate kinase (AK1) gene

The state of the s

	Transcription Factor Met? Alt Solice 2	Death domain containing profein CRADD mRNA	Acetolactate synthase homolog mRNA	Methylmalowl-CoA mitasa (MCM) mbnia	IKBL mRNA	Dopamine D1A recentor dene complete exon 1 and exon 2 5, and	Unknown gene extracted from Human HLA class III region containing	receptor for advanced glycosylation end products (RAGE) gene, and 6	Uniderfulled das, complete sequence	Doe of the control of	GUCTA2 Guandate exclase 1 soluble alpha 2	EST: Human mRNA sequence containing Alu repetitive elements.	(from Genbank)	MYO54 Myosin VA (heavy notymentide 12 myosin)	MDS1B (MDS1) mRNA	M20747_s_a SLC2A4 Solute carrier family 2 (facilitated glucose transporter), member 4	GABPA GA-binding protein transcription factor, alpha subunit (A001)	F variable segment 5' to antithrombin III gene (AT III)	EST: 43h11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA, mRNA sequence, (from Genbank)	CLU Clusterin (complement lysis inhibitor; testosterone-repressed prostate message 2: apolipoprotein J)	Squamous cell carcinoma antigen 2 (SCCA2) mRNA	CELL SURFACE GLYCOPROTEIN MUC18 PRECLIRSOR	CÇAAT BOX-BINDING TRANSCRIPTION FACTOR 1
HG4668-	113003_s_d	at	ät	M65131_rna 1_at	X77909 at	M85247 at		36_cds	ŧ	Шa	at		ਜ਼ _ਾ ਜ਼					1	0.17177361 W28229 at		U19557_s_a t	M28882_s_a t	
,	0.172899471	0.17287736 U84388	0.17278095 U61263	0.17272903 1 at	0.17265637 X77909	0.17258646 M85247		U893	0.17247929 U37251	X63E	0.17231564 Z50053	0.0000000000000000000000000000000000000	0.17225973 U51704	0.172133831.19401 at	0.1721126	0.17206554	0.17202441 U13044 at	0.17192478 X00237_at	0.17177361	0.1717327 M63379	0.17169896	0.17163287	0.17160499 X12492 at
	0.302917	0.302887	0.302865	0.302772	0.302751	0.302667		0 302625	0.302574	0 302574	0.302536	270000	0.302375	0.302309	0.302209	0.302098	0.301988	0.301944	0.301922	0.301869	0.301818	0.301776	0.301723
	0.3667952	0.3667437	0.3664827	0.3664717	0.3663333	0.3662105		0.3662004	1	0.3660156	0.3659922	0.3650600	0.3657061	0.3656631	0.3655565	0.3654885	0.3654729	0.3654238	0.3653984	0,3653928	0.3653437	0.3653304	0.3653186
	0.3046137	0.304464	0.3043042	0.3042852	0.3042667	0.3041199		0.3041064	0.3037222	0.303679	0.303647	0.3035386	0.3033458	0.3032986	0.3030077	0.3030002	0.3029182	0.3029045	0.3028929	0.3026291	0.3025326	0.3019649	0.3019368
	979 Renal	980 Renal	981 Renal	982 Renal	983 Renal	984 Renal		985 Renal	986 Renal	987 Renal	988 Renal	080 Renal	990 Renal	991 Renal	992 Renal	993 Renal	994 Renal	995 Renal	996 Renal	997 Renal	998 Renal	999 Renal	1000 Renal

FIG. 13N

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

DNA for cellular retinol binding protein (CRBP) exons 3 and 4 0.4906163 t 0.8014274 0.7546642 0.655026

FIG. 14A

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Docket Inc.. 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Uterus 2 deno	A SI	0.7885609	0.7049133	0.609112	0.45793012 X63187_at		HE4 mRNA for extracellular proteinase inhibitor homologue
Uterus 3 deno	A SI	0.7596874	0.6836953	0.58733	0.4409759 U19718	U19718_at	MFAP2 Microfibrillar-associated protein 2
Uterus_4 deno	A St	0.7034049	0.6724176	0.569706	0.4280845 t	HG2815- HT4023_s_a t	HG2815- HT4023_s_a Myosin, Light Chain, Alkali, Smooth Muscle (Gb:U02629), Smooth t
Uterus 5 deno	JS A	0.7029994	0.6652874	0.557462	0.41891643 U71207 at	U71207 at	Eyes absent homolog (Eab1) mRNA
Uterus	A St					8	
6 deno	A S	0.6847081	0.6558477	0.548483	0,41156512 08 at	08 at	cDNA clone 503374 3', mRNA sequence. (from Genbank)
7 deno		0.6783209	0.6473196	0.544136	0.40528116 X03635_at	X03635_at	ESR Estrogen receptor
Uterus 8 deno	A SI	0.6780892	0.6394708	0.537258	0.39963865	M97676 at-2	0.39963865 M97676 at-2 Msh (Drosophila) homeo box homolog 1 (formerly homeo box 7)
Uterus	A SI						MSX1 Msh (Drosophila) homeo box homolog 1 (formerly homeo box
9 deno		0.6780892	0.63345	0.532624	0.3945808 M97676	M97676 at	()
Uterus_ 10 deno	AS. A	0.6749753	0.629061	0.527834	HG4058- 0.3909843 HT4328_at	HG4058- HT4328_at	Oncogene Am11-Evi-1, Fusion Activated
Uterus_	A_sn	0.69569.0	:	0.000	000000000	X98833_ma	7:00 11 11 11 11 11 11 11 11 11 11 11 11 1
o dello		0.0350329	0.021/121	0.52485	0.38738698 1 at	1 at	Zing ringer protein, risari
Uterus_ 12 deno	JS_A	0.6193135	0.622245	0.521983	0.38387653 X65724_at	X65724_at	NDP Norrie disease (pseudoglioma) protein
Uterus	US_A					AF005037_a	
13 deno		0.6115471	0.6184411	0.517686	0.3806994		Secretory carrier membrane protein (SCAMP1) mRNA
Uterus 14 deno	US_A	0.6094357	0.6157311	0.514617	0.37791827 U22398 at	U22398 at	Cdk-inhibitor p57KIP2 (KIP2) mRNA
Uterus	A Su	1					
ouap ci		0.00/10/93	0.011495	60021.0.0	0.3752558 U8448/ at	U8448/ at	CA3C chemokine precursor, mkina, alternatively spliced
Oterus_ 16 deno	A C	0.6031231	0.6084949	0.508376	0.37256134 X13839 at	X13839 at	LCAT Lecithin-cholesterol acyltransferase
Uterus_17 deno	NS A	0.5878692	0.6043285	0.505912	0.3704882 M29277	M29277 at	CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR
Uterus 18 deno	US A	0.5859218	ľ	0.50366	0.36809826 D11151 at	D11151 at	EDNRA Endothelin receptor type A
Uterus 19 deno	us A	0.5841683	0.5993426	0.50194	0.36599654	X03794 s_a	HOXB5 Homeo box B5 (2.1 protein)
Uterus 20 deno	us_A	0.5811234		0.499428		U40271_s_a t	PTK7 Protein-tyrosine kinase 7

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Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

			H. Auth	T. And dad H. and dad		
Uterus_A				R 800000	C_AA4769 E	RC_AA4769 EST: zu38e07.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
- 1	0.5789183	0.5938608	0.497127	0.3617493844 at		CIONE 140232 3, IIININA SEQUENCE. (ILOM CENTERM)
Uterus_A	0.578205	0.5909106	0.495523	0.35991812 M61906 at		SUBUNIT
Uterus A				A	α,	
23 deno	0.5779814	0.5893356	0.493304	0.3580341 t)	GLIA MATURATION FACTOR BETA
Uterus_A]	000	0000	107770M 90100700	†	DAM Dowlidydyding alpha-amidaling monooxydenase
24 deno	0.5/12/14	0.5886418	0.490790	0.3300400 10	ซี	Awi Tepinajigiyano apna amaanig moraga
1	0.5687109	0.5881904	0.489792	0.3543079 M11433_at		RBP1 Cellular retinol-binding protein
Uterus A 26 deno	0.5675042	0.5866073	0.487726	0.3526019 L06419_at		PLOD Lysyl hydroxylase
Uterus_A deno	0.5631672	0.5845363	0.485729	0.3512763 X06614 at		Receptor of retinoic acid
Uterus_A 28 deno	0.5605159	0.5819351	0.482978	0.34989554 U09210_at		SLC18A3 Solute carrier family 18 (vesicular acetylcholine), member 3
Uterus_A	0.5587613	0.5801027	0.481242	0.34846714 X57766_at		PSG11 Pregnancy-specific beta-1 glycoprotein 11
Uterus_A		0.5795479	0,480028	0.34698954 X66945 at		FGFR1 Basic fibroblast growth factor (bFGF) receptor (shorter form)
Uterus A	+			IL.	0	RC_AA1490 EST: zl46b12.s1 Soares pregnant uterus NbHPU Homo sapiens
	0.5411475	0.5774937	0.479182	0.34542534 51_at		cDNA clone 504959 3', mRNA sequence. (from Genbank)
Uterus_A	0.5400556	0.5752281	0.476929	0.34430408 t	M24122_s_a t	MYL3 Myosin, light polypeptide 3, alkali; ventricular, skeletal, slow
Uterus A			0.478487	X0444E	X04445_ma 1 s at	InhA gene exon 1 (and joined CDS)
Uterus A			0.475155	0 34153652 t	X57351_s_a	RPS3 Ribosomal protein S3
	7100000					Unknown gene extracted from Human HLA class III region containing NOTCH4 gene, partial sequence, homeobox PBX2 (HPBX) gene,
Uterus_A	0.5336916	0.5701175	0.473583	0.34040645 7_at	336_cds	receptor for advanced glycosylation end products (RAGE) gene, and 6 unidentified cds, complete sequence
Uterus A		,	0.47246	0.3393251 U65011	U65011_at	Preferentially expressed antigen of melanoma (PRAME) mRNA
Uterus A	0.5303065	0.5678923	0.471609	0.33834442 X95876	X95876_at	G-protein coupled receptor
Uterus A	4 0.5295582	0.5676312	0.470674	0.3373514	D43772_at	Squamous cell carcinama of esophagus mklvA lof GKD-7 3112 domain protein
S	A 0.52907	0 5675115	0.469849	0.33613598	D26561_cds 2_at	ORF for E6 protein gene extracted from Human papilioniavirus on genome integrated into human carcinoma DNA
20120	0.070	•				

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A						
59 deno	0.494047	7 0.5464213	0.452428	0.3190701	AB000449_a	VRK1
Uterus A 60 deno	0.4938313	0.545815	<u> </u>		HG2190-	Caracter and Colored and Color
Uterus_A	-				ווולבטט מו	Orystamin, Deta 53 (50.X15144)
- 1	0.493098	3 0.5443705	0.451477	0.3176218	0.3176218 S81914 at	EX-1
Uterus_A 62 deno	N 0 4930396	0 5444296	0.454067			
Uferus A		f	2		0.31/03/4 L41351 at	Prostasin mRNA
İ	0.4914521	0.5429288	0.44993	RC_A 0.31620046 41_at	KC_AA3941	RC_AA3941 EST: zt49f05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
Uterus_A					5	Gold (2007) 3, IIIKIVA Sequence. (Ifom Genbank)
64 deno	0.4908763	0.5424645	0.449569		0.3158707 M26880 at	UBA52 I Biquitin A-52 racidus ribocomo arctain facilis
Uterus_A 65 deno	0.4905528	0.5420473	0.449265			GSN Geleptin (converted control of the control of t
Uterus_A		1	1		_	ody odbolin (dili)(didosis, Fillilish type)
	0.4882318	0.5410122	0.4488	0.31429195 t	1	RPL32 Ribosomal protein L32
67 deno	0.4876482	0.5403776	0.44799	0.31386706	0.31386706 U15131 at	HTS1
Uterie A					HG3342-	
	0.4874155	0.5394405	0.447206	0.313191951	113519_s_a	
Uterus_A	-	1				
	0.4860205	0.5388785	0.446016	0.3126637	0.3126637 X90908 at	Ileal linid hinding protein mRNA
Uterus_A					N71513 s a	N71513 s a EST: vw32h09.r1 Homo saniens cDNA clone 253085 5' (from
/U deno	0.4841321	0.5383306	0.445569	0.312083071	1	Genbank)
1	0.4841264	0.5370155	0.445193	0.31147408 M95787 at		22kDs ermooth muscle protein (CNISS) - DNA
Uterus_A	0.4835203	0 500000	1007		NB000450_a	CENCO OFFICIAL (SINGE) HIRINA
Uterus A	70700010	- 1	0.444037	0.3110561/1	10004	VRK2
	0.4826925	0.534344	0.444267	0.31066507 33 s at	365	Frontronic viral integration site 4
Uterus_A	0.4022020	1		-	5 a	Total of the state
Uterus A	0.4023329	0.5338963	0.443608	0.31011337	+	DNA for H4 histone
	0.4802965	0.5334052	0.443057	0.3095204	0.3095204 U68385 at 1	Meist-related protein 2 (MBC2) mBNA
Uterus_A						resolucione processi z (withoz), sirving, parual cus
- 1	0.47686	0.532887	0.442853	0.30924416 X64707_at		60S RIBOSOMAL PROTEIN L13
deno	0.4761102	0.5325905	0.442243	0.30867124 at	393164_s	Mammaglobin 2

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

FIG. 14E

78	Uterus_A deno	0.4757585	0.5318888	0.441369	0.30804583 273478	Y73/78 of	UDTDA ACTUA
70	Uterus A	┼	1			AB000897_a	
2	Uterus A		1807166.0	0.441369	0.30752692	1	Cadherin FIB3, partial cds
80	deno	0.4726467	0.5311901	0.440723	0.3069651	A/3005_S_d	AMB2 I amining hote 3 (Inmining C)
	Uterus_A	├	1				LAWIDZ Lahilinin, Deta Z (laminin S)
81	deno	0.4698234	0.5305458	0.440097	0.30624396 M85289 at		HSPG2 Henaran sulfate professionan
C	Uterus_A		!			1	is of reparent salicate protecting
Z Z	- 1	0.4687507	0.5304906	0.439276	0.3057988	0.3057988 X01703 at	Alpha-tubulin mRNA
83	Uterus_A	0.4685047	0 5900977	0.00000			
3	Uterus A			0.439009	0.30532092 006155	at	Chromosome 1q subtelomeric sequence D1S553
84 (1 1	0.4679755	0.5295302	0.438081	0.30494124 66 s at	4α	Homo eanians homoshov A44 (UOVA44)
85.0	Uterus_A 85 deno	0 4661969	0 5290954	0.497072	N TOOTEON	sa	capital strained and records ATT (TICAATT) gene, complete cas
-	Uterus A	+			0.30438073	140000	MYL1 Myosin light chain (alkali)
98		0.4630819	0.5285833	0.436526	0.30407998	40369_ma	Spermidine/enermine N4 and throughous (COAT)
	Uterus_A		1			5	oponimento por mine INI-acciviu ansierase (55A1) gene
87 (0.4607104	0.5269665	0.43646	0.3036926	0.3036926 D42123 at	ESP1/CRP2
388	Uterus_A 88 deno	0.4566061	0.5265443	0.435804	U 30324002 4	22970_rna	6-16 gene (interferon-inducible peptide precursor) extracted from
	Uterus A				2000-0	ם מו	riunan interreron-inducible peptide (6-16) gene
88	1	0.4551983	0.5255779	0.435288	0.30284992 302947	s at	SOD3 Superoxide dismutase 3 extracellular
	Uterus_A					cds	יייי ביייי ביייי ביייי ביייי בייייי בייייי בייייי בייייי ביייייי
8	1	0.4551933	0.5252157	0.43494	0.30238762 s at		Laminin gamma? chain gene (1 AMC2)
	Uterus_A						
910	ı	0.4549561	0.5250371	0.433915	0.30181777 L03411	S	at RD Radin blood group
99	Uterus_A	0.4545004	0 5048400	40007			Jan. C
7	Uterus A	16000+0+.0	0.3240432	0.43334	0.30125198 D86975_at	- 1	KIAA0222 gene
93 d		0.4530377	0.5247809	0.433075	0.3009687 U49260 at		Mevalonate nyronhosobate decerboodass (MBD) 2001.
ر	Uterus_A				1	a	ANNIII (d. Ini) sepidos control de la contro
94 d		0.4521654	0.5243944	0.432646	0.3003403 t		Steroidogenic factor 1 mRNA
<u>- ر</u>	Uterus_A					1	
oueb ca		0.4497136	0.5234382	0.432204	0.2999253 U73843 at		Epithelial-specific transcription factor ESE-1b (ESE-1) mRNA
ر 96 ط	96 deno	0.4468888	0.5233313	0.432046	0.299599 X69910 af		DG3 mDNIA for tronom combinance and it.
دا	Uterus_A						
97 deno	leno	0.4462032	0.5226997	0,431335	0.29919237 X81372 at		Biphenyl hydrolase-related protein

								ſ	itl	entc	Ger	ne	tic Maidha	Iar r R	kei an	rs f	or	Tu	у,	et al										
A: gamma-3 5' flank	Ribosomal protein 130		s_at CD24 signal transducer mRNA and 3' region	Diatelet-endothelial tetrasman antionn 3 mDMA		MACH-alpha-2 protein	HSPB1 Heat chack 27kD protein 1	ייסי בין ייסי פוסטו בואף לוסופון ו	A cell surface protein	DNA polymerace della small subunit mDNA		mRNA, clone RES4-24C, exon 1, 2, 3	Homo saniens chromosome 19 cos	Kidney mRNA for putative membrane protein with histidine rich charge	clusters		Clone 23748 mRNA		CTNNB1 Catenin (cadherin-associated protein), beta 1 (88kD)		WANTED TO GEOGRAPH OF THE STREET	KIAA0088 gene, partial cds		PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78		Semapnorin E	A2M Alpha-2-macroclobulin	Homo canions mDMA oncoding DAMAD4		CBG Corticosteroid binding globulin
5_at	D79205 at	00000	L3393U s at	D29963 at		X98176_at	Z23090 at		D/9985 at	U21090 at	B00046		RC_AA3992 26 at		D82060_at	***************************************	U79294_at		X87838_at	U45878_s_a t		D42041 at		M80359_at	AB000220_a	0, 0, 1	M11313_s_a t	RC_AA1332	5	J02943_at
0.29872197 5_at	0.2984027 0.79205	000000180000000	0.23/3/208	0.29751363 D29963		0.2972376 X98176	0.29665336 223090		0.236480Z D79985	0.29596934 U21090		0.29556844 t	RC_A 0.2951474 26 at		0.29460874 D82060		0.29419395 U79294		0.29396734 X87838_at	U.293521581		0.29320568 D42041 at		0.29294837 M80359 at	A 2002COC 0	0.43430003	0.2920456 t	RC 0.29187736.15		0.2915053 302943
0.431001	0.430228	0.420008	0.443330	0.429478		0.429269	0.42907	0,100,100	71 /074.0	0.427838		0.427346	0.426986		0.426346		0.426339		0.425803	0.42561	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	0.425395		0.42503	0 424445	0.1424.0	0.423693	0.423252	110000	0.423017
0.522201	0.5215474		- 1	0.5205852	l .	0.5200284	0.5200284	7,0000	í	0.5197809	1	0,5193853	0.5188586		0.5186184		0.5182504	1	0.5179058	0.5176738		0.5175284		0.5164073	0 5158703	27.00.0	0.5152394	0.5147505	0.00000	0.0142239
0.444212	0.4441896	0.4437682	700 101	0.4422355	0 4 4000A	0.4422310	0.437993	7.000000	0.100000	0.4365739	047770040	0.4304/42	0.4363791		0.4362825	2000	0.4360177	, C	0.4352084	0.4333916		0.4333183		0.4328869	0.4324418		0.4320297	0.4314195	7997000	0.4017007
	Uterus_A 99 deno	Uterus A	Herris A	1	Uterus A	٥	103 deno	Uterus_A	A Sural		Uterus_A		Uterus_A 107 deno	Uterus_A	i	Uterus_A	- 1	Uterus_A		Uterus_A 111 deno	Uterus_A	112 deno	Uterus_A		Uterus_A	Ilfarie A		Uterus_A 116 deno	Uterus A	O DO DO DO DO DO DO DO DO DO DO DO DO DO

Uterus
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S_A 0.4299999 S_A 0.4284449 S_A 0.4257057 S_A 0.4252054 S_A 0.4252054 S_A 0.4209878 S_A 0.4209878 S_A 0.4209878 S_A 0.4209878 S_A 0.4209878 S_A 0.4180424 S_A 0.4180424 S_A 0.4169104 S_A 0.4169104 S_A 0.4169104 S_A 0.4169104

The state of the s	AFFX. M27830 M		X99720_ma	TPRC gene	-	of at K-Cl cotransporter (hKCC1) mRNA	. to	To at Inna Polymerase II, 14.5 Kda Subunit	18_at IF I factor (complement)		at		99 s. a	Homeo box B5		ja,	, ;	or at Muscie, Art. Spirce 2	4 at SSR2 Signal continuous continuos	1	at YMPHOTOXIN, BETA DECEDED IN COTOR	T	3_at Catgizzarin		CDINA GONE 491136 3' similar to contains element THR repetitive element :: mRNA sequence (from Genhank)		6_at Type II iodothyronine deiodinase mRNA	AA043111_s EST: zk48b08.r1 Soares pregnant uterus NbHPU Homo sapiens	CDINA Clone 486039 5', mRNA sequence, (from Genbank)	7 at Homeo box c1 protein mBNA		7 at P37NB mRNA
Total Street Street Street	AFFX-	0.2848366 at	7997	0.28447035 1_at	0.284190241165054	000 4000 4077	0.2839762 HT2370	11140	0.2836857 Y00318		0.28339228 J02783	0.28313938 25084 24	M92299 s	0.28283542 t		0.2825081 M94250	HG2815-	0.40440 111 43.	0.28198045 X74104 at		0.2816157 L04270 at		0.28139827 D38583_at	BC 001370	0.28103173 34 at		0.28074732 U53506_at	AA043	בחחטב+טו מו	0.28032324 M16937 at		0.2799537 U32907
:22		0.416028		0.415906	0.415704	5	0.414831	1	0.414825		0.414653	0.414653 0		0.414322 0		0.413557	0 413405		0.41308 0		0.412883		0.412349 0,		0.412031 0.		0.411938 0.	0.411706		0.411481 0.	<u></u>	0.411437 0
		0.5054011		0.5052038	0.5041894		0.5039822		0.5039408	, C	0.4102130 0.5031565	0.5023284		0.5023284		0.5019749	0.5016758		0.5014106		0.5013072		0.4999831		0.4991259		0.4991158	0.4988249)	0.4981218	00074000	0.4971882
		0.4155762	0 444020	0.414638	0.412925		0.4128701		0.4121329	7.007	0.4102133	0.409792		0.4081467	07.7	0.407142	0,4067512		0.4067289		0.4049592		0.4045934		0.4042062		0.4039962	0.4036855		0.4036092	7 4030600	0.4032089 0.49/1882
	Uterus_A	- 1	Uterus_A	0	139 deno	Uterus A	1	Uterus_A	141 deno	Uterus_A	Uterus A		Uterus_A		145 dong	Ulterus A	1	Uterus_A		s_A		IS_A	149 deno	S A	<	151 dong	<	ζ,	A		Uterus_A	

FIG. 12

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	Mac 2 hinding actain and Data	wacz birunig protein mena	Complement C8 gamma subunit precursor (C8G) gene	akalatal hota transmissis	Overeign Deta-LupolityOsin	Boto orbinoit of 1811 in 1911	pera subunit of epithelial amiloride-sensitive sodium channel		280	Ma 190	PTGER3 Prostaglandin E receptor 3 (subtype EP3) {alternative	products}		KGP3 MKNA	Opromonomy 12 do 0 de 1 de 1	Circuitosofile 17412-21 IIIRIVA, clone pUV-2, partial cds	MMP2 Matrix metalloprofeinase 2			Mucin 1, Epithelial, Alt. Splice 9	TEBA protoin mona	LD PIOCEIL IIIKINA	ADD Amyddid Ad martain as All the	An invitation At protein of Alzheimer's disease	mRNA export protein Rae1 (BAE1) mBNA		0.2738917 L27624 s_at TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR		LISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR	DROBABLE ATO DEPENDENT DAYS 1771 OF 1	CONDITION FINE RIVA HELICASE P34	CAMILG Calcium modulating ligand	PURPLE DURING	Forkhead (Drosophila)-like 13
	0.27968997113210 at	U08198_rna	1 at	M12125 at		X87150 at	100 at	X60838 of	אמסססס מו	0.2784675 1468864 24	X83857_s_a	+	1107666 24	02/035 at	0.2775925 1118919 at	D86331 s a		HG371-	HT26388_s_	AEOOOso4 c	A 003301_a		Ť	ij,	aţ		2/624 s at			π	į,		ma	
	0.27968997	-00010500	0.2734220/ 1 at	0.2792073 M12125		0.2788841 X87159	1000	0.27867562 X60838	700 100 1	0.2784675		0.278120431	0.277848841127665	0.2.11.04004	0.2775925		0.27730173 t		H H	0.2770937	0.27688951		0.2764627 Y00264		0.2762043 U84720		0.2758917	0 27569007	0.21 300001 DZ333Z at	0.27544108 1017532		0.27503148 U18242 at		0.27481934 1 at-2
	0.411241	0 440	1.0	0.410798		0.410675		0.410111		0.409397	L	0.409253	0.409253		0.409176		0.409168		7010010		0.408144		0.408116		0.407863	17110	0.407797	0.407555	20101:0	0.40723		0.407132		0.40615
	0.4968431	0.4066155	1	0.4958473		0.4956109	1	0.4954442		0.4954442	1		0.4950701		0.4948221		0.4933896		0.4920247		0.4918493		0.4918493		0.4915251	0.4045054	1070104.0	0.4913622		0.491362		0.4911715	100	0.4907261
	0.4014092	0.4012508		0.4006594		0.4001233		0.3984343		0.3980627	0.3970766	00101000	0.3970429		0.395334		0.3951663		0.3948417		0.3941645		0.3931555		0.3923586	0.3023443	2010700	0.3920158		0.3917662		0.3899161	0.00000	0.3899072
Uterus A		Uterus_A 156 deno	Uterus_A	ļ	Uterus_A	158 deno	Uterus_A	159 deno	Uterus_A	160 deno	Uterus_A 161 deno	Uterus A		Uterus_A	163 deno	Uterus_A	164 deno		165 deno	Uterus_A	166 deno	Uterus_A	deno	Uterus_A	- 1	Uterus_A	Uterus A	1	Uterus A		Uterus_A		A_A	
	15.	156		157		158		155		160	161		162		163		164		165		166		167	(168	169		170		171		172(Uter.	-

Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors

HFH4_cds gene extracted from H.sapiens HFH4 gene, exon 1 and PCI gene (plasminogen activator inhibitor 3) extracted from Human AA197134_a EST: zq11b11.r1 Stratagene muscle 937209 Homo sapiens cDNA MAJOR GASTROINTESTINAL TUMOR-ASSOCIATED PROTEIN CYP4A11 Cytochrome P450, subfamily IVA, polypeptide 11 EIF4C Eukaryotic translation initiation factor 4C (eIF-4C) Y07829_xpt3 Exon A1 from H.sapiens gene encoding RING finger clone 629373 5', mRNA sequence. (from Genbank) Poly(ADP-ribose) glycohydrolase (hPARG) mRNA Fork head domain protein (FKHR) mRNA, 3' end Axonal transporter of synaptic vesicles MPI Mannose phosphate isomerase Phosphomevalonate kinase mRNA TRANSCRIPTION FACTOR P65 protein./ntype=DNA /annot=exon Glutamine transaminase K Cadherin FIB1, partial cds protein C inhibitor gene GA733-2 PRECURSOR 14-3-3 epsilon mRNA CSN2 Beta-casein KIAA0334 gene CW-1 mRNA oined CDS LIMK-2 at AB000895_a AF005043_a M68516_rna (99350_rna AB002332_a X13766 s a 0.27439705|D50663 at 0.2740964 L04751_at 0.27183247|L77213_at 0.27272266|X76057 at 0.2724144|X82224 at 0.27211398 D45906_at 0.27294514 L18960 at 0.27087584|L19067_at 0.27079478 U36922_at 0.27008152 X90840 at 0.2703186 U54778 at 0.2698614 M93036_at 0.274604 1_at 0.2732578 1_at 0.27345976|t 0.27387777 0.27124965|t 0.2722671 0.27148208 0.27059072 0.406119 0.405871 0.405731 0.40554 0.405248 0.3861356 | 0.4867556 | 0.403763 0.405248 0.404647 0.3870421 | 0.4870125 | 0.403855 | 0.3863457 | 0.4868404 | 0.403763 0.4036530.404321 0.404207 0.403512 0.402748 0.402705 0.402921 0.4025530.402357 0.402321 0.389556 0.4902203 0.3890103 0.4899243 0.3899072 0.4907112 0.3886735 | 0.4883817 0.3889893 0.4886434 0.3884962 0.4876038 0.3860179 0.4867483 0.4881 0.3877835 | 0.4874873 0.3874409 | 0.4872577 | 0.384951 | 0.4860813 0.3858946 | 0.4865684 | 0.3855798 0.4861995 0.3854379 0.4861572 0.3845308 | 0.4860763 0.384253 0.4858058 0.3837801 | 0.4852167 0.3885605 Uterus_A Uterus A Uterus A Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus 174 deno 175|deno 177 deno 178 deno 179 deno 183 deno 176 deno 181 deno 182|deno 184 deno 180 deno 185 deno 186 deno 187 deno 188|deno 189 deno 190 deno 191 deno 192 deno 193 deno

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. The first ser of the first that the first series of the first seri

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	(clone PK2J) CDC2-related protein kinase (PISSLRE) mRNA	Dystroglycan (DAG1) mRNA	Zinc finger protein, clone RES4-26	Mitogen inducible gene mig-2	C1NH Complement component 1 inhibitor (angioedema, hereditary)	citizen in contraint	Reliculocalulii	GCSH Glycine cleavage system protein H (aminomethyl carrier)	Defensin 6 (HD-6) gene	Nouronal nicotinic acetylcholine recentor beta-2 subunit	Neul Olia Historii ila averyna iomia i cochoa a caracia	Carboxypeptidase Z precursor, mRNA	DNA-DIRECTED RNA POLYMERASE II 23 KD POLYPEPTIDE		UPA gene	C1R Complement component C1r	CCND1 Cyclin D1 (PRAD1; parathyroid adenomatosis 1)	GGTB2 Glycoprotein-4-beta-galactosyltransferase 2	MGMT 6-O-methylguanine-DNA methyltransferase (MGMT)	MaxiK potassium channel beta subunit mRNA	Tubulin, Beta 2	Antioxidant enzyme AOE37-2 mRNA	cDNA clone 504502 3', mRNA sequence. (from Genbank)
	₩,	at	AB000468_a t	Z24725_at	M13690_s_a t	1004	D42013 at	0.2683764 D00723_at	U33317_rna 1_at		U02431_al	U83411_at	D38251_s_a t	X02419 rna	1 s at	M14058_at	X59798_at	D29805_at	M29971_at	U25138_at	HG1980- 0.26572043 HT2023_at	0.26556104 U25182 at	RC_AA1513 33_at
	0.26950815 X78342	0.26931265 L19711	0.26912433	0.26903847 Z24725_at	0.26890865 t	00000	0.2686522 1742013	0.2683764	U333 0.26800755 1_at	0 06775846 163437	0.26773510	0.26748958 U83411_at	0.2672902		0,2669887	0.26671186 M14058	0.26652628 X59798	0.26627892 D29805	0.2661012 M29971	0.26592505 U25138	0.26572043	0.26556104	RC_A 0.26524332 33_at
	0.401799	0.401634	0.401283	0.401202	0,400843		0.400781	0.400064	0.399878	0.5000	0.399773	0.399639	0.399602		0.399596	0.399211	0.399085	0.398452	0.398359	0.398147	0.398064	0.397796	0.397595
	0.4851144	0.4850967	0.4842905	0,4840759	0.4840454		0.4837295	0.483696	0.4835097	00000	0.4833969	0.4833184			0.4826117	0.4819224	0.4817348	0.4816919	0.4816005	0.4812906	0.481163	0.4808285	0.4807644
	0.3834412	0.3831369	0.3826602	0.3823716	1		0.3813474	0.3812963	0.3796422	11000	0.3/92/52	0.378675	0.3784726		0.3783565	0.378039	0.377782	0.3774269	0.3770593	0.3761662	0.3757033	0.3754145	0.3752081
Í	Uterus_A 194 deno	Uterus A	Uterus_A	Uterus_A	Uterus A	Uterus_A	1	Uterus_A 200 deno	Uterus_A 201 deno	Uterus_A		Urerus_A 203 deno	Otherns A	I Herris A	1	Uterus_A 206 deno	Uterus_A 207 deno	Uterus_A 208 deno	Uterus A 209 deno	Uterus A 210 deno	Uterus_A 211 deno	Uterus_A 212 deno	Uterus A 213 deno
	197	196	196	19.	19	2	19	50	20		20	20	2	3	20	2	8	20	28	23	21	21	27

Docket No.: 2825.2020-002

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	INTERFERON-ALPHA INDUCED 11.5 KD PROTEIN	TCF11 Transcription factor 11 (basic leucine zipper type)	CDC37 homolog mRNA		Platelet activating factor acetylhydrolase IB gamma-subunit		- Landana	i ype ii ccivir-dependent protein Kinase	at MATRILYSIN PRECURSOR	at FDHX1 Enovide hydrolese 1 microscond (constitution)	CEDENT CONTROLL IN THE CONTROL (ACTIONION)	ISTBE4 IISUIII-IIKE Growth factor-binding protein 4	CALT Caltractin (20kD calcium-binding protein)		Diriaj normorg (cb. Xossos), Air. Splice Form 2	Pax8 mRNA		Authorations COMA	Autoantigen mkiva	Integrin, alpha subunit	AF001548_r 815A9.1 gene (myosin heavy chain) extracted from Homo sapiens na1 at chromosome 16 BAC clone CIT987SK-815A9 complete sequence	CD59 CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, E.116, E.130, Fl 32 and G344)	FRAP FK506 hinding protein 12-rangewin accordated protein	Profein-fvrosine nhosphatase mRNA	י איני ווויניסטיונים אויניסטיונים איניסטיונים איניטטיוניטטיוניטטיוניטטייטטיוניטטיוניטטייטטי
100107	18 675/0Y	X77366_at	U43077 at		0.26433152 D63391_at	D17408_s_a	04640	734012 at	တ	u.	ျှံလ		at	HG3395- HT3573_s_a +	,	X69699 at	AA482319_f at		170000 at	at	AF001548_r na1_at	ਲ			7
7 70007000	0.20490914 Ab/ 325 at	0.26464757 X77366	0.26452804 U43077	and arrange of the second of t	0.26433152	0.26405442 t	0.0828878 V04640	0.20001.0	0.263626 L22524	0.26336345125878	0.2631806	0.520	0.26291057 X72964	0.08273808	0.5051 0000	0.26267448 X69699 at	0.26241487	0.262477621.26330	0.50511105.0	0.2621099 X68742	AF0018 0.26185763 na1 at	0.26169914 M84349	0.26155105 M75099 at	0.26136196 U27193 at	
0 207472	0.391473	0.39724	0.397118		0.396897	0.396417	0.306346	0	0.396224	0.396123	0.395993		0.395783	0.395687	200000	0.395679	0.395208	0.395109	2000	0.394917	0.394725	0.39457	0.394216	0.394134	
0.4804749	0.100	0.4799234	0.4795054		0.4783845	0.4779314	0.4777744	- 1	0.4771564	0.4770376	0.3711425 0.4769517		0.4767917	0.4767409		0.4766974	0.47627	0.476121		0.4760983	0.4758993	0.4756543	0.474995	0.4747753	
0 3749906	000	0.3744172	0.3740618		0.3727394	0.3724615	0.3723084		0.3721785	0.3716648	0.3711425		0.3706329	0.3705975		0.3696799	0.3682101	0.3671481		0.3651912 0.4760983	0.3649179 0.4758993	0.3640831	0.3627926	0.3625371 0.4747753	
Uterus_A	Uterus_A		Uterus A 216 deno	Uterus_A		Uterus A 218 deno	Uterus_A 219 deno	Uterus A	1 1	Uterus_A 221 deno	Uterus A 222 deno	Uterus_A	223 deno	Uterus_A	Uterus A	1 1	Uterus_A 226 deno	Uterus_A 227 deno	Uterus A	228 deno	Uterus_A 229 deno	Uterus_A 230 deno	Uterus_A deno	Uterus_A 232 deno	,
214	i	21.	216		21	218	216		22(221	222		222	224		225	226	227		228	229	230	231	232	

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Uterus 233 deno	A 0.3617034	0.4746594	0.393886	0.2610491	0.2610491 M64098 at	High density lipoprofein binding profein (HRP) mRNA
Uterus	A 0.3611303	0.4743144		0.26083332 S62539	S62539 at	Institute recentor cubetrate of Thuman aboletal minoria mana 1000.
Uterus 235 deno	A 0.3608667	1		0.2605413	M55998_s_a	Maho 4 college to 1
	A 0.3597587			0.26036203	M81182 s	Alpria - Louisgen type I gene, 3 end a PXMP1 Peroxisomal membrane protein 1 (70kD, Zellweger syndrome)
Uterus	A 0.3596351	0.4736839	0.392947	0.260103261	J52696_s_a	Adrenal Creb-rp homolog (Creb-rp), and tenascin-X (XB), partial cds, mRNA
	A 0.3595874	0.4734863	0.392907	0.26001436 L07594 at	L07594 at	TGFBR3 Transforming growth factor, beta receptor III (betaglycan, 300kD))
	A 0.3591667	0.4725641	0.392651	0.25984654 M84739 at		CALR Autoantidan calcationing
	A 0.3587261	0.472512	0.392112	0.25960776 X75593 at		Rab 13
	A 0.3581595	0.4724179	0.392011	0.25940916 U79258	at	Clone 23732 mRNA partial cds
	A 0.3570312	0.4719178	0.391713	0.2591425	at	Sarcolipin (SLN) mRNA
Uterus	A 0.356487	0.4718776	0.39159	0.25892106.J02854 at		20-kDa myosin light chain (MI C 2) mDNA
Uterus	A 0.3561977	0.4717351	0.391412	X 0.258748861	(53586_ma	Integrin alpha 6 (or alpha E) protein gene extracted from Human mRNA for integrin alpha 6
	A 0.3558232	0.4714233	0.39104	0.25867283 t	⟨03363_s_a	ERBB2 V-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/dioblastoma derived oncogene homolog 2)
	A 0.3556713	0.4710527	0.390892	0.25841162	M24486_s_a t	P4HA Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), albha polynentide
Uterus / 247 deno	A 0.3556233	0.4709223	0.390831	HG2271- 0.2583091 HT2367_at		Profilagarin
Uterus_A 248 deno	٩ 0.3556163	0.4707972	0.390526	0.258133564	, a	I state of the sta
<u>s</u>	A 0.3545109	i		0.2579129 L42379	at a	Oulescin (Q6) mRNA partial cds
	A 0.3540901	0.4699484	0.390185	0.257637 D14823	at	Chimeric mRNA derived from AML1 gene and MTG8(ETO) gene, partial sequence
Uterus / 251 deno	A 0.3539492	0.4696537	0.390015	0.2574368 U24576	at	Breast tumor autoantigen mRNA, complete seguence
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Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Uterus

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Uterus

258 deno

Inventors: Sridhar Ramaswamy, et al. EST: zw57b01.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) FGFR2 Fibroblast growth factor receptor 2 (bacteria-expressed MYL2 Myosin, light polypeptide 2, regulatory, cardiac, slow clone 774121 3', mRNA sequence. (from Genbank) UBIQUITIN-CONJUGATING ENZYME E2-CDC34 FUSE binding protein 2 (FBP2) mRNA, partial cds Homo sapiens LIM protein mRNA, complete cds Mitochondrial short-chain enoyl-CoA hydratase PI3 Protease inhibitor 3, skin-derived (SKALP) Cysteine-rich heart protein (hCRHP) mRNA Homogentisate 1,2-dioxygenase gene Cell adhesion protein (SQM1) mRNA Prostate differentiation factor mRNA Cell surface protein HCAR mRNA Clone 23665 mRNA sequence KIAA0123 gene, partial cds 59 protein mRNA, 3' end ARSA Arylsulfatase A STX5A Syntaxin 5A COMPLEMENTING TESK1 U69126_s_a 0.25612065 69 at AB000584_a 0.25431052 09_at 0.25521854 U90716 at AF000573 0.2568196|D13900_at Ħ, 0.25656405|D50913_at 0.25637862 L10343_at 0.25598252 D50863_at 0.2556767 X52151_at 0.2544843 M33374 at 0.25552478 M87770 at 0.25473884 U90913 at 0.2540986 U09770_at 0.25390607|X66141_at 0.25583646 L19267 at 0.25487748 L22005 at 0.25713515 U26648 0.2572328 na1_at 0.2551098 0.2567428 0.38973 0.389273 0.389174 0.388905 0.389785 0.389601 0.389446 0.388633 0.388615 0.388422 0.388389 0.388296 0.388105 0.387877 0.387862 0.387506 0.387342 0.387128 0.387524 0.3518259 0.4692048 0.468998 0.349875 0.4678672 0.3493615 0.4669909 0.346028 0.4656386 0.3535267 0.4693585 0.3501498 0.4683319 0.3483551 0.4666338 0.3483136 0.4666338 0.3467862 0.4656529 0.3518513 0.4692196 0.468677 0.3503282 0.4685783 0.3486268 0.4669909 0.3471859 0.4657836 0.4693475 0.3475202 0.4665211 0.3474691 | 0.4664369 0.3469153 0.4657298 0.3526265 0.3516677 0.3515681

Uterus

265 deno

Uterus

264 deno

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269 deno

Uterus

268 deno

2825.2020-002

Title: Genetic Markers for Tumors

Docket No.:

Uterus_A

Uferus

deno

Uterus

260 deno

259 deno

Uterus

262 deno

FIG. 140

					please in the case of		Staff Vector Vereit world world Vereit Verei
27.		0.3456708	0.4655994	0.386753	0.2538055	RC_AA4466	RC_AA4466 EST: zw89g02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA
27.7	Uterus_A 272 deno	0.3454163	0.4654715	<u> </u>		190362 at	To 737 m DNA
	Uterus_A	} -	1			מבמססב מו	1970/ HINNINA
27.	273 deno	0.3453842	0.4649046	0.386738	0.25333798 U48959 at	J48959 at	Myosin light chain kinges (MI CV) mBNA
274	Uterus_A 274 deno	0.3447059	0.4647908		0.25315666 7. 04	U62317_rna	Hypothetical protein 384D8 7 gene extracted from Chromosome
	Uterus A	+	1		0.23313000	W.	ZZq13 BAC Clone CIT987SK-384D8 complete sequence
27.5	275 deno	0.3443086	0.4642941	0.386583	0.25298345 748633 at	748633 at	Retrotransmonan
	Uterus_A				100000000000000000000000000000000000000	ייססס מ	i veri ori eri sposori i
27£	276 deno	0.3441027	0.4641958	0.386236	0.25278383 M34423 at	134423 at	I By By Control of the Control of th
	Uterus_A		ł			אוס דיבט מו	orbi beta-b-garactosidase
277	277 deno	0.3437606	0.4637237	0.386213	0.2525776 Y08639 at	708639 at	Miclear orphan recentor DOD Lots
	Uterus_A				14.	100	EST: 7w72c12 e1 Soares factic NIHT Home conjune on 1.
278		0.3431605	0.4636868	0.386145	0.2523856 51 at		781750 3', mRNA sequence, (from Genhank)
	Oterus_A				- -	HG3227-	
275		0.3427788	0.4636477	0.385899	0.25221294 HT3404	ä	Guanine Nucleotide-Binding Protein Herd
-	Uterus_A						
780		0.3424358	0.4631247	0.385883	0.2520823 Y09267	709267 at	Flavin-containing monooxygenase 2
	Uterus_A						7 Deptingly Control Co
281	281 deno	0.3415793	0.3415793 0.4630214	0.385833	0.25197226 U72508 at	172508 at	B7 mRNA
	Uterus_A					1	
282	- 1	0.3415793	0.4628754	0.385484	0.25167248 U	172508 at-2	0.25167248 U72508 at-2 Human B7 mRNA complete cds
	Uterus_A					The state of the s	Clone 350/2 melanoma ubiquitous mutatad prataia (Mutata 4)
283	283 deno	0.3415338	0.4622342	0.385347	0.25159296 U20908 at		partial cds
	Uterus_A				æ	1	EST: 779h07 s1 Soares NhHMDI, S1 Homo conjune about along
284	284 deno	0.3410251	0.4621983	0.385255	0.25129947 62 at		681877 3", mRNA sentience (from Genhank)
	Uterus_A				ix	RC AA4820	
285		0.3408567	0.4619737	0,385178	0.2511995 31_at		Ribosomal protein L37
	Oterus_A						
286	286 deno	0.340582	0.4619737	0.38501	0.2509831 U76189	aţ	EXTL2 (FXTL2) mBNA partial cds
	Uterus_A		the state of the s				יייין אין אין אין אין אין אין אין אין אי
287		0.3400451	0.4616603	0.384639	0.2507244 L40397 at		(clone S31i125) mRNA 3' and of cds
	Uterus_A					T	Solid Ordinary of Gild of Odd
288	288 deno	0.3399361	0.4614886	0.384433	0.25058222 M19645	ă,	78 KD GLUCOSE REGLII ATEN PROTEIN BECCUESOB
Ç	Uterus_A	6					THE COUNTY OF THE LANGE OF THE COUNTY OF THE
697		0.3399325	0.4613862	0.384144	0.25039697 U73682 at		Meningioma-expressed antigen 6 (MEA6) mRNA
290	290 deno	0.3393976	0.4610068	0 384093	0.05005040	00100	
		200000	0000101-0	0.00702.0	7/0100000770	22333 S at 1	U.230339 13/222333 s at Activin A receptor type II-like 1

Indian hedgehog protein (IHH) mRNA, 5' end	11 Macrophage migration inhibitory factor (MIF) gene	AGA Aspartudul massiminidaes			ALDH8 Aldenyde denydrogenase 8	ME491 gene extracted from H.sapiens gene for Me491/CD63 antigen					sequence. (from Genbank)	DNAJ PROTEIN HOMOLOG 1	0 2/8127671 ORDAL e at TEE3 Trafail factor 3 (intentinal)	at 111 o 116011 labiol o (iliteorifia)	ar- Trefoil factor 3 (intestinal)	a Cysteine protease Mch2 isoform alpha (Mch2) mRNA						ဟ
L38517_at	L19686_ma1 _at	X55330 at	102082 at	002002	U3/519_at	X62654_rna 1_at	X17254 at	U89606 at	167849 at	RC_AA3479	/3_at	D85429_at	, a NAORO I	00044 3	Lugu44_s_ar 2	U20536_s_a t	X57025 at	RC AA4822	D86973 at	D21262 at	K03460 at	M11437_cds 2_at
0.25013983 L38517_at	0.2499281	0.94071911 X55330	0.2437 1211 730330 at	20.0001-1.0	0.24940549 U37519_at	X 0.24922764	0.24906518 X17254	0.24891324 U89606	0.24873494 167849 at		0.24852309 73_at	0.24827251 D85429_at	0.94849767	0.24012101	0.24792191 ₂	0.24772425 t	0.24762948 X57025 at	0 24749441 24	0.24740446 D86973	0.24726626 D21262 at	0.24716893 K03460 at	M114 0.24698804 2_at
0.383996	0.383678	0 383378	0.383313	0.000.0	0.382/00	0.38273	0.382649	0.382618	0.38253	0 000 0	0.382419	0.382309	0.382081	0.007001	0.382012	0.381873	0.381707	0 38159	0.381433	0.381338	0.38128	0.380931
0.4604204	0.4604124	0.4601698	0.4600778	700070	0.4000404	0.459957	0.4597787	0.4596771	0.4593989	0 450470	0.459173	0.4590025	0.458764	0.000	0.4579214	0.4572246	0.4572246	0 4570327	0.4569894	0.4556952	0.455655	0.4548651
0.339082	0.3388332	0.3386539				0.3372519	0.3371888	0.3371089	0.3369807		0.3360/91	0.3358634	0.3353862	7000000	0.3353862	0.3347316	0.3344394	0.334328	0.3339888	0.3331699	0.3329813	0.3326526 0.4548651
Uterus_A deno	Uterus_A deno	Uterus_A	Uterus A	Uterus_A		Uterus_A 296 deno	Uterus_A deno	Uterus_A deno	Uterus_A	Uterus_A	deno	deno	Uterus_A	I Harsie	303 deno	Uterus_A 304 deno	Uterus A 305 deno	Uterus_A	Uterus_A 307 deno	Uterus_A 308 deno	Uterus_A	Uterus_A 310 deno
291	292	293	294	205	627	296	297	298	299	300	3	301	302	1	303	304	305	306	307	308	309	310

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

7G 14C

	A 0.3324483	0.4548494	0.380931	0.246704 M59371_at		TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR
Uterus	A 0.3308183	0.4547785	0.380809	0.24665685 M27492_at	492_at	INTERLEUKIN-1 RECEPTOR, TYPE I PRECURSOR
Uterus313 deno	A 0.3305241	0.4546936	0.380557	0.24642128 M38258 at	258 at	RABG Retinoic acid recontor gamma 1
2	A			7000	10	control returned and receptor, gariffia 1
314 deno	0.329749	0.4545722	0.380493	0.24626747 J05633_at	33_at	ITGB5 Integrin beta-5 subunit
Uterus315 deno	A 0.3293291	0.4545722	0.380216	U332 0.24603835 t	U33202_s_a	Mdm2-D (mdm2) mRNA
Uterus	A					
316 deno	0.3292323	0.4543243	0.380164	0.2459015 Y00282 at	282 at	RPN2 Ribophorin II
Uterus	A 0 3201355	0 4540360	0.2004.05	309040 30494540 0	, oc.	17. A CO A A C.
S	A	1	0.000.0	0.2430707042.0	122431 c a	NAMOTI gene
	0.3287892	0.453737	0.379975	0.24565186 t	3 - -	MOP1 mRNA
2	A					
319 deno	0.3287064	0.4537318	0.379734	0.24545638 X54938_at		ITPKA Inositol 1,4,5-trisphosphate 3-kinase A
Uterus 320 deno	A 0 3286694	0.4537264	0.379662	U244 0 24526131 t	488 s.a	U24488_s_a CYP21 Cytochrome P450, subfamily XXI (steroid 21-hydroxylase,
S	A		1000	1010201		congenital autona hyperplasia)
321 deno	0.3284178	0.4536604	0.379592	0.24514027 D50645 at		SDF2
S	Ą			RC	RC_AA1612	
322 deno	0.3283114	0.4535351	0.379519	0.24498405 92_s_at	at	Interferon, alpha-inducible protein 27
2	Α.					
323 deno	0.3280039	0.4532845	0.379276	0.24476415 1.37347	147_at	NRAMP2 Natural resistance-associated macrophage protein 2
<u>s</u>	A		10000	70007700	-	
- 1	0.3275977	0.4529636	0.379065	0.2446961 U86602	502_at	Nucleolar protein p40 mRNA
Uterus	A 0 3260334	0.4520374	0.37904	0.04453083 D87303 04		و مدمولات ال
S	A			7100 0000011-70		i vi oddi jeso
	0.3268973	0.452558	0.37904	0.24430916 X79204 at	:04 at	SCA1 Ataxin 1
s	Y.					
	0.3264969	0.4522962	0.378937	0.24416241 U50330_at	330_at	BMP1 Bone morphogenetic protein 1
Uterus/ 328 deno	A 0.3261698	0.4522531	0.378848	0.24404605 L76702	.02 at	Protein phosphatase 2A 74 kDa regulatory subunit (delta or B" subunit)
S	A	1				
329 deno	0.325877	0.4517606	0.378592	0.24384515 X52947 at		GJA1 Cardiac gap junction protein
Uterus/ 330 deno	A 0.3253962	0.451715	0.378352	0.24366722 [135139 at		NECDIN related profein mRNA
				220 22 22 22	ı	

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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Herie	Δ					The control of the co
1 1	0.3249705	5 0.4516403	3 0.378289		0.24358681 D84361 at	P52 and p64 isoforms of N Ch.
<u>s</u>	A.				AC002115 r	AC002115 r chromosome 19 cosmids R31396 F25451 and P31076 containing
332 deno	0.3242988	8 0.4515868	3 0.378083	0.24339214 na2_at	na2_at	COX6B and UPKA, genomic sequence
	0.3236986	6 0.4515263	0.377919	X606 0.24331963 1 at	X60673_rna	AK3 mDNIA for all all all all all all all all all al
Uterus	A 0 323500		<u> </u>	_	3	AND HIMMA IOI adenyiate kinase 3
S	A 0.323336	0 0.4512817	0.377855	0.24318363 U59914	U59914_at	Chromosome 15 Mad homolog Smad6 mRNA
1 1	0.3230597	7 0.4510961	0.377426	0.24341537 044520 4		
S	V .		<u> </u>		7	GC-Box binding protein BTEB2
336 deno	0.3230261	0.450872	0.377287	0.24284379 U09953_at		RPL9 Ribosomal protein L9
i	0.3228814	1 0 4506879	0.377256			
8	A	-		0.24200913 U41515 at		Deleted in split hand/split foot 1 (DSS1) mRNA
338 deno	0.3224655	0.450321	0.37703	0.24238089 1179241 at		John 22750 ministration
Uterus_A					1	Owie 20/09 IIIRNA, partial cds
oca deno	0.3224182	0.4501603	0.376843	0.2422535	at	CNN3 Calponin 3, acidic
Uterus_A						
340 deno	0.3222949	0.4500964	0.376777	0.24220291	1112201_5_8	Solare Timo Vii Alaka 4
Uterus_A					U82108 s a	Collage, Type VII, Alpha T
Uerio Ufferiis A	0.3222534	0.4499819	0.376495	0.24200976 t	1	SIP-1 mRNA
1	0.3222534	0.449921	0.376491	U8 0 2417886 t-2	U82108_s_a	U82108_s_a Solute carrier family 9 (sodium/hydrogen exchanger), Isoform 3
Uterus_A					7.	regulatory tactor z
040 deno	0.3218622	0.4496649	0.376375	0.24173036 U65785 at		150 kDa oxygen-regulated protein ORP150 mRNA
Uterus_A					1 1 1 1 1 1	LISCH7 gene (liver-specific bHLH-Zip transcription factor) extracted
344 deno	0.3213359	0.4495851	0.37634	0.24150029 ds1_at	1s1_at c	ds1_at containing USF2, genomic semilence
345 deno	0.3212643	0.4495544	0.376289	0.24139899	1	
Uterus_A		1			1	FIGURIN distultide isomerase-related protein P5
346 deno	0.320374	0.4493822	0.376224	0.24126476 18 at		clone 785941 3', mRNA sequence. (from Genbank)
1 1	0.3199958	0.449273	0.376102	0.2411686 U09550 at		Ovidintal alwansatais m DNIA
Uterus_A	0.3409464		1000			aracia giyobi otgil i i Niya
2		0.4487265	0.375982	0.24103151 D85418 at		Phosphatidylinositol-glycan-class C (PIG-C)

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			V	A 100010	7100.00 at 0.000 f. f. f. f. f. f. f. f. f. f. f. f. f.
319664	0.319664 0.4486223	0.375716	0.240924791	AU10324_a	AAU 10324_al ziuscus.ri soares tetai liver spieen 1NFLS s1 Homo sapiens cund t t
0.319585	0.4485313	0.375704	0.24059117 M55621 at	55621 at	MGAT1 N-acetvlolucosaminyltransferase I
0.3194803	0.4484961	0.375632	0.24051295 0.26362	26362 at	KIAA0043 gana
0.319375			0 24038925 Vecess -4	בפססד מו	
0 3103633			0.24000000	00000 at	ACTR- gene for adrenocorticotropic hormone receptor
2000		0.37 3407	0.24014301 D86869 at	gosos at	KIAAU215 gene
0.319358	0.4480884	0.375282	0.23999971 U28386 at	28386 at	RCH1 RAG (recombination activating gans) popur 1
					control activating galley collect i
0.3188474	0.4479365	0.3751	0.23992673 D42063 at	42063 at	RanBP2 (Ran-binding protein 2)
0.3182724	0.4475956	0.375024	0.23975044 t	J60808_s_a	CDP-diacylnlyreard cynthase (CDS) mDNA
0.3180091	0.4475429	0.374935	0.23956417 X74801	74801_at	T-COMPLEX PROTEIN 1, GAMMA SUBUNIT
0.3179981	0.4472666	0.374915	M 0 23940325 t	M10321_s_a	GOSCHOSED EACTOR OF THE GOSCHOOL OF THE GOSCHO
	3			HG2604-	VON WIETELDIAND I ACTON TOLOGONO
0.3169152	0.4468046	0.374913	0.23922215 HT2700_at		Pan-2
0 3466372	0.4466934	0.074000	70000	, ,	
710001		0.374009	0.23907527 D63874	D638/4 at	HMG1 High-mobility group (nonhistone chromosomal) protein 1
165043	0.3165043 0.4461813	0.374809	0.23887782 HT2375 at	32273- F2375 at	Triosephosphate Isomerase
7007	0100011			X01038_rna	
104000	0.3 104000 0.44002/8	0.3/4463	0.238790781	s at	Fetal gene for apolipoprotein Al precursor
0.3164475	0.4460184	0.37427	0.2386381 U52522	Ť	Arfantin 2 putativa target protein of ADB-ribosylation factor mBNA
					יייידן דיייניס ייין פסי דייסיין פייסיין ארא אייידיין דייידיין דייידיין ארא
0.3164171	0.4458409	0.374163	0.23852523 M77698_at		YY1 YY1 transcription factor
03462400	0.4458000	0.974067	74 00076060 0		INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3
20170	1	0.374007	0.23037 3U9 M330878	326/8 at	FKECUKSOK
0.313632	0.4456559	0.374018	0.23816937 U85611	35611 at	Snk interacting protein 2-28 mRNA
			Party (Marty)		
0.3134979	0.4455278	0.373949	0.23811185 U37690	37690_at	RNA polymerase II subunit (hsRPB10) mRNA
134503	0.3134503 0.4450367	0 373850	0.9378677	7	Nicologia interest
2000	יייייייייייייייייייייייייייייייייייייי	0.01	0.2010011100	ซี	Nuclear protein, NP220

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors

FIG 14'

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us_A 0.3132919 0.4449785 (us_A 0.3132757 0.4449585 (us_A 0.3132757 0.4449585 (us_A 0.3130562 0.4443128 (us_A 0.3129298 0.4441189 (us_A 0.3129298 0.4440747 (us_A 0.3126976 0.4430238 (us_A 0.3124268 0.4440747 (us_A 0.311838 0.4436725 (us_A 0.3117394 0.4436725 (us_A 0.3117394 0.4436725 (us_A 0.3118838 0.4432444 (us_A 0.3109515 0.4433298 (us_A 0.3105853 0.4433298 (us_A 0.310385 0.4433298 (us_A 0.310385 0.4432471 (us_A 0.3098956 0.4432471 (us_A 0.3098956 0.4432471 (us_A 0.3098956 0.4432471 (us_A 0.3098956 0.4432471 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3098956 (us_A 0.3008956 (us_A 0.3008050 (us_A 0.300805
us_A 0.3132919 us_A 0.3132757 us_A 0.3132918 us_A 0.3130562 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298 us_A 0.3129298
370 371 371 372 374 377 378 378 378 380 380 380 380 380

										nve	entor	s: \$	Sri	dha	ir J	rker Ram	as	wai	ny,	et a	il.				_			
VI DI R Verv low density linoprotein recentor	No description for gene: GMCSF at	RC_AA4060 EST: zu65a10.s1 Soares testis NHT Homo sapiens cDNA clone	742842 3', mRNA sequence. (from Genbank)	AA009826_a EST: ze82b02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA	de la contra del contra de la contra del la contra del la contra del la contra del la contra del la contra de la contra del la cont	Cathepsin B	ITGA2B Integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex,	GADD Chemidatina 2 about the debut of the	On Dolyceraldery-propriate deriyarogeriase	TST Thiosulfate sulfurtransferase (rhodanese)	NADP dependent leukotriene b4 12-hydroxydehydrogenase, partial	000	DNA-binding protein (HRC1) mRNA	- Company of the Comp	Ladinin (LAD) mRNA	EST: zv08e05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753056 31 mRNA sequence (from Genhank)		Cysteine-rich secretory protein-3		Exit normal sapiens in ymus mKNA (randomly primed, normalized), single-pass segmence, mRNA segmence, (from (2enhank)	or grade deduction and conduction (notification)	HXC-26 mRNA	EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 1	PRECURSOR	Regulatory factor X-associated ankyrin-containing protein	HMGCL 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase	(hydroxymethylglutaricaciduria)	Chemokine HCC-1
D16532 at	0.23511226 GMCSF at	RC_AA4060	54_at	AA009826_a t	HG417-	HT417 s at	M34344 ot	D00763 at	3	X59434 at	II .	III	M91083 at		U42408_at	RC_AA4364 71 at	X95240 s a			L44538 at		i i		M5//30_at	AA459542_s at		.07033_at	249269_at
0.23524748 D16532 at	0.23511226		0.23492418 54_at	0.2348472		0.23478754 HT417	0 23456080 M34344	0 23442553 D00763 at		0.23429397 X59434	0.2341576 D49387		0.23400204 M91083		0.23388658 U42408_at	RC_A 0.2338644 71 at		0.23367557		0.233571 L44538		0.23350069		0.23330177 M57730 at	0.23312435		0.23291077 L07033	0.232675 Z49269
0.371156	0.371114		0.370909	0.370874		0.370486	0.370318	0.370079		0.370008	0.36979		0.369777		0.369695	0.369326		0.369159		0.368907		0.368834	0	0.368//9	0.368694		0.368437	0.368408
0.4430744	0.4430103	ě.	0.4428861	0.4428766		0.4427666	0.442739	0.442721		0.4426495	0.4426138		0.4425674		0.4424902	0.4419999		0.4419858		0.4419595		0.4417441	T 4 4 4 0 0	0.4410243	0.4416104		0.4415439	0.4415279
0.3092669	0.3088878		0.3088586	0.3087997		0.3075095	0.3074018	0.3073979		0.3072291	0.3070417		0.3069941		0.3059313	0.3058104		0.3057342		0.3049663		0.3036065	7 900000	0.3032004	0.3030933		0.3025794	0.3025116 0.4415279
Uterus_A 387 deno	Uterus_A 388 deno	Uterus_A		Uterus_A 390 deno	Uterus_A	391 deno	Uterus_A	Uterus_A 393 deno	Uterus A	394 deno	Uterus_A 395 deno	Uterus_A	396 deno	Uterus_A		Uterus_A 398 deno	Uterus_A		Uterus A	1	Uterus_A	401 deno	Uterus_A		403 deno	Uterus_A		Uterus_A 405 deno
387	388	Č	383	390		391	392	393		394	395		396	0	387	398		399		400		401	402	705	403	-	404	405

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FIG. 147

																						ding)							
WHITE TABLE TRAIL TRAIL	Diadenosine tetraphosphatase mRNA	KINESIN I GHT CHAIN		KH type splicing regulatory protein KSRP mRNA	SERIM AMYLOID A DDOTEIN DDECLIDEOD	CERCON AND LEGIS AT INCITED TO THE CONSOCIAL	0.23208181.22647_s_at Prostaglandin E receptor 1 (subtype EP1), 42kD	Chromocome cegrenation and production OAC month	ANIII OAO BOINI NIBO INDIA NIBO INIBO INDIA NIBO INDIA NIBO INDIA NIBO INDIA NIBO INDIA NIBO INDIA	Dual specific protein phosphatase mKNA	Surface antigen mRNA		Immunoglobulin superfamily containing leucine-rich repeat		rzy pumoceptol mikaya	H19 RNA gene		GTP cyclohydrolase I feedback regulatory protein gene	OO OWOU NIETOGO ETIHM	WILLE PROTEIN HOMOLOG	Mammaglobin mRNA	Mitochondrial RNA polymerase mRNA, nuclear gene encoding	mitochondrial protein	TO STATE INTO SIRCE INCOMINANT ININCITORISTE HIM	MOLTIFONO TONAL AMINOACYL-TRNA SYNTHETASE	TMOD Tropomodulin		Lysyi nydroxylase isoform 2 (PLOD2) mRNA	HLA-H MHC protein HLA-H (heredilary haemochromatosis)	
1991, 1992, 1997, 1998,	U30313 at	L04733 at		U94832_at	X51441 at		L22647_s_at	1133286 at	100001	040001 at	M60922 at	H61361 s a	 	AF000234_a	-	M32053 at	U78190_rna	1_at	Xa124a at	7512+3 at	U33147 at		U75370_at	VE/1306 of	704920 at				U60319 at	
anni anni in anni anni a	0.23256662 U30313	0.23243715 L04733 at	A de la communicación de l	0.23237877 U94832	0.23224539 X51441 at		0.2320818	0.23198555 1133286 at	7000N11070777000	0.23111010	0.23162402 M60922 at		0.23149961	0 23141015+	2010	0.23138271 M32053 at		0.2311929	0 23111738 XQ124Q	0.50111100.	0.23103131 U33147 at	A CONTRACTOR OF THE PROPERTY O	0.23085783 U75370_at	0 23081134 VEA226 of	10002.0	0.2307061 M77016 at	000000	U.23U4310 U643/3 at	0.23028168 U60319 at	
	0.368154	0.368094		0.367995	0.367898		0.30/79/	0.367663	0.987849		0.367598		0.367447	0.36725	041000	0.367212		0.36715	0.36709	2000	0.36694		0.366922	0.366808		0.366468		0.30043/	0.366299	
	0.4414794	0.4414436	1	0.4413044	0.4411463		0.4411403	0.4410265	0.4400084	1000011-0	0.4408862	,	0.4407882	0.4407098		0.4405996		0.4404657	0.4403853		0.440361		0.4403432	0.4400919		0.4400919	0 4400046	0.4400310	0.4400395	
	0.3024692	0.3021389		0.3017629	0.3017367	0.3047098	0701106.0	0.3016791	0 3015491		0.3014864		0.3011269	0.3007341		0.3003851		0.3003795	0.3000679		0.3000638		0.2997915	0 2997595		0.299703	0.3000000	0.2330003	0.2996515	
1	Uterus_A 406 deno	Uterus_A deno	Uterus_A	- 1	409 deno	Uterus_A	Herric A	2	Uterus_A	Uterus A	deno	Uterus_A	deno	Uterus_A deno	Uterus_A	leno	Uterus_A	- 1	Uterus_A deno	Uterus_A		S_A	<	deno	S A	1	S_A	A S		R A
	406	407	9	408	409	410,0		411 deno	Uteru 412 deno		4130		414	415		416 deno		41/0	418		419 deno		420 deno	421 d		422 d	Uteru 123 deno	7 7	424 deno	Uter

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswanıy, et al.

FIG. 14W

426	Uterus A		0.2991064 0.4309162	0.9860	RC A	RC_AA2332	
	Uterus A	0.000	70100010	0.00044	0.43013133	0/_al	Harisionning growth ractor beta 1 Induced transcript 1
427	1	0.2990786	0.2990786 0.4397017	0.366108	0.229932 M32879	M32879 at	CYP11B1 Cytochrome P450 11 beta
428	Uterus_A 428 deno	0.2981855	0.439625	0.365865	0.22976169 X15187	11	TRA1 Homologija of mojisa tijmor rajacijon antigan 2008
	Uterus_A						osella libraria i compara de la compara de l
429	429 deno	0.2981116	0.4396184	0.365784	0.22962955 U68494 at	U68494 at	Hbc647 mRNA sequence
430	Uterus_A 430 deno	0.2980832	0.4391629	0.365689	0.22958684	Z25821_rna 1_s_at	Dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
	Uterus_A					-' ₹	
431	431 deno	0.2980207	0.438918	0.365606	0.22950916	1	AQP3 Aquaporin 3
	Uterus_A						
432	432 deno	0.2979845	0.4387482	0.365586	0.22923166 X07767_at	X07767_at	PRKACA Protein kinase, cAMP-dependent, catalytic, albha
133	Uterus_A	0.0070074	400400	100			
2		0.2370371	0.23/65/1 0.438/255	0.303474	0.22910094 D13634	D13634_at	KIAA0009 gene
434 (Uterus_A 434 deno	0.297305	0.297305 0.4384107	0.365052	0.22900726 X13916 at	X13916 at	LDL-receptor related protein
	Uterus_A						
432 (435 deno	0.2971269	0.4383769	0.364907	0.22889222 Z80777 at	Z80777 at	H2A/k gene
	Uterus_A					The state of the s	
436	436 deno	0.2970312	0.4382743	0.364553	0.22881934 D86956 at	D86956 at	KIAA0201 gene
	Uterus_A		MATERIAL CONTRACTOR				
437 (437 deno	0.2969605	0.4381124	0.364552	0.22862452 U14550	U14550 at	Sialytransferase SThM (sthm) mRNA
	Uterus_A						
438 (438 deno	0.296619	0.4377558	0.364335	0.2285323 U89505	U89505 at	Hlark mRNA
	Uterus_A						
439 (439 deno	0.2962874	0.2962874 0.4369476	0.364117	0.22844386	1	PAX2 Paired box homeotic gene 2
	Uterus_A						
440 (440 deno	0.2962253	0.2962253 0.4367364	0.364032	0.2283235 U13369_at	U13369_at	Ribosomal DNA complete repeating unit
-	Uterus_A						TATA-binding protein associated factor 30 kDa subunit (tafl130)
441 0	441 deno	0.2962041	0.4366629	0.363854	0.2282466 U13991	U13991_at	mRNA
- 077	Uterus_A	7,000,000,0	10000	1000			
717		0.2300017		0.505550	0.2280918 056418	ä	Lysophosphatidic acid acyltransferase-beta mRNA
443	443 deno	0.2959577	0.4361742	0.363456	0.22799143 X16665 at	X16665 at	HOXB2 Homeo box B2
	Uterus_A					AF001900 a	
444 deno	deno	0.2954874	0.4361716	0.36343	0.22783183	1	Secreted frizzled-related protein 1
	Uterus_A						
445 deno	deno	0.2953545	0.2953545 0.4361492	0.363421	0.22774851 L40391	ੜ	(clone s153) mRNA fragment

FIG. 14X

										_				-,																		
EST: 43e1 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA mRNA segmence (from Genhank)	EST, yh81g01.r1 Homo sapiens cDNA clone 136176 5' similar to contains MSR1 reneflive element: (from Genhant)	Trismand and the control of the cont	at mKNA translocon-associated protein delta subunit precursor		Calcium Channel, Voltage-Gated, Alpha 1e Subunit, Alt. Splice 3	G-myc binding profein		Amplaxin (EMS1) mRNA		IFRU	RPS11 Ribosomal proteip S11	HS1 binding profein HAX-1 mRNA purloar gana encoding	mitochondrial protein		Decorin. All. Splice 1		Melanoma growth stimulatory activity (MGSA)	(LOCAL) (MARCH TOTAL)	at-2 Growth factor receptor-bound protein 14		Grb14 mRNA	11 - 170	Giant larvae homolog		SURF1 Surfeit 1		inositoi 1,3,4-trispnosphate 5/6-kinase mKNA	Protoporphyripogen ovidase	ocepor propert concase	PSMB5 Proteasome (prosome, macropain) subunit, beta type, 5	MANA Director biometer biometer beautiful properties of the property of the pr	rniviz ryiuvate Kiliase, muscie
W27993 at	R33301 at			HG3242- HT4231_s_a]	D89667 at		M98343_at	70070	D04294_at	0.2267837 D28137 at	Land,	U68566 at	HG3431- HT3616 s a	31	X54489 rna	1 at				_76687 at		X87342_at		Z35093 at			L3033/_s_a		at	1	1
0.22761446 W27993	0.2273876 R33301	000000000	0.22726029 269043 \$	7 7	0.227 1009	0.22701234 D89667		0.22692072 M98343_at	0 0000000000000000000000000000000000000	0.2200340	0.2267837		0.22662352 U68566 at		0.22646135		0.22628474		0.22619678 L76687		0.2261087 L76687		0.22587514 X87342		0.2257998 Z35093	0 00579407	0.22313121 US1330 at	0.22567737		0.22547948 X95586	0 22543862 256404 24	0.243730021
0.363283	0.363267			097696	0.000	0.363146		0.363121	0 269446		0.362707		0.362705		0.362467		0.362298		0.36224		0.362107		0.362004		0.361973	0 26404	10100.0	0.361697		0.361647	0.361429	0.501750
0.4360268	0.4360268	1		0.4359497	1	0.4357618	I	0.4357099	0.435594	1700010	0.4351829		0.4351318		0.434964		0.4349208		0.4348293		0.4348207		0.4344747		0.4344587	0.4344587	Joseph Chr.	0.4342676		0.43423	0 4342046	2.10.10.10
0.2951211	0.2948279	0.2047705	0.2341103	0.2044304	1001107:0	0.2944256		0.2934274	0.2030351	1000001	0.2928565		0.2926317		0.2924196		0.2921097		0.2920352		0.2920352		0.291668		0.2911482	0.2908663	2000	0.2902213		0.289964	0.2899492	
Uterus_A 446 deno	Uterus_A 447 deno	Uterus_A	OT ION	Uterus A	I Heris A	1	Uterus_A	deno	Uterus_A	Uterus A	453 deno	Uterus_A	454 deno	Uterus_A	455 deno	Uterus_A	456 deno	Uterus_A	457 deno	Uterus_A	458 deno	Uterus_A		Uterus_A		Uterus_A	Herris A		Uterus A	463 deno	Uferus_A deno	
446	447	448	2	449	2	450		451	452		453		454	-,	455		456		457		458		429	6	460	461		462		463 (Uteru 464 deno	

Docket No.:

2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. And Service and the service of the s

Inventors: Sridhar Ramaswamy, et al EST: zf20c08.s1 Soares fetal heart NbHH19W Homo sapiens cDNA sapiens DNA from chromosome 19p13.2 cosmids R31240, R30272 RC_AA4046 | EST: zt43h04.s1 Soares ovary tumor NbHOT Homo sapiens cDNA PTPRF Protein tyrosine phosphatase, receptor type, f polypeptide RAD23A gene (human RAD23A homolog) extracted from Homo Msh (Drosophila) homeo box homolog 1 (formerly homeo box 7) and R28549 containing the EKLF, GCDH, CRTC, and RAD23A EST: ygg1d04.r1 Homo sapiens cDNA clone 40987 5'. (from Genbank) DDB1 Damage-specific DNA binding protein 1 (127 kD) Endogenous retrovirus envelope region mRNA (PL1) clone 377486 3', mRNA sequence. (from Genbank) clone 725143 3', mRNA sequence. (from Genbank) LAMP1 Lysosome-associated membrane protein 1 Prostate carcinoma tumor antigen (pcta-1) mRNA HEK2 mRNA for protein tyrosine kinase receptor Carnitine palmitoyltransferase (CPT1) mRNA UDP-Galactose 4 epimerase (GALE) gene Integrin-linked kinase (ILK) mRNA PMM1 Phosphomannomutase genes, genomic sequence Selenoprotein P JunD mRNA Ini1 mRNA Imogen 38 AD000092_c RC_AA0558 L41668_rna7 AA039806_a X56681_s_a J32986_s_a 0.2232224 U86070_at 0.22360732 Y00815 at 0.22336929|X75208_at Ħ 0.22371829 R56174 at 0.2249255 M11119 at 0.22439732 U04847_at 0.22511102 U09646_at 0.22433487 L78132 at 0.22537497 Z11793_at 0.22520113 J04182_at 0.22458471 Z68747_at 0.22383574 ds7_s_at 0.22386107 U40282_ 0.22404896 09_s_at 0.22351962 41 at 0.22329307 at 0.22413822|t 0.22421539 0.2249325 0.359516 0.3595680.359608 0.359553 0.359879 0,359874 0.360556 0.360522 0.360287 0.360117 0.360665 0.36066 0.360814 0.360799 0.361345 0,360986 0.361167 0.361124 0.361032 0.2847927 0.4316029 0.2845995 | 0.4314997 0.2859086 0.4320048 0.2855813 0.4317689 0.28547 0.4317689 0.2852781 | 0.4316954 0.2872125 0.4324769 0.4321163 0.2856298 0.4318539 0.2874659 0.4329076 0.2878524 0.4331787 0.2886791 0.4335316 0.2881754 0.4334388 0.433137 0.2875306 | 0.4331364 0.2890282 0.4335746 0.4335316 0.2898663 0.4340635 0.2894121 0.4340261 0.2868869 0.2877404 0.2886999 Uterus A Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus 481 deno 482 deno 479 deno 480 deno 483 deno 477 deno 478 denò 473 deno 474 deno 475 deno 467 deno 468 deno 469 deno 470 deno 471 deno 472 deno 476 deno 466 deno 465 deno

Docket No.:

2825.2020-002

Title: Genetic Markers for Tullors

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COVED Cydorhome c ovidase subunit Vh	סטטטט סטטטטט פרטטטטטטטטטטטטטטטטטטטטטטטטט	KIAA0062 gene, partial cds	. C3f mRNA	SERUM AMYLOID A PROTEIN PRECURSOR		I-Plastin	I andstainer Wiener Blood Groun Glycoprotein (1 w) (Gb:1 27671)	EST: zt18g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone 713538 3', mRNA sequence. (from Genbank)	Alpha(1,2)fucosytransferase, 5'UTR partial sequence		(clone 14VS) metallothionein-IG (MT1G) gene	Tazarotene-induced gene 2 (TIG2) mRNA	Glycine receptor beta subunit (GLRB) mRNA	Darisharal muslin aratein-22 (PMP22) gene non-cading exon 18	Poventa Procedure (1 M) 22/ gene, non occurs	BCKDHA Branched cnain Keto add derlydrogeriase E.i., alpria polypeptide (maple syrup urine disease)	EST: zt25h08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA	clone /1420/ 3', mKNA sequence. (Ironi Genbarik)	Albha1-antichymotrypsin, exon 1	EST: zr57d06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667499 3. mRNA sequence. (from Genbank)	Putative DNA-binding protein mRNA, partial cds	Nucleolar autoantigen No55 mRNA	
	\top	at	U72515_at	J03474_at			HG3954- HT4224_s_a	AA2909	91 s at	D87937 at	J03910_rna1	at	0.2219429 U77594_at	U33267 at		Unougo at	Z14093_at	RC_AA2935	68_at	X68733_rna 1_at	RC_AA2279	U49278 at		at ≰
40 700741 1000000	0.223101041	0.22304858 D31887	0.22273396 U72515_at	0.22260329 J03474_at	1000	0.22253384 H12862 at	000077070	0.222.13003	0.22226422 91	0.22222547 D87937 at		0.2219732	0.2219429	0.22173133 U33267	0.00467400	0.22107428 000030	0.2215458 Z14093		0.22138602 68_at	X687 0 22127473 1 at	RC_A	0.22111517 U49278	0.22106889 U47621	RC_/ 0.22098492 57_f
	0.359454	0.359438	0.359248	0.359248		0.358861	0.000	0.3300 12	0.358686	0.358633		0.3585	0.358422	0.358257	0.00	0.358122	0.357958		0.357843	0.357614	0.357482	0.357412	0.357312	0.357238
	0.4313016	0.4309928	0,4307328	0.4305675		0.430433		0.43027.30	0.4299765	0.4299765	ŧ	0.4293582	0.4293129	0.4290204		0.4286917	0.4285328	1	0.4284139	0.4283401				
	0.2845324	0.2841438		0.2838041		0.2834567	0000	0.2033400	0.2832195	0.2832159		0.2831684	0.2831166	0.2826918		0.2822928	0.2818125		0.2817415	0.284605	0.0846604	0.2803111	0.2799788	0.2799
S_A		Uterus_A 485 deno	S A	Uterus_A 487 deno	Uterus_A	488 deno	Uterus_A	Uterus A	490 deno	Uterus_A	Uterus A	492 deno	Uterus_A 493 deno	Uterus A	Uterus_A		Uterus_A	Uterus_A	497 deno	Uterus_A	Uterus_A	Uterus A	Uterus_A	Uterus_A 502 deno
	484 (485	486	487		488	9	664	490	491		492	493	404		495	496		497	408	8	439	501	502

Inventors: Sridhar Ramaswamy, et al. RECA Replication protein A (E coli RecA homolog, RAD51 homolog) DBT Dihydrolipoamide branched chain transacylase (E2 component ERYTHROCYTE PLASMA MEMBRANE 50 KD GLYCOPROTEIN AA380393_a EST: EST93352 Supt cells Homo sapiens cDNA 5' end, mRNA INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR COX7A2 Cytochrome c oxidase VIIa subunit (liver specific) FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE of branched chain keto acid dehydrogenase complex) EIF4E Eukaryotic translation initiation factor 4E Cytoplasmic dynein light chain 1 (hdlc1) mRNA MTAP Methylthioadenosine phosphorylase FKBP4 FK506-binding protein 4 (59kD) ANX11 Annexin XI (56kD autoantigen) G protein gamma-11 subunit mRNA Heat shock protein (hsp 70) gene Randomly sequenced mRNA Importin beta subunit mRNA sequence. (from Genbank) Male Enhanced Antigen Ribosomal Protein S20 Nip3 (NIP3) mRNA PACAP receptor M11717_rna 0.21908528 HT1823 at 0.2188031 U15174_at 0.22014561 M88279_at 0.21982065|U32944_at 0.22073737 U22233 at 0.22054973|HT1904 at 0.21991216 M15353_at 0.21913551 U31384_at 0.21868214 L19605 at 0.22083832 D25274 at 0.22048616|X64594_at 0.22002916|X69141_at 0.21979056 L38951_at 0.21964961 D17516 at ਲ 0.2192977 X15822_at 0.2202547 L07493 at 0.22013626|L34600_at HG1800-HG1869-0.21955003 X66785 0.21945575 1 at 0.21892498 0.355574 0.355355 0.3569660.356919 0.356695 0.356595 0.356593 0.356395 0.356352 0.356271 0.35604 0.356040.355878 0.355802 0.355705 0.355598 0.355581 0.355367 0.356732 0.356643 0.425627 0.2756592 0.4256174 0.2778782 0.4268214 0.426542 0.2764907 | 0.4265125 0.2764285 0.4264167 0.2760856 0.4263303 0.279361 0.4274165 0.42726 0.2784306 0.4270774 0.2781857 0.4268785 0.2757418 0.4256781 0.2797954 | 0.4277055 0.2797235 0.4275312 0.2793272 0.4274165 0.2791519 0.4273974 0.2788312 0.4272924 0.2768742 0.4267413 0.2767665 0.4266193 0.2776918 0.4267844 0.2756682 0.2766471 0.2786267 Uterus_A Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus 505 deno 506 deno 507 deno 511 deno 512 deno 514 deno 515 deno 516 deno 517 deno 519 deno 520 deno 521 deno 508 deno 509 deno 510 deno 513 deno 518 deno 522 deno 504 deno

2825.2020-002

Genetic Markers for Tumors

Docket No.:

Title:

FIG. 14B

Docket No.: 2825.2020-002
Title: Genetic Markers for Tumors
Inventors: Sridhar Ramaswamy, et al.

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FIG. 14C

Conf. 1970,

SNRP70 U1 snRNP 70K protein	Transportin (TRN) mRNA	Nucleosome assembly profein 2 mRNA	ainha 2 (VII) collegen	, aiplia-2 (vi) cuiageii	UBIQUITIN-LIKE PROTEIN GDX	T(3:5)(a25.1:b34) fusion gene NPM-MI F1 mRNA		ENOT Enolase 1, (alpha)	RPS28 Ribosomal profein S28	KIAANDES gang nartial cds	Mind gelle, palual cus	Tissue specific mRNA	EST: zx97c05.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 811688 3' similar to CW-DB26 DADIT DAGGOODAG DELIATED			at Epoxide hydrolase 1, microsomal (xenobiotic)	UBIQUITIN CARBOXYI -TERMINAL HYDROLASE T		EEF1G Translation elongation factor 1 gamma		transferases +L-billianing protein 1 pseudogene, p-dopacting ine- tautomerase pseudogene ESTs and polymorphic CA repeat	Lamin-Like Protein (Gb:M24732)	M31520_ma Unknown protein gene extracted from Human ribosomal protein S24
X04654_s_a t	0.2163793 U70322 at	U77456 at			J03589 at	L49054 at	M14328_s_a	-	U58682 at		מו	X67698_at	RC AAAR3R	61 at		S	7		X05855_at	784718 ode	1 at	HG1078- 0.2150529 HT1078 at	M31520_rna 1_s_at
0.21656726	0.2163793	0.21627219 U77456	0.21611719 M20777	0.1014.0	0.21608192 J03589	0.21597868 L49054_at	0.0040	1 51 560 17:0	0.21585877 U58682 at	0.21574046.031763	2011	0.21572573 X67698		0.21567973 61 at		0.21557063 L25880	0.21547543 U47927		0.21533197 X05855_		0.21524751	0.2150529	M3152 0.21499753 1_s_at
0.353227	0.353132	0.353098	0.352804	1007000	0.352744	0.352632	0.252512	71070000	0.352192	0.352192		0.352116		0.352067		0.352013	0.351914		0.351889		0.351782	0.351759	0.351702
0.4237284	0.4236468	0.423574	0.423483		0.4233583	0.4233548	0.2703614 0.4227634	0.4227034	0.2699578 0.4227304	0.4227235		0.4226134		0.4225569		0.422502	0.4224213		0.4223568		0.4223372	0.4222952	0.4221923
0.2714271	0.2713856	0.271137	0.2709395		0.270704	0.2705061	0.2703614	4100014	0.2699578	0.2699567		0.2696941		0.269311		0.2688356	0.2688137 0.4224213		0.268597		0.2683244	0.2681485	0.2681193
Uterus A 542 deno	Uterus_A 543 deno	Uterus_A 544 deno	Uterus_A 545 deno	Uterus A	ì l	Uterus_A 547 deno	Uterus_A	Utenis A	1	Uterus_A 550 deno	Uterus A	551 deno	Uterus A	l	Uterus_A	553 deno	Uterus_A 554 deno	Uterus A	555 deno	Uterus A	ı	Uterus_A	Uterus_A 558 deno
542	543	547	545		54E	547	548	5	546	550		551		552		553	554		555		556	557	558

										I	nvei	nto:	rs:	Srid	ha	r R	am	as	wa	my	у, е	t a	ıl.		_							
	E1V4 Ets Variant gene 4 (E1A enhancer-binding protein, E1AF)	ALCOHOL DEHYDROGENASE	CDEDD 4 m DNIA	SINEDI-1 IIININA	CCT6 Chaperonin containing T-complex subunit 6		Protein tyrosine kinase mRNA	at ARF41 ADP-rihosvlation factor 4-like		mRNA KKIALRE for serine/threonine protein kinase		Lyniphocyte Orlemoattractant Factor	TRANSDUCIN-LIKE ENHANCER PROTEIN 1		COMPLEMENT OF PRECURSOR	ATP SYNTHASE GAMMA CHAIN MITOCHONDRIAL PRECLIRSOR		LTF Lactotransferrín		Selenophosphate synthetase 2 (SPS2) mRNA		RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M1 CHAIN		Orphan nuclear hormone receptor	Laminin, alpha 3 (nicein (150kD), kalinin (165kD), BM600 (150kD), enilegrin)		Laminin-related protein (LamA3) mRNA		KIAA0257 gene, partial cds	TRPC1 Transient receptor potential channel 1	The state of the s	Potassium Channel, Voltage-Gated Kcnc1
	UIBUIB at	J04794 at	Innaka at	200200 at	L27706 at		U02680 at	ဟ		X66358 at		11210 at	M99435 at		מסלקט	043951 at	1	X53961 at		J43286 at	} [X59543_at		4/9/50_at	0.21331818 L34155 at-2		.34155_at		J87446_at	K89066 at	HG2507-	-TZ603_at
1.70	0.21491011 018018	0.2147938 J04794	0.21471241100968	17111170	0.21459487 L27706		0.21447521 U02680	0.21439157 L38490		0.21421917 X66358	HG270	20061112:0	0.21404296 M99435	0.042000026	0.51330030	0.21391523 D43951		0.21382193 X53961		0.21369071 U43286		0.21353564 X59543		0.213429/3 R/9/50	0.21331818		0.2131184 L34155		0.21306536 D8/446	0.21302578 X89066		0.21291442 HT2603
	0,331000	0.351577	0.351509		0.351285		0.351256	0.351084		0.350938	0.350864	00000	0.350818	0.350787	100000	0.350746		0.350449		0.350301		0.350181		0.350089	0.35005		0.349992	0.00	0.349967	0.349785		0.349753
4004647	0.424.017	0.4219514	0.2679596 0.4217643		0.4216982		0.2677929 0.4215668	0.2673985 0.4214301		0.4212584	0.2672976 0.4211393	000	0.2672949 0.4211275	0.424414	11171	0.4210816		0.4209127		0.4208286		0.4207057		0.4200284	0.4201897		0.4201707	0.400004.0	0.4200040	0.4198795		0.4198719
7600036 0	0.2000331	0.2680175	0.2679596		0.2679467		0.2677929	0.2673985		0.2673255	0.2672976		0.2672949	0.2671263	0.10	0.2670027		0.2667579		0.2667247		0.2664374	0,000	0.2004333	0.2662248		0.2662248	7.4000000	0.2000047	0.2659003		0,2658926 0,4198719
Uterus A	Uterus A	1	Uterus_A 561 deno	Uterus A	562 deno	Uterus_A		Uterus_A 564 deno	Uterus_A	ļ	Uterus_A 566 deno	Uterus A	567 deno	Uterus_A	Iterie A	1	Uterus_A	570 deno	Uterus_A	571 deno	Uterus_A	- 1	Uterus_A		574 deno	Uterus_A	- 1	Uterus_A	-	577 deno	Uterus_A	578 deno
550	3	560	561		562	i	263	564		565	566		267	568		569		570		571	Î	5/2	570	2/2	574] 	5/2	576	0/0	577		578

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0.2	0.2658202	0.4198377	0.34964	0.21282695 U67171_at	167171_at	Selenoprotein W (selW) mRNA
0.2657732	22	0.4196101	0.349455	0.212732 X76105_at	76105_at	DAP-1 mRNA
0.2649265	5	0.4194946	_ C	0.21267319	X62083_s_a	RING3 DROTEIN
			'			
0.264836	36	0.4194618	0.349288	0.21256402 L25270_at	25270_at	XE169 PROTEIN
0.2648053	53	0.4193648	0.349227	0.21251966 U31383 at	31383 at	G protein gamma-10 subunit mRNA
					4	
0.264574	74	0.4193594	0.349227	0.21235517 J04501	04501 at	GYS1 Glycogen synthase 1 (muscle)
720773	7	0.4400000	7,000			
0.60443			0.04500	0.212082/ LUD14/ at	uo 147 at	(clone SY11) golgin-95 mKNA
0.2644895	95	0.4192634	0.349007	0.21205798 U52840 at	52840 at	Cri-du-chat region mRNA. clone CSA1
0.0644794	707	0.44000074	700070	0000		
0.204	5		0.340307	0.21203339123083	25085 at	PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT
0.2638043	043	0.4191681	0.348983	0.2119637 U21128 at		LUM Lumican
0100000	2	1				
0.2030	000	0.4191001	0.34884	0.21184/16/256281 at	256281 at	Interreron regulatory factor 3
0.2636525	525	0.4190968	0.34881	0.21170548 HT3686 at	T3686 at	Uncounting Profein Hen
		1				
0.2635278	278	0.4188384	0.348783	0.21163805 D50920	50920 at	KIAA0130 gene
0.000000	2,5			11 70 20 770 0		
0.2034	212	0.4104200	0.348391	0.21163581 072514	72514_at	C:zt mKNA
0.263129	129	0.4183771	0.348472	0.21141809 215108	15108 at	PRKCZ Protein kinase C. zeta
						(genomic clones lambda-[SK2-T2, HS578T]; cDNA clones RS-[3,4, 6])
0.2630199	199	0.4183332	0.348444	0.21138875 J00277	30277_at	c-Ha-ras1 proto-oncogene, complete coding sequence
0.2628559	559	0.4183297	0.348396	0.21120284 U18934 at	18934 at	TYRO3 Receptor protein-tyrosine kinase sky
0.2628134	134	0.4182341	0.348382	0.2111348 U79751	79751_at	Basic-leucine zipper nuclear factor (JEM-1) mRNA
0.2625636	336	0.4180861	0.348353	0.21101585 L39061	39061 at	Transcription factor SL1 mRNA, partial cds
0.2625419	419	0.4178532	0.348108	HG1139-	HG1139- HT4040 at	EVENS Binding Dratain Alt Caling 9
2	5		201010	111.01001.4:0	2012	ו מסטיטוועוווען דוטיפווו, הינ. טאיוטק ג

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

Inventors: Sridhar Ramaswamy, et al. J04152_rna1 M1S1 gene extracted from Human gastrointestinal tumor-associated EST; zu99d05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:746121 3', mRNA sequence. (from Genbank) INPPL1 Inositol polyphosphate phosphatase-like protein 1 (51C Thyroid receptor interactor (TRIP11) mRNA, 3' end of cds Translation initiation factor eIF-2alpha mRNA, 3'UTR MYH9 Myosin, heavy polypeptide 9, non-muscle Protein Phosphatase 1, Alpha Catalytic Subunit antigen GA733-1 protein gene, clone 05516 Phosphoethanolamine cytidylyltransferase Thiol-specific antioxidant protein mRNA OX40L RECEPTOR PRECURSOR Metallothionein-If gene (hMT-If) ANX2 Annexin II (lipocortin II) X BOX BINDING PROTEIN-1 CKS1 CDC28 protein kinase KIAA0213 gene, partial cds Aquaporin-5 (AQP5) gene Placental bikunin mRNA Glycogenin Calcyclin protein) HT4604_s_a RC_AA4194 0.20911497 M10943_at Ħ, 0.20929463 D00017_at 0.20926517 U46569 at 0.20898302 X75962_at 0.20966943 HT1614 at 0.20938765 L40380_at 0.21017759|D86968_at ä 0.21073449 U78095_at 0.21061045 HT2896_at 0.2103696 M31013_at 0.21025482 D84307 at 0.2100078 Z22548 at 0.20975152 L36818_at 0.2107923 X54941_at HG1614-0.20953403 M31627 0.21009575 U26032 HG2788-0.210412 61 at 0.21050337 s_at 0.20962179 0.345788 0.34636 0.34603 0.346443 0.34622 0.346461 0.347013 0.346846 0.348006 0.347378 0.347358 0.347024 0.346992 0.346570.348098 0.347748 0.347449 0.348106 0.347977 0.2582242 0.4161993 0.2595041 0.4167566 0,2589543 0.416486 0.2583682 0.4162008 0.2601779 0.4169285 0.2591497 0.4165642 0.2587756 0.4162321 0.2612912 0.4174601 0.2610937 0.4173998 0.2601918 0.4169976 0.2617883 0.4175743 0.2616552 0.4174962 0.26039 0.4170809 0.2595922 0.4168607 0.2623431 0.4178353 0.4178126 0.4177389 0.2608421 | 0.4172757 0.2619094 | 0.4175922 0.2622514 0.2620153 Uterus_A Uterus A Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus Uterus 616 deno 612 deno 613 deno 614 deno 615 deno 617 deno 607 deno 608 deno 610 deno 611 deno 606 deno 609 deno 604 deno 605|deno 600 deno 601 deno 602 deno 603 deno 599 deno

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FIG. 14G2

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	الماموم المامو	retal orain (239rB) mRNA, from the WAGR region	100 kDa coactivator mDMA		cDNA clone 471671 3', mRNA sequence. (from Genbank)	, co O3F	ISC-22 protein mRNA	MINES	מובואס ו ווועואל	Glycoden synthasa kinasa 3 m DNA	Chimeric mRNA derived from AML1 gene and MTG8(ETO) gene,	partial sequence	17. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Land 1. Carry 1. Carry 1. Land 1. Carry 1. Carr	DI Dorlacenay Commission Addition	accertoyr-coertsyllie A delta Isomerase (3,2 trans-enoylat) Coenzyme A isomerase)		NIAAUZbb gene	Drothous and the state of the s	rioteasorire acrivator nPA28 subunit beta	NF2 Neurofibromin 2 (bilateral acoustic neuroma)		Cbl-b mRNA	יייייייייייייייייייייייייייייייייייייי	r Br' Prostatic binding protein	DMCH Dra malania constituti	nort i contentini concentrating hormone	FFF1G Translation alongation footby 1	The second and lacin I garring	KIAA0183 gene, partial cds		PRKAR1B Protein kinase, cAMP-dependent, regulatory, type I, beta	DDNI1 Dikonkonin	N NIDOLIOIRI I	RalGDS-like 2 (RGI 2) mBNA continuodo
	0.2088752411157944 at	201311 91	0.20883551 U22055 at	RC_AA0353	oo at	1135048 0+	033040 at	X80199 at	20000	L40027 at	0.000	U 14022 at	729083 24	בבטטטט פו	တ	D87466 21	201435 at	145248 at	מביים מביים	-11353 at		J26710_at	(75050 24	1522 at	1410//03_s_a		A11353 at				ä		+	
		1	0.20883551		0.2000 103 00 at	0.20855607 1135048 -+	0.5000000	0.20841019 X80199 at		0.20836684 L40027 at	0 20825005	0.2002.0033	0.20813176 729083 2		0.20804895 L24774	0.20701467 087465	0.50101407	0.20790617 0.45248 9		0.2078381 L11353		0.20774677 U26710	0.20763738	20010010	0.20748435		0.20742702 M11353 at		0.20732033 D80005 at	. 004000	0.20129133 Mibbubb	0.20722334 Y00284 at		0.20709082 U68142 at
	0.345744		0.34551	0 345443	3	0.345349	2	0.345224		0.345082	0 34505		0.344815		0.344791	0.344776		0.344729		0.344678		0.344592	0.344576		0.344563		0.344456		0.344356	0 344 202	20244600	0.344206		0.344153
	0.4159587		0.4159102	0.4159014		0.4158571		0.4156796		0.4154275	0.4154163	1	0.4153165	1	0.4149506	0.414668	The state of the s	0.4144479		0.4142088	777777	0.4141737	0.4141395		0.4138413		0.4136742		0.4135049	0.4134337	201011	0.413304		0.41278
	0.2578333		0.2578289	0.2577869		0.2574125		0.257185		0.2569321	0.2569108		0.2569098		0.2567879	0.2563604		0.2563132		0.2559661	0.2550404	0.2000104	0.2556659	7	0.2554102		0.2550506		0.2550402	0.2550168	. 1	0.2550134		0.2547998
Uterus A	1 1	Uterus_A	619 deno	Uterus_A 620 deno	Uterus A]]	Uterus_A	622 deno	Uterus_A	- 1	624 deno	Uterus A	625 deno	Uterus_A	020 deno	627 deno	Uterus A	628 deno	Uterus_A	629 deno	630 deno	Uterus A	1	Uterus_A		Y Y	1	Y 	<	635 deno	S A	636 deno	Uterus_A	
	618		616	620		62.		622		27.9	624		625		070	627		628	Č	629	630		631		632		633	627	450	635 (929	_	637 deno

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FIG. 14H2

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Clone 23587 mRNA sequence	KIAA0090 gene, partial cds	Carbonic anhydrase-related protein VIII (CA8) mRNA, partial cds	VII 2 VIIIn 2 (ezrin)	Tumor-associated 120 kDa nuclear protein p120, partial cds(carboxvl	(terminus)	UROS Uroporphyrinogen III synthase	RAP1GA1 RAP1, GTPase activating protein 1	DNA sequence from PAC 452H17 on chromosome X contains sodium and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs	Clone 23574 mRNA sequence	SSBP Single-stranded DNA-binding protein	LGALS1 Ubiquinol-cvtochrome c reductase core protein II	LGALS3 Lectin, galactoside-binding, soluble, 3 (galectin 3) (NOTE:		G1P2 Interferon, apna-inducible protein (clone IFI-15K)	218kD Mi-2 protein	CENPB Centromere protein B (80kD)	Bcr (breakpoint cluster region) gene in Philadelphia chromosome	NADH-CYTOCHROME B5 REDUCTASE	RNA polymerase II largest subunit gene extracted from H.sapiens	CUL-2 (cul-2) mRNA
at	at.			a					U90905 at	M94556 at	J04456 at	to		M13/55_at	X86691_at	X05299 at	X02596 at	M28713 at	-	1
0.2069234 U90914	0.2069172 D42044_	0.20680265 L04656 at	0 20664568 X51521 at		0.20659515	0.20650668 J03824 at	0.20639172 M64788_at	0.20637465 Z96810	0.20626236 U90905	0.20620517 M94556	0.20606036 J04456 at	0.20592916 M57710	0107070	0.20589109 M13/55 at	0.20581552 X86691_	0.20570503 X05299 at	0.20554873 X02596	0.20548111 M28713 at	0.20536642	0.20533037 U83410_at
0.34411	0.343995	0.343954	0.343852		0.343824	0.343672	0.343545	0.343459	0.343439	0.343396	0.343351	0 343318		0.343197	0.343179	0.343091	0.342987	0.342944	0.342787	0.342761
0.4125558	0.4125383	0.4123448	0.4122883		0.4122883	0.4121573	0.4121376	0.4117497	0.4116872	0.4116798	I	0.4116021		0.4115909	0.4115728	0.4114385	1	0.4113905	0.444280	0.2507451 0.4112571
0.2546377	0.2544473	0,2544405	0.2544229		0.2538336 0.4122883	0.2537045	0.2533985	0.2529826	0.2525482	0.2520984	0.2519337	0.2518845 0.4116021		7568167.0	0.2517993	0.2516725	0.2511663	0.2509293	0.2508778	0.2507451
Uterus_A 638 deno	Uterus_A 639 deno	Uterus_A 640 deno	Uterus_A 641 deno	Uterus A		Uterus_A 643 deno	Uterus_A 644 deno	Uterus_A 645 deno	Uterus_A 646 deno	Uterus_A 647 deno	Uterus_A 648 deno	Oterus A	Uterus_A	opo deno		Uterus_A 652 deno	Uterus A 653 deno	Uterus_A 654 deno	Uterus A	Uterus_A 656 deno
638	369	640	641		642	643	644	645	646	647	648	646		00	651	652	653	654	654	656

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswanıy, *et al.*

FIG. 14]

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Uncoupling protein homolog (UCPH) mRNA	Major astrocytic phosphoprotein PEA-15	B94 PROTEIN	Mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA encoding mitochondrial protein	J00207 rna2 IFNA gene (interferon alpha-a) extracted from Human leukocyte at interferon (leif) alpha-a gene	B12 protein mRNA	Transcriptional activator hSNF2b	EST: aa45a12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 823870 3', mRNA sequence. (from Genbank)		KK I & Keratin &	Immunoglobulin lambda gene locus DNA, clone:92H4	HARS Histidyl-tRNA synthetase	COL6A1 Collagen, type VI, alpha 1	Transmembrane 4 superfamily protein (SAS) mRNA	NDUFV3 gene, exon 3	EEE2 Eukarvotic translation elongation factor 2	EST: HFBEST-40 Human fetal brain QBoqin2 Homo saplens cDNA,	Mucin 3, Intestinal (Gb:M55405)	r_at Transcription Factor Btf3 Homolog (Gb:M90355)	Putative OSP like protein mRNA, partial cds
			ät	100207_ma2 at	W80783_at		_AA4904 at	X74929_s_a				X15880 at		X99728_at	X97074 at	N89563_s_a	HG2147- HT2217 at		ज
0.20531571 U94592_at	0.20518886 X86809_at	0.20493752 M92357_at	0.20487504 U65579	0.20482738	0.20468934 M80783	0.2045756 U29175_at	0.20450786 61	1	0.204455/81	0.20429668 D87024_at	0.20420502 X05345	0.20409995 X15880	0.20394151 U01160_at	0.20387729 X99728	0.20375377 X97074 at	A MAGGGGGG	0.20352738 HT2217	HG4518 0.20349981 HT4921	0.20338908 U89916
0.342705	0.342575	0.342562	0.342525	0.342445	0.34231	0.342191	0.342164		0.342137	0.341987	0.341978	0.341835	0.341788	0.341773	0.341508	0.044444	0.341392	0.341341	0.341262
0.4112431	0.4111953	0.4111344	0.4110905	0.4110051	0.4108851	0.4108338	0.4107993		0.4107896	0.4105617	0.4104435	0.4103316	0.410291	0.4101844	0.4404575			0.4099067	0.4098116
0.2505027	0.2504852 0.4111953	0.2504227	0.2503917	0.2503327	0.2502797	0.250184	0.2501272		0.2499178	0.2498905	0.249839	0.2498355	0.2495216	0.2495123	0.2404593	000000000000000000000000000000000000000	0.2486922	0.2485079	0.2485042
Uterus_A 657 deno	Uterus_A 658 deno	Uterus_A 659 deno	Uterus_A	Uterus_A 661 deno	Uterus_A 662 deno	Uterus_A 663 deno	Uterus_A 664 deno	Uterus_A	oob deno Uterus A		Uterus_A 667 deno	Uterus_A 668 deno	Uterus_A 669 deno	Uterus_A 670 deno	Uterus_A	Uterus_A	Uterus A 673 deno	Uterus_A 674 deno	Uterus_A 675 deno
657	658	629	099	661	662	663	664	C	caa	999	199	899	699	029	671		673	674	675

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		6 0.4097788 0.34116 0.20337161 D38305_at Tob	5 0 4096659 0 341127 0 2033072 M60614 at WT1 Wilms tumor 1		3 0.4096152 0.341061 0.20315552 D50922_at KIAA0132 gene	0.4095904 0.341047 0.20313679 D42084 at		8 0.4095649 0.340946 0.20292272 D14874_at ADM Adrenomedullin	AA004987_a	2 0.4092398 0.340837 0.20291898 t Homo sapiens HRIHFB2017 mRNA, partial cds	59 0.4091134 0.34083 0.20289299 X81003_at HCG V mRNA	55 0.4087214 0.340802 0.2028687 U23070 at Putative transmembrane protein (nma) mRNA	0.4085421 0.340801 0.2027938 M61176 at	M35851_s_a	0.40050474 0.40050400 0.40050400 11	AA137107	0.408259 0.340387 0.202427 D25248 at Randomly sequenced mRNA	0.4081624	36 0.4081178 0.3403 0.20235871 U06631 at IEF SSP 9502 mRNA	29 0.408109 0.340285 0.20226054 M36341_at ARF4 ADP-ribosylation factor 4	0	75 0.4080064 0.340005 0.2020316 U85625 at Ribonuclease 6 precursor	0.4078902 0.339905 0.20191616 S74728_at	o o coccess o coccosto coccostata of ATD2A2 ATDaca Cart francharting regular muerle clow fwifth ?
:)										
	IS_A	0.2484186	IS_A 0 2483445	IS A	0.2483443	IS_A 0.2481566	A S	0.2480698	S_A	0.2480122	IS_A 0.2479959	s_A 0.2479685	s_A 0.2477644	IS_A 0.2478759	0.24	S_A 0.2476614	IS_A 0.2475609	s_A 0.2474507	s_A 0.2471866	JS_A 0.2471129	s_A 0.2470499	s_A 0.2469575	s_A 0.246885,	IS_A
	Uterus	676 deno	Uterus 677 deno	Uterus	678 deno	Uterus_ 679 deno	Uterus	680 deno	Uterus	681 deno	Uterus 682 deno	Uterus 683 deno	Uterus 684 deno	Uterus	0100000	Orierus_ 686 deno	Uterus 687 deno	Uterus 688 deno	Uterus 689 deno	Uterus 690 deno	Uterus 691 deno	Uterus 692 deno	Uterus 693 deno	Uterus

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in the first the state of the s	0.4078249 0.330833		0.4076308 0.339725 0.20160927	0.4076252 0.339718 0.20140246 c.t.	01/24/07:0	0.4075416 0.339676 0.20132491	0.000000	0.4072084 0.339456 0.201289251	0.4071463 0.330307	0.20175889 M29550 at	0.4070459 0.339267 0.20114507 112404		0.4070299 0.339235 0.20096983 D87469 at	EST: 2x80d02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA	AA465016	0.2446809 0.4070299 0.33905 0.20089798 t Genbank)		0.4069985 0.338941 0.2008418	0 406780E 0 339830 2 2 3 2 3 3 4 16 s. a	0.20072708	0.4065297 0.338829 0.00074437	. 1 /21 / / / / / / / / / / / / / / / / /	725 0.4061399 0.338755 0.2006228 X71490 at 31kn		0.2436445 0.4060523 0.338715 0.20057796 M34057 at LTBP1 Latent transforming growth factor heta hinding protein 4	0.4059398 0.338673 0.20048787		0.405756 0.338579		0.405722 0.33844 0.200292	0.4055416 0.338424 0.2001aaaa515 4	ABOUNTED	0.40559 0.338980
	0,4078249			0.4076252			7000207	0.4072084	0.4071463	2			_				_	- 1									1						
	0.2457927	 	0.245791	0.2457024		0.2451821		0.2431198	0.2449466	+	0.2448869	0,700	0.2448439			0.2446809		0.2444632	0.2439893		0.2439373		0.2436725 (0.2436445	0.2434871	+	0.2433659		0.2432338	0.2430875 0		7000000
- 1	Orierus A 695 deno	Uterus A	Uterus A		Uterus_A		699 deno	Uferus A	1	Uterus_A	701 deno	Uterus_A	102 06110		Uterus_A	/03 deno	704 deno	Uterus A		Uterus_A	706 deno	Uterus_A	- 1	Vierus_A	Uterus A	1	Uterus_A	- 1	Oterus A	O I I dello	1 1	Uterus_A	-

714 (Uterus_A 714 deno	0.2424154	0.4049967	0.338116	Y08682 0.20004942 1 s at	Y08682_rna 1 s at	Carnitine palmitoyltransferase I type I
715	Uterus_A deno	0.2423697	0.4049794	0.337872	RC_A 0.19983758 13_at	RC_AA6091 13_at	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0503
716	Uterus_A 716 deno	0.2419224	0.4049338	0.337824	0.19976324 S65738	at	Actin depolymerizing factor [human, fetal brain, mRNA, 1452 nt]
717	Uterus_A 717 deno	0.2417723	0.4047661	0.337817	0.19967079 M59979 at		PTGS1 Prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
718	Uterus_A 718 deno	0.2413999	0.4043337	0.337802	0.19956286 J03278 at		PDGFRB Platelet-derived growth factor recentor beta notypentide
	Uterus_A		ş			AA477978_s	
719(719 deno	0.2409703	0.4043114	0.337776	0.19948545	at	Short-chain dehydrogenase/reductase 1
720	Uterus_A	0.2408781	0.4043111	0.337591	0.19943006		EST: zt55h02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA AA292745_a clone 726291 5' similar to TR:G984317 G984317 TRYPSIN-IR:I ATED PROTEIN: mRNA section central Genhank)
	Uterus_A		1			Z35402_ma	
721	721 deno	0.2403585	0.4041506	0.33754	0.19932517 1_	1_s_at	Gene encoding E-cadherin, exon 3 and joined CDS
722	Uterus_A 722 deno	0.2403563	0.4041416	0.337367	0.1993059 L42572	at	Motor protein
723	Uterus_A deno	0.2401321	0.4040065	0.337208	0.19921875 D89052	D89052 at	Proton-ATPase-like protein
724 (Uterus_A 724 deno	0.240064	0.4037657	0.337196	0.19912402 L38941 at		RPL37 Ribosomal protein L37
<u> </u>	Uterus_A					Control of the Contro	
725(725 deno	0.2400631	0.4037277	0.337097	0.19908763 D86985_at		KIAA0232 gene
726	Uterus_A 726 deno	0.2399433	0.4035304	0.337026	RC_A 0.19897778 01_at	RC_AA1570 01_at	RC_AA1570 EST: z119f07.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA 01_at clone 502405 3', mRNA sequence. (from Genbank)
727	Uterus_A deno	0.2396292	0.4033691	0.336926	0.19897367 D79994 at		KIAA0172 gene, partial cds
7287	Uterus_A	0.230414	0.4033473	0 336014	0 40875054	0.40875854 1440684 04	Albha 1 Chanasa a capara batalar aisam attaca 1 chal
	Uterus_A	700000		1 0000	1000 1001 10		יייייייייייייייייייייייייייייייייייייי
) R7)	-	0.2392691	0.4031408	0.330860	0.198/44/4 033032	U33032_at	IWO P-domain K+ channel IWIK-I mRINA
730	Urerus_A 730 deno	0.2389883	0.4029934	0.336761	0.19868517 J04611	J04611_at	G22P1 Thyroid autoantigen 70kD (Ku antigen)
731	Uterus_A	0.2389594	0.4028815	0.336745	0 19857195 X57206	at	ITDKR Inocitol 1 4 5-trisphoenhate 3-kinase R
Uter.	Uterus A	0.2384095	1		0.19854063 X86163 at		RDKRB2 Bradvkinin recentor R2
70	2122	0.001002.0	0.70207		0.1000100	7	בייייייייייייייייייייייייייייייייייייי

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

FIG 14M

Ulerus
S
S
S
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S_A 0.2382978 0.2382975 0.2382975 0.2382975 0.2377442 0.2377442 0.2365575 0.2365575 0.2365548 0.2365048 0.2365722 0.2365048 0.2364722 0.2365048 0.2365022
S_A 0.2382978 S_A 0.2382975 S_A 0.237756 S_A 0.2377442 S_A 0.2377442 S_A 0.2365575 S_A 0.2365575 S_A 0.2365364 S_A 0.2365364 S_A 0.23653648
8 8

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*

FIG. 14N2

0.2346534 0.3999384 0.335254 0.19669877 D84110 at RBP-MS/type 1	0.2344288 0.3997569 0.335208 0.19661027 J03934 s. at NMOR1 NAD(P)H:menadione oxidoreductase	0.2343063 0.3996253 0.335072 0.19656943 2_at glucose-6-phosphate dehydrogenase	0.2342788 0.3992167 0.33491 0.19651958 X56932 at LCAT Lecithin-cholesterol acyltransferase	0.233977 0.3991958 0.334874 0.19645308 L76703 at B56epsilon mRNA	0.2338666 0.3989463 0.334818 0.19640778 D87447 at KIAA0258 gene	0.2338324 0.3988006 0.334733 0.19628781 D38521 at KIAA0077 gene, partial cds	0.2337794 0.3987582 0.334612 0.19624043 Y13620 at BCL9 gene	0.2335423 0.3986899 0.334552 0.19611062	+	 	0.2331807 0.3984479 0.334214 0.1958741 U50733_at Dynamitin mRNA	0.2328755 0.3983392 0.334125 0.19585091	0.2328523 0.3982097 0.33405 0.1957263	 	0.2324877 0.3981585 0.333776 0.19558929 D28476 at KIAA0045 gene		0.2321644 0.3978292 0.333649 0.1954881 X93921_at Protein-tyrosine-phosphatase (tissue type: testis)	0.2320411 0.3977866 0.333561 0.19535936 U24683_at
1,2346534 0.3	ţ.	1	1	١	}	1	1	1	-	<u> </u>			1	1	1		1	
Uterus_A 753 deno 0	A si	Uterus_A	IS_A	Uterus_A 757 deno	S. A	Y SI	S A	A SI	A_S	IS A	Uterus_A 764 deno	Uterus_A 765 deno	Uterus_A 766 deno	Uterus_A 767 deno	Uterus_A 768 deno	Uterus A 769 deno	Uterus_A 770 deno	Uterus_A 771 deno

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	Tumor susceptiblity protein (TSG101) mRNA	COL6A2 Collagen, type VI. alpha 2		L-3-hvdroxvacyl-CoA dehydrogenase	-	1056222 3', mRNA sequence. (from Genbank)	CTMMM Cotonin (coult air and included actains)	SI COA1 Solits corrier family 0 (codium the decay)	1 (antinorter, Na+/H+ amiloride sensitive)		ITGB8 Integrin, beta 8	K/AA0059 gene		SMAD5 (Smad5) mRNA		TFIIB related factor hBRF (HBRF) mRNA		Guanine nucleotide exchange factor mss4 mRNA		Mg81		RPL37A Ribosomal protein L37a	MO11 IM domain only 1 (rhombotin 1)		KIAA0240 gene, partial cds	EST: ab15c03.r1 Stratagene lung (#937210) Homo sapiens cDNA	clone 840868 5', mRNA sequence. (from Genbank)	KIAA0205 nana	_			KIAA0017 gene	Listano LOA 4 (LOA) acco	nisione nza, i (nza) gene
	U82130_at	X15882 at		X96752 at	RC_AA6210	41_at	1103100 at	2000	X76180 at		M73780 at	D31883 at		U59913 at	U75276 s a			U/4324_at		H 1 909 at		L06499_at	M26682 at		D87077_at	AA482319_i	at	786960 at	162293 rna	1 s at		013642_at	MENTED of	אוטטו טב מו
	0.19531338 U82130_at	0.19519822 X15882		0.19514258 X96752 at		0.19507122 41	0 19498265 LI03100 at	2070010110	0.19475788 X76180 at		0.19468385 M73780	0.19462924		0.19455749 U59913 at		0.19444549	0101010	0.19431679 U/4324	0 40407400	0.1942/429 H1909		0.1941988 L06499	0.19413875 M26682 at		0.19407034 D87077_at		0.19391/32	0.19390087 D86960 at		0.1938536 1 s at		0.19381486 D13642	0 10370328 M60752 at	0.100100201
	0.333463	0.333454		0.333316		0.333158	0.333121		0.333		0.332975	0.332936		0.332872		0.332798	070000	0.33212	0020000	0.332008	0	0.332523	0.332385		0.33227		0.332202	0.332068		0.332008		0.331949	0 331021	1.201.00.0
	0.3976886	0.3976808		0.3974064	l .	0.39/4034	0.3974002		0.3973968		0.39/35/6	0.3972426		0.3971692		0.3971491	0.0074064	0.397 1331	1,0077000	0.037 1.034	0.000	0.39/12/8	0.3970439		0.3969169	00000	0.390898	0.3967957		0.3965802		0.3964263	0.3963582	0,0000004
	0.2314513	0.2311976		0.2311372	0000	0.2310928	0.230896		0.2303467		0.2303291	0.2303227		0.2301527		0.2300359	0.2200542	0.4293040	0 2200018	0.7253010	0.0000	0.2298452	0.2297839	1	0.2295767	0.000000	0.2292312	0.2283888	1	0.2281222	1	0.2280639	0.2276432	
Uterus_A	deno	Uterus_A deno	Uterus_A		Uterus_A	- 1	Uterus_A 776 deno	Uterus A	deno	Uterus_A	uerio Herrio	779 deno	Uterus_A	780 deno	Uterus_A	deno	Uterus_A		783 deno		Oterus_A	7 84 Geno	785 deno	Uterus_A	786 deno	Uterus_A	UEIO Herio		Uterus A		Uterus_A		Uterus_A	7
	772	773		774	775	677	776		777	770	0	779		780		781	782	7	783	3	707	/ 04	785		786	787		788		789		790	767	- ,

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FIG. 14PZ

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2	9763760	0 3063303	0 22402	0.40350034	RU_AAK302	TC_AA2302 E31. Z34E12.S1 Sodres Milhiwifu 31 Homo Sapiens CLINA Glone
		0.3903392	0.33182	0.19358824 /b at		667246 3, mKINA sequence. (from Genbank)
S	A.				_D55590	EST: Human fetal brain cDNA 3'-end GEN-183D04, mRNA sequence.
793 deno	0.2274526	0.3960518	0.331661	0.1934462	t	(from Genbank)
<u>s</u>	Α.				A2428	EST: zr65e10.s1 Soares NhHMPu S1 Homo sapiens cDNA clone
794 deno	0.2273864	0.3960518	0.331624	0.19343604 23_at		668298 3', mRNA sequence. (from Genbank)
Uterus/	A 0.2273716	0 3080065	0.22467	0 409900994 VE4477 £	7	Mathianii
0,	A 0.2213110		401000	0.19330031	A04111 al	at interallution tells
		0.2273713 0.3958992	0.331521	0 19328187 1107231 at		GBSE1 G-rich DNA contence kinding factor 1
S	A		2000	2000	α	Total Guide Salanda Sa
		0.2273325 0.3958559	0.331473	0.19320635	1	EEF1G Translation elongation factor 1 gamma
Uterus/	A				X12876 s a	
798 deno	0.2272773	0.2272773 0.3956159	0.331357	0.1931426 t	 	KRT18 Keratin 18
Uterus/	A 0.2272036	0.2272036 0.3956129	0.331346	0.19299792 159423 at		Mad-related protein MADB4 mBNA
	+-	2	2	0.1000100	1	יייים על ייייים איייים איייים איייים איייים איייים איייים איייים איייים איייים איייים איייים איייים איייים איי
800 deno	0.2271893	0.3955437	0.331226	0.19296314 U41060 at		breast cancer, estrogen regulated LIV-1 protein (LIV-1) mKNA, partial cds
<u>s</u>	l A					
801 deno	0.2271715	0.3954002	0.331224	0.19287054 X13956_at	X13956_at	9 KD PROTEIN
S	A	0.00	0	1000	383_cds	subunit 63 kda isoform/membrane skeleton protein (alternatively
ouz deno	0.227 1464	0.227 1464 0.3953812	0.33115	0.19285284 1_at	1_at	spliced, exon 10 to 13 region} [human, Genomic, 4499 nt 3 segments]
Uterus	Α,				RC AA1610	EST: zo62h09.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 591521 3' similar to SW:PPAP_RAT P20646 PROSTATIC ACID PHOSPHATASE PRECURSOR:, mRNA
803 deno	0.2270525	0.2270525 0.3951676	0.331136	0.19272555 85 at		sequence. (from Genbank)
S	A					
804 deno	0.2269973	0.3949719	0.331	0.19258632 X64037_at		GTF2F1 General transcription factor IIF, polypeptide 1 (74kD subunit)
S	A.		0000		U90552_s_a	
- 1	0.220023	0.3949148	0.330948	0.19249186	•	Butyrophilin (BTF5) mKNA
Uterus / 806 deno	A 0.2265343	0.3948469	0.330855	0.19245616 U79254 at		Clone 23693 mRNA sequence
S	A				AA5051	EST: aa65e04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone
	0.2263038	0.3947555	0.330841	0.19244628 41	41_at	IMAGE:825822 3', mRNA sequence. (from Genbank)
Uterus/ 808 deno	A 0.2260586	0.2260586 0.3946863	0.330795	0.19230844	AF000560_a	TTF-I interacting peptide 20 mRNA, partial cds

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TRUSSIKAV Ribosomal protein Sik kinasea 90kU polypantida 2	0 19220942 1 07597 at				
		217859	0.19		.330721
r0	RC_AA0355	0.19207966 14 at	0.192		.330721
	0.19195788 M65199 at	95788	0.191	0.330532 0.191	0.3944922 0.330532
	0.19189903 U59752 at	89903	0.191		.330378
1	HG33- HT33 at	0.19182348 HT33	0.197		0.330358
	0.19168772 L13977 at	168772	0.19	0.330248 0.19	.330248
T	0.19163452 U37689 at	63452	0.191	0.330098 0.191	330098
	0.1915269 U53445_at	915269	0.19	0.329969 0.19	.329969
_a PML Probable transcription factor PML {alternative products}	X63131_s_a t	0.19140352		0.329914 0.191	.329914
	0.19135886 M29877 at	35886		0.329914 0.1913	.329914
		3415			.329837
AC002115_c chromosome 19 cosmids R31396, F25451, and R31076 containing ds1_at COX6B and LIPKA_genomic sequence	AC002115_c	31549	0.1913	0.329771 0.1913	
	0.19120951 L48513 at	0951	0.1912		329648
σ,	X16609_s_a t	2635	0.19112635 t	0.329618 0.1911	329618
 	0.1911092 J04970_at	1092	0.191	0.32951 0.191	
	0.19100827 D86972 at	0827	0.1910	0.329414 0.1910	329414
	0.19095838 M96982_at	95838	0.1909	0.329368 0.1909	.329368
at RPS3A Ribosomal protein S3A	0.19090745 M84711_at	0745	0.1909	0.329347 0.1909	.329347

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswany, *et al.*

FIG. 14RZ

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F	Uterus A				The second secon		
828 deno		0.2210563	0.3931398	0.329226	0.19085993 D25328_at		PFKP Phosphofructokinase, platelet
Uteru 829 deno	Uterus_A deno	0.2210487	0.3930356	0.329107	RC_A 0.19082682 63_at	A1557	EST: zo52g12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 590566 3, mRNA sequence. (from Genbank)
	Uterus_A				AA09	1752_a	Protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform
8300	- 1	0.2209396	0.3927349	0.329104	0.190611151		(calcineurin A beta)
831	Uterus_A deno	0.2208063	0.3927211	0.329035	0.19058026 X69111 at		ID3 Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein
Uteru 832 deno	Uterus_A deno	0.2205668	1	0.328885	0.1905006824 s at	9	EST: zt45e11.s1 Soares ovary fumor NbHOT Homo sapiens cDNA clone 725324 31 mRNA sequence (from Genhank)
	Uterus_A						
833 deno	Jeno	0.2203584	0.3926899	0.328875	0.190399 L09260	at	(chromosome 3p25) membrane protein mRNA
	Uterus_A					-	
834 deno	deno	0.2203135	0.3926258	0.328757	0.19037071 Z27113 at		DNA-DIRECTED RNA POLYMERASE II 14.4 KD POLYPEPTIDE
Uteru 835 deno	Uterus_A deno	0.2202485	0.3926057	0.328752	RC_A 0.19024087 34 at	A4632	KIAA0792 gene product
	Uterus_A				A COLUMN TO THE		
836 0		0.2201656	0.3925739	0.328696	0.19013503 D38128	të,	PTGIR Prostaglandin I2 (prostacyclin) receptor (IP)
768	Uterus_A	7700000					
02/50	Uerio A	0.2200211	0.392552	0.328696	0.19007593 X75535	at.	33 KD HOUSEKEEPING PROTEIN
838 deno	2	0.2196897	0.3925354	0.328503	0 189990461 33243	_	DKD1 Dolvovetic kidnav disassa protain 1
1	Uterus_A		1			;	מוסטים אינויים אינויים אינויים אינויים אינויים אינויים אינויים אינויים אינויים אינויים אינויים אינויים אינויים
839 deno	leno	0.2195956	0.3924983	0.328482	0.18995152 U26424	ä	Stress responsive serine/threonine protein kinase Krs-1 mRNA
ر	Uterus_A					T	
840 deno	leno	0.2195145	0.3923914	0.328342	0.18983406 D23662	at	UBL1 Ubiquitin-like protein
	Uterus_A						
841 deno		0.2194871	0.392348	0.328262	0.18979727 D80001	at	KIAA0179 gene, partial cds
. ر_	Uterus_A				HG2855-		
842 deno		0.2192769	0.3922077	0.328238	0.1897162 HT2995	at_	Heat Shock Protein, 70 Kda (Gb:Y00371)
0 843 d	Uterus_A	0.2188253	0 3921473	0 328225	0.18062407	ŧ	DETA LIEVOSAMINIDASE AL DIJA OLIANI DEFOLIDOSO
	Uterus A				1000 OT 2000 O	5 ,	SELECTION OF THE SELECT
844 deno	leno	0.2186754	0.3921363	0.328185	0.18959355 D84454	aţ	UDP-galactose translocator
<u>ر</u> ا	Uterus_A				M22403	s a	
845 deno	leno	0.2183199	0.3920519	0,328171	0.18950279t		PLATELET GLYCOPROTEIN IB ALPHA CHAIN PRECURSOR
Uteru 846 deno	Uterus_A	0.2181793	0.301078	0 328458	0.18046074		END Endedin (Orler Dender Wohen a managed 1)
2		201121	1		0,10040014	ō,	The Ericognii (earling independent and indepen
847 deno	2	0.2181419	0.3916428	0.328117	0.18941845 L40393_at		(clone S171) mRNA
				-	The state of the s		

Docket No.: 2825.2020-002

Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al. Estrogen receptor-related protein (hERRa1) mRNA, 3' end, partial cds COX7A1 Cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) U41766_s_a | Metalloprotease/disintegrin/cysteine-rich protein precursor (MDC9) RC_AA4890 EST: aa54f09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone Smooth muscle myosin heavy chain isoform SMemb [human, E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA IMAGE:824777 3', mRNA sequence. (from Genbank) Plasma cell membrane glycoprotein (PC-1) mRNA 0.18884222|S67247_s_at|umbilical cord, fetal aorta, mRNA Partial, 971 nt] Alpha-1 collagen type II gene, exons 1, 2 and 3 43 kDa inositol polyphosphate 5-phosphatase SRP9 Signal recognition particle 9 kD protein Growth-arrest-specific protein (gas) mRNA Iduronate 2-sulfatase (Hunter syndrome) COUP TRANSCRIPTION FACTOR 0.18848702|Z74616_s_at|COL1A2 Collagen, type I, alpha-2 0.1883928 D89501_at-2 Human PBI gene, complete cds Myosin VIIa transcript 2 mRNA 0.18879755|S69272_s_at|Cytoplasmic antiproteinase ORF, Xq terminal portion FH Fumarate hydratase PBI gene mRNA AA452625_a 0.18909398 M83186_at ä 0.18787563 M60299 at 0.18780664 M37197 at 0.18784288 U55209 at 0.18916298 D16469 at 0.18887334 U39317 at 0.18799828 U59309 at 0.18791752|U20998_at ਜ਼ ਙ 0.18835962|Z31695 at 0.18806374 L13720 at 0.18898879 D12485 0.18841834 D89501 0.18926829 L38487 0.18871094 63 at 0.18903786|t 0.18866172 0.326678 0.328019 0.327975 0.32743 0.327298 0.327274 0.326948 0.326938 0.326936 0.32682 0.327917 0.327868 0.327681 0.327657 0.327458 0.327156 0.327038 0.327832 0.327261 0.327242 0.2160996 0.3901967 0.2168844 0.3910093 0.2170451 0.3911894 0.2165489 0.3909825 0.216281 0.3904407 0.2162152 0.3904098 0.2161932 0.3902636 0.2180451 0.3916329 0.2179092 0.3913852 0.2177311 0.3913164 0.2176722 0.3912907 0.2175078 0.3912492 0.2173687 0.3912196 0.2170184 0.391046 0.390965 0.2164272 0.3906802 0.2179884 0.3915557 0.2165359 0.3907785 0.2164264 0.3906361 0.2161681 0.3902329

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2825.2020-002

Docket No.: Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, et al.

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Uterus 868 deno	_A 0.2159223	23 0.3901786	0.326655	0.18769714	AA036900_a	AA036900_a EST: zk29e11.r1 Soares pregnant uterus NbHPU Homo sapiens t
Uterus 869 deno	A 0.2158823	23 0.390174	0.326548	0.18764181 L19314	at	HRY gene
Uterus 870 deno	A 0.2158697	97 0.3901598	0.32623	0.18763767 D50911 at		KIAA0121 gene
Uterus 871 deno	A 0.2157742	42 0.3901439	0.326055	0.18754317 t	F006609_a	RGS3 mRNA, 5' UTR
Uterus	Y_		1	0.0000000000000000000000000000000000000	0000	+ v • C C
8/2 deno		56 0.390073	0.325800	0.18/32888	2/4/92_s_at	0.18/32888 Z/4/92_s_attCCAA1 transcription binding factor subunit gamma
Uterus 873 deno	A 0,2154192	92 0.3900648	0.32573	0.1872749 L08666	at	VDAC2 Voltage-dependent anion channel 2
Uterus 874 deno	A 0.2153729	29 0.3900135	0.325729	0.18723059 M83772	at	FMO2 Flavin-containing monooxygenase 2
Uterus 875 deno	_A 0.2152882	82 0.3899862	0.325652		0.18716176 J03077 s at	PSAP Sulfated divcoprotein 1
Uterus	A.				1 7	OTA Citable Leaves
0/0 dello	0.2.14885	65 U.3899649	0.325023	0.18699339 764330	ส	ATF-citrate iyase
877 deno		09 0.38994	0.325549	0.18695594 Z50853	ä	СГРР
Uterus 878 deno	A 0.2146991	91 0.3898827	0.325549	0.18680224 M62762	at	ATP6C Vacuolar H+ ATPase proton channel subunit
Uterus	A.	3				
879 deno	0.2146418	18 0.3898788	0.325455	0.18680006 X84908 at		Phosphorylase-kinase, beta subunit
Uterus 880 deno	A 0.2141112	12 0.3898322	0.325386	RC_A 0.18666598 65 at	A0404	EST: zk46h09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485921 3', mRNA sequence, (from Genbank)
Uterus	Y,					
881 deno	- 1	43 0.389818	0.32537	0.18656534 D63475	at .	KIAA0109 gene
Uterus 882 deno	A 0.9137322	22 0 3898152	0.325361	0 18643631113616 at		ANK3 Ankvrin G
Uferus	A				-	EST: zm27e01.s1 Stratagene pancreas (#937208) Homo sapiens
883 deno		17 0.3896319	0.325349	0.18640657		cDNA clone 526872 3', mRNA sequence. (from Genbank)
Uterus 884 deno	_A 0.2134041	41 0.3895733	0.325204	RC_A 0.18634397 90_at	A4343	EST: zw31a06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 770866 3', mRNA sequence. (from Genbank)
Uterus 885 deno	۷	33 0 3895175	0.325204	0.18630908 Z34897	äţ	HRH1 Histamine receptor H1
Uterus	A				s_a	Protein encoded by a candidate gene, DXS6673E, for mental
886 deno	0.2131764	64 0.3893924	0.325166	0.18622774	t	retardation
Uterus 887 deno	A 0.213163	63 0.389187	0.325166	0.18616542 U45285_at		Specific 116-kDa vacuolar proton pump subunit (OC-116KDa) mRNA

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				-		Ì	NUT THE THE THE THE THE THE THE THE THE TH
ç	Uterus_A						
∞	888 deno	0.2130594	0.3891805	0.325129	0.18610477 D88378	Ħ,	Proteasome inhibitor hPl31 subunit
(Uterus_A					A4814	EST: zv45a05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA
[מכ	- 1	0.2129396	0.3891524	0.324892	0.18605664 40 at	40 at	clone 756560 3', mRNA sequence. (from Genbank)
3	Uterus_A					C00810_s_a	
Şĺ		0.2128476	0.3890407	0.324798	0.18591151		Homo sapiens clone 24733 mRNA sequence
	UterusA 891 deno	0.2127736	0.3889237	0.324723	0.18574932 M57567 at	M57567 at	ARES ADD-ribosolation factor 5
	Uterus A	 				35	י שיייי פיייי פייייי פייייי פייייי פיייייי פיייייי
2	1		0.2126237 0.3889156	0.324492	0.18571627 M27878 at		ZNF84 Zinc finger protein 84 (HPE2)
-	Uterus A	 		The second secon		AA012885 a	AA012885 a EST; ze27f07.r1 Soares retina N2b4HR Homo saniens cDNA clone
8	893 deno	0.212453	0.3888914	0.324312	0.18565921	+	360229 5', mRNA sequence. (from Genbank)
7	Uterus_A			1,700	27.07.0	-	U30999 Homo sapiens MV3 melanoma Homo sapiens cDNA clone
4	ueilo Herus A	0.2124312	0.3887673	0.32417	0.18564533 U30999 at	U30999 at	memd, mRNA sequence
35		0.2124234	0.3887493	0.324127	0.18562196	AA443230_a t	Casein kinase 2. albha 1 nolvneptide
	Uterus_A	┼					
ဖ	896 deno	0.2124129	0.3887451	0.324108	0.18562196 U67319	U67319_at	Mch3 isoform alpha (Mch3) mRNA
7	Uterus_A 897 deno	0.2121364	0.3887233	0.32399	RC_A 0 1854949191 at	45999	
	Uterus_A	+				HG2239-	
8	898 deno	0.2118426	0.388687	0.323895	0.18537976 HT2324	HT2324_at	Potassium Channel Protein (Gb:Z11585)
	Uterus_A				A CONTRACTOR OF THE CONTRACTOR		
9	899 deno	0.2118247	0.3886782	0.323885	0.18536246 X70476_at	X70476_at	COATOMER BETA' SUBUNIT
9	Uterus_A						
2		0.2117503	0.3886605	0.323654	0.18533596 D87683_at		KIAA0243 gene, partial cds
$\overline{}$	UterusA	0.2117159	0.3886469	0.323579	0 18513113	735491 at	Noval attracentarional recentarios established
	Uterus A	+					איניטן שיניטים והספקים בספקים איניסים איניסים שיניסים איניסים
2	902 deno	0.2115579	0.3884025	0.323459	0.1850868	0.1850868 X04106_at	CAPN4 Calpain, small polypeptide
2	Uterus_A	0.0444040	70000000	0000000	0.4010000		
2	I Herric A			0.525320	0.1000000	- (SEC 14L SEC 14 (S. Cel evisiae)-iike
7		0.2113917	0.3883212	0.323286	0.18500431	L03174_s_d	CBP1 Collagen-binding protein 1
	Uterus_A				Permitten management of the control		
2	1	0.2111866	0.3882014	0.323258	0.18494545 D26018_at		KIAA0039 gene, partial cds
9	Uterus_A 906 deno	0.2111419	0.3881112	0.32316	0.18489355 X05610 at	X05610 at	COL4A2 Collagen, type IV, alpha 2
<u> </u>	Uterus_A	0.2110081	0.2110081 0.3880424	0.32316	0.18488622	S54005 s at	0.1848R622 S54005 s at THYMOSIN RETA_10
7			1 20000	0.020.0	0.10100	a 2001.00	

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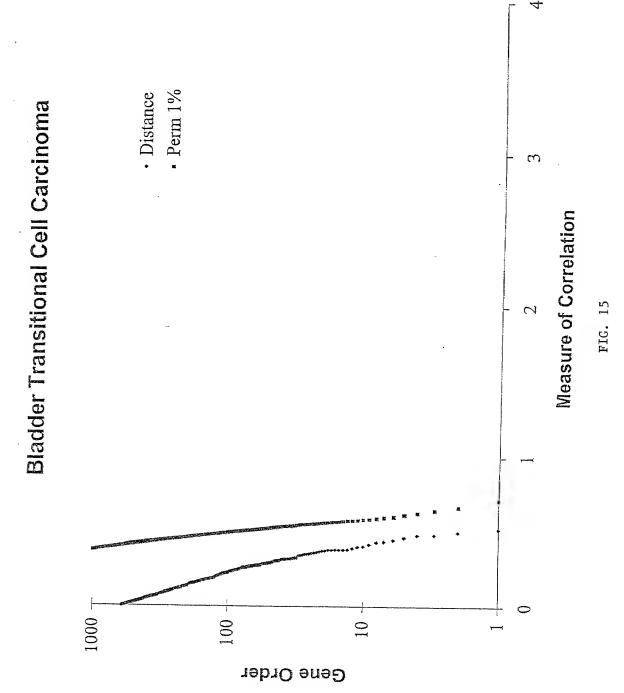
भूग पुरुष्ट पुत्रमें क्षित क्षिती भूताने पुरुष्ट क्षिती भूताने पुरुष्ट क्षिती भूताने भूताने क्षिताने भूतान	0.2081375 0.3866959 0.321457 0.18326777 X87843 at Cyclin H assembly factor	0.2080586 0.3864307 0.321449 0.18320964 U58048 at PRSM1 Metallopeptidase 1 (33 kD)	0.40000400	0.3004307	0.2077635 0.3863581 0.3213 0.18308832 X59373 at HOX4D mRNA for a homeobox protein		0.207701 0.3862331 0.321278 0.18306522 M65085 at FSHR Follicle stimulating hormone receptor	0.2073369	0.1020120 001001	0.2072935 0.3861527 0.321172 0.18287313 Z28407 at RPL8 Ribosomal protein L8	0.2070523 0.3861446 0.321143 0.18286061 1120499 at Estronom cultotraneferace mDNA	10 000000000000000000000000000000000000	0.2069973 0.3861243 0.32109 0.18269487 X99325 at Alpha-tubulin mRNA		0.206596 0.3860807 0.32105 0.18259509 L25286 s_at COL15A1 Collagen, type XV, alpha 1	0.2063607 0.3860218 0.320913 0.1825639 U60061 at RPS26 Ribosomal protein S26		0.2062834 0.3856179 0.320848 0.18246435 U31814 at Transcriptional regulator homolog RPD3 mRNA	the state of the s	0.2060707 0.3854891 0.320722 0.18238516 R74226 at Homo sapiens mRNA for ATP synthase subunit e, complete cds		0.3634396 0.320636 0.16230672 D14658 at	0.2056348 0.3851745 0.320637 0.18222739 t Metabotropic alutamate receptor 4 mRNA		0.2055/81 0.38514/6 0.32055 0.18216674 D83782_at KIAA0199 gene, partial cds	0.2055413 0.3849975 0.320471 0.18203042 t mRNA sequence. (from Genbank)		0.2054722 0.3849196 0.320453 0.18199 L38810 at Thyroid receptor interactor (TRIP1) mRNA	0.2053742 0.38483 0.320388 0.18195434 s at mRNA	1 384750 0 320370 0 18487532 54	0.3041.39 0.32031.9 0.10101.322 1/2121
	8_A	A A	S A	S A		S_A		A A	s A		S A	A		S A	•	<u>s</u>	Uterus A		S A		A_s	A		S_A		S A	S A		S	A_st	
	Uteru 928 deno	Uteru 929 deno	Oteru 930 deno	Ute	931 deno	Offe Coo	932 deno	Uteru 933 deno	Ute	934 deno	Uteru 935 deno	Ute	936 deno	Ute	937 deno	Uteru 938 deno	Ute	939 deno	Ute	940 deno	Uteru 94.1 deno	L Ife	942 deno	Ute	943 deno	Uteru 944 deno	Ute	945 deno	Uteru 946 deno	Uteru 947 deno	22 - 12

deno 0.2017264 0.3831523 0.319426 0.18038586 1 at Ulerus A 0.2010871 0.3830653 0.319319 0.18029657 U79209 at deno A 0.2010566 0.3828281 0.319221 0.18029657 U72209 at Ulerus A 0.2009065 0.3828281 0.319221 0.18029657 U78029657 U78029657 U78029667 U78029657 U78029657 U78029687 U78029687 U78029687 U78029688 U78029688 U7802968 U7780299 U7790299 U7790299 U7790299	<u> </u>	Uterus_A				×	X15525_ma	Lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 1 (and joined
Uterus A deno 0.2010871 0.3830653 0.319319 0.18034121 X97335_at deno Uterus A deno 0.2010566 0.382831 0.319221 0.18026657 U72209_at deno Uterus A deno 0.2006699 0.382772 0.319187 0.18019491 X63097_at deno Uterus A deno 0.2006699 0.382772 0.319187 0.18019491 X63097_at deno Uterus A deno 0.2006699 0.382772 0.319185 0.18002176 HT3688_at deno Uterus A deno 0.2002342 0.3825721 0.319818 0.17992198 U42359_at deno Uterus A deno 0.2002342 0.3825721 0.31878 0.17978184 Z28876_at deno Uterus A deno 0.20001837 0.3825721 0.31878 0.1797627_at deno Uterus A deno 0.2000612 0.3819756 0.31878 0.1795627_at deno Uterus A deno 0.199635 0.3817549 0.318262 0.17956562 U73864-at deno Uterus A deno 0.1996475 0.3817845 0.1795666 0.1795666 1141564 at deno	296		0.2017264			0.18038586 1		CDS)
Ulerus_A 0.2010566 0.382831 0.319221 0.18029657 U72209_at Ulerus_A 0.2000605 0.3828281 0.319221 0.18026663 D63881_at Ulerus_A 0.2006949 0.382779 0.319187 0.18019491 X63097_at Ulerus_A 0.2006699 0.3827249 0.319185 0.180019491 X63097_at Ulerus_A 0.2006599 0.3827249 0.319185 0.18002176 H73688_at Ulerus_A 0.2002562 0.382721 0.318913 0.17992198 U42359_at Ulerus_A 0.2002562 0.3827221 0.318913 0.17992198 U42359_at Ulerus_A 0.2001334 0.3822296 0.31878 0.17978184 226876_at Ulerus_A 0.2001334 0.3822296 0.31878 0.17978184 226876_at Ulerus_A 0.2000612 0.3817549 0.31845 0.17959562 U7365062 141690_at Ulerus_A 0.1995483 0.3817549 0.318386 0.179529562 U7363652 H74154_at	968	တ		0.3830653		0.18034121 X8	at	Kinase A anchor protein
Uterus_A deno 0.2009065 0.3828281 0.319221 0.18026663 D63881_at Uterus_A deno 0.2006699 0.3827249 0.319187 0.18019491 X63097_at Uterus_A deno 0.2006699 0.3827249 0.319185 0.18002176 HT3688_at Uterus_A deno 0.2002562 0.3827249 0.319185 0.18002176 HT3688_at Uterus_A deno 0.2002342 0.382722 0.318793 0.17992198 U42359_at Uterus_A deno 0.2001837 0.3824891 0.31878 0.17976818 226876_at Uterus_A deno 0.20001304 0.3822296 0.31878 0.1797627 at Uterus_A deno 0.2000612 0.3819756 0.31878 0.17959687 U73377_at Uterus_A deno 0.1998273 0.3817549 0.31845 0.17959687 U741690_at Uterus_A deno 0.19954757 0.381786 0.318254 0.17926956 U74154_at Uterus_A deno 0.19954757 0.3817842 0.17926956 U77929956 U7306871 <t< td=""><td>696</td><td><u>ω</u></td><td>0.2010566</td><td></td><td></td><td>0.18029657 U.</td><td>aţ</td><td>YY1-associated factor 2 (YAF2) mRNA</td></t<>	696	<u>ω</u>	0.2010566			0.18029657 U.	aţ	YY1-associated factor 2 (YAF2) mRNA
Uterus A 0.2006949 0.382779 0.319187 0.18019491 X63097_at deno Uterus A 0.2006699 0.3827249 0.319185 0.18002176 H73688_at HG3494-deno Uterus A 0.2002397 0.382712 0.319037 0.18001038 X82153_at HG3494-deno Uterus A 0.2002342 0.3826212 0.318913 0.17992198 U42359_at U42359_at Uterus A 0.2002342 0.3824891 0.318819 0.17978184 Z26876_at U42359_at Uterus A 0.2001304 0.3822286 0.318788 0.17978184 Z26876_at U42359_at Uterus A 0.2000612 0.3819756 0.31878 0.1797627_at D1797627_at D1797627_at D1797627_at D1797627_at D1797627_at D1797627_at D179762966_at >970</td> <td><u>S</u></td> <td></td> <td></td> <td></td> <td>0.18026663 Dt</td> <td>स्र</td> <td>KIAA0160 gene, partial cds</td>	970	<u>S</u>				0.18026663 Dt	स्र	KIAA0160 gene, partial cds
Uterus A 0.2006699 0.3827249 0.319185 0.18001038 X82153 at deno Uterus A 0.2006699 0.3827249 0.319185 0.18001038 X82153 at deno Uterus A 0.2002562 0.3826212 0.318913 0.17992198 U42359 at deno Uterus A 0.2002342 0.3825721 0.318913 0.17992198 U42359 at deno Uterus A 0.2002342 0.3825721 0.318918 0.17978184 226876 at deno Uterus A 0.2001837 0.3822296 0.31878 0.1797627 at deno Uterus A 0.2000612 0.3819756 0.31878 0.1795627 at deno Uterus A 0.2000612 0.3819756 0.31845 0.17959627 At HG30 at deno Uterus A 0.1995483 0.3817549 0.318356 0.17942125 M60091 at deno Uterus A 0.1995483 0.3816814 0.318254 0.17926956 U7326956 U7328956 U732884- </td <td></td> <td>8</td> <td></td> <td></td> <td></td> <td>0.18019491</td> <td>7</td> <td>RHD Rhasus blood aroun. D antigen</td>		8				0.18019491	7	RHD Rhasus blood aroun. D antigen
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Uterus A 0.2002562 0.3826212 0.318913 0.17992198 U42359 at Uterus A 0.2002342 0.3825721 0.318906 0.17980315 D30756 at Uterus A 0.2001837 0.3824891 0.318788 0.17978184 226876 at Uterus A 0.2001304 0.3822296 0.318778 0.1797627 at Uterus A 0.2000882 0.3819756 0.31878 0.17955957 X04366 at Uterus A 0.2000612 0.3819756 0.318582 0.17953672 U73377 at Uterus A 0.1998273 0.3817549 0.318386 0.17942125 M60091 at Uterus A 0.1995483 0.3817649 0.318254 0.179329956 U73029956 U73028844 deno 0.1995483 0.3814793 0.317842 0.17926956 U73028956 U73028956 U73028956 U73028956 U73028956 U73028956 U73028956 U730289	973	Uterus				0.18001038 X8	at i	CATHEPSIN K PRECURSOR
Uterus A 0.2002342 0.3825721 0.318906 0.17980315 D30756 at Uterus A 0.2001837 0.3824891 0.318819 0.17978184 226876 at Uterus A 0.2001304 0.3822296 0.31878 0.1797627 at Uterus A 0.2000882 0.3819756 0.31873 0.17959587 X04366 at Uterus A 0.2000612 0.3819015 0.318582 0.17953672 U73377 at Uterus A 0.1998273 0.318386 0.17951201 L41690 at Uterus A 0.1995483 0.3817845 0.1795562 U73377 at Uterus A 0.1995483 0.381583 0.318386 0.17942125 M60091 at Uterus A 0.1995483 0.381583 0.317977 0.17929956 U23028 at Uterus A 0.1993721 0.3812621 0.317842 0.17926472 t HG162 Uterus A 0.1992204 0.3812249 0.317721	974	က္ဆ				0.17992198 U.	at	N33 protein form 1 (N33) gene, exon 10 and complete cds
deno 0.2002342 0.3825721 0.318906 0.179980315 D30756 at Uterus A 0.2001837 0.3824891 0.318819 0.17978184 226876 at Uterus A 0.2001304 0.3822296 0.31873 0.1797627 at Uterus A 0.2000882 0.3819756 0.31873 0.17959587 X04366 at Uterus A 0.2000612 0.3819015 0.318582 0.17953672 U73377 at Uterus A 0.1998273 0.318386 0.17953672 U73377 at Uterus A 0.1995483 0.3816814 0.318386 0.17942125 M60091 at Uterus A 0.1995483 0.3815814 0.318254 0.17936562 HT4154 at Uterus A 0.19954757 0.381583 0.317845 0.17929956 U230288 at Uterus A 0.1992306 0.3812621 0.377842 0.17928956 U73928472 Uterus A 0.19922306 0.38		<u></u>	-	1				
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Uterus_A deno 0.2001304 0.3822296 0.318788 0.1797627 at Uterus_A deno 0.2000882 0.3819756 0.31873 0.17959587 X04366_at Uterus_A deno 0.199835 0.3817549 0.31845 0.17953672 U73377_at Uterus_A deno 0.1998273 0.3817549 0.318386 0.17951201 L41690_at Uterus_A deno 0.1995483 0.3817814 0.318386 0.17942125 M60091_at Uterus_A deno 0.1995483 0.381583 0.317977 0.17929956 U23028_at Uterus_A deno 0.1993721 0.3814793 0.317842 0.17926472 M79463_s_a Uterus_A deno 0.1992306 0.3812621 0.317814 0.17926472 HG162- Uterus_A deno 0.1992306 0.3812621 0.317814 0.17918429 HT3165_at Uterus_A deno 0.1992204 0.3812621 0.317721 0.17908818 U13165-at	976	္တ				0.17978184 Z:		LTBP1 Latent transforming growth factor beta binding protein 1
deno 0.2001304 0.3822296 0.318788 0.1797627 at Uterus A 0.2000882 0.3819756 0.31873 0.17959687 X04366_at Uterus A 0.2000612 0.3819015 0.318582 0.17953672 U73377_at Uterus A 0.199835 0.3817549 0.31845 0.17951201 L41690_at Uterus A 0.1998273 0.3817186 0.318386 0.17942125 M60091_at Uterus A 0.1995483 0.3816814 0.318254 0.17942125 M60091_at Uterus A 0.19954757 0.381583 0.317977 0.17929956 U23028_at Uterus A 0.1993721 0.3814793 0.317842 0.17929956 U23028_at Uterus A 0.1992306 0.3812621 0.317842 0.17926472 t Uterus A 0.1992204 0.3812621 0.317721 0.17918429 HT3165_at		S	-			1	·	EST: Human fetal brain cDNA 3'-end GEN-098C12, mRNA sequence.
Uterus A deno 0.2000882 0.3819756 0.31873 0.17959587 X04366_at Uterus A deno 0.2000612 0.3819015 0.318582 0.17953672 U73377_at Uterus A deno 0.1998273 0.3817549 0.31836 0.17951201 L41690_at Uterus A deno 0.1995483 0.381786 0.31836 0.17942125 M60091_at Uterus A deno 0.1995483 0.3815814 0.318254 0.17936562 HT4154_at Uterus A deno 0.1994757 0.381583 0.317877 0.17926956 U23028_at Uterus A deno 0.1993721 0.3812621 0.17926472 t HG162- Uterus A deno 0.1992306 0.3812621 0.317814 0.17928472 t Uterus A deno 0.1992306 0.3812621 0.317814 0.17918429 HT3165_at Uterus A deno 0.1992306 0.3812621 0.317814 0.17918429 HT3165_at	977		0.2001304				at	(from Genbank)
Uterus A 0.2000612 0.3819015 0.318582 0.17953672 U73377 at Uterus A 0.199835 0.3817549 0.31845 0.17953672 U73377 at Uterus A 0.1998273 0.3817549 0.318386 0.17951201 L41690 at Uterus A 0.1995483 0.3817814 0.318386 0.17942125 M60091 at Uterus A 0.1995483 0.3816814 0.318254 0.17936562 H74154 at Otherus A 0.1994757 0.381583 0.317977 0.17929956 U23028 at Otherus A 0.1992306 0.3817877 0.17929956 U23028 at Otherus A 0.1992306 0.3812621 0.317814 0.17918429 HT3165 at Otherus A 0.1992204 0.38128249 0.317721 0.17908818 U88871 at	978	2			0.31873	0 17959587 X	ā	CAI PAIN 1 - ABGE
deno 0.2000612 0.3819015 0.318582 0.17953672 U73377_at Uterus_A deno 0.1998273 0.3817549 0.31845 0.17951201 L41690_at Uterus_A deno 0.1995483 0.3817186 0.318386 0.17942125 M60091_at Uterus_A deno 0.1995483 0.3816814 0.318254 0.17936562 HT4154_at Uterus_A deno 0.1994757 0.381583 0.317977 0.17929956 U23028_at Uterus_A deno 0.1993721 0.3814793 0.317842 0.17926472_t HG162 Uterus_A deno 0.1992306 0.3812621 0.317814 0.17918429 HT3165_at Uterus_A deno 0.1992204 0.3812621 0.317721 0.17908818 U88871_at		0	- -		200	70000	รี	O'THE TAIL I'T WOLL
Uterus A deno 0.199835 0.3817549 0.31845 0.17951201 L41690 at L41630 at	979	ام				0.17953672 U		SKI V-ski avian sarcoma viral oncogene homolog
deno 0.199835 0.3817549 0.31845 0.17951201 L41690 at Uterus_Acho 0.1998273 0.3817186 0.318386 0.17942125 M60091 at Uterus_Acho 0.1995483 0.3816814 0.318254 0.17936562 HT4154 at Uterus_Acho 0.1994757 0.381583 0.317977 0.17929956 U23028 at Uterus_Acho 0.1993721 0.3814793 0.317842 0.17926472 t Uterus_Acho 0.1992306 0.3812621 0.317814 0.17918429 HT3165_at Uterus_Acho 0.1992204 0.3812349 0.317721 0.17908818 U88871 at		1 1		1				
Uterus A deno 0.1998273 0.3817186 0.318386 0.17942125 M60091 at HG3884- Uterus A deno 0.1995483 0.3816814 0.318254 0.17936562 HT4154 at HG3884- Uterus A deno 0.1994757 0.381583 0.317977 0.17929956 U23028 at M79463 s a M79463 s a HG162- Uterus A deno 0.1992306 0.3812621 0.317814 0.17918429 HT3165 at HG162- Uterus A deno 0.1992206 0.3812621 0.317721 0.17908818 U88871 at HG162-	980	deno	0.199835	-	0.31845	0.17951201 L		TNF receptor-1 associated protein (TRADD) mRNA, 3' end of cds
Uterus A HG3884- deno 0.1995483 0.3816814 0.318254 0.17936562 HT4154 at Uterus A 0.1994757 0.381583 0.317977 0.17929956 U23028 at Uterus A 0.1993721 0.3814793 0.317842 0.17926472 HG162- Uterus A 0.1992306 0.3812621 0.317814 0.17918429 HT3165 at Uterus A 0.1992204 0.3812349 0.317721 0.17908818 U88871 at	981	ည				0.17942125 M		GALT Galactose-1-phosphate uridyl transferase
Uterus_A 0.1994757 0.381583 0.317977 0.17929956 U23028_at Otherus_A 0.1993721 0.3814793 0.317842 0.17926472 t Uterus_A 0.1992306 0.3812621 0.317814 0.17918429 HT3165_at Uterus_A 0.1992204 0.3812349 0.317721 0.17908818 U88871 at	080	Uterus	-	1		H 0 47036562 L	, 7	Lormontic Drotain Hay 43
S	202	Herus	+	- 1		0.17 930302 11	ซี	
1S_A 0.1992204 0.3812349 0.317721 0.17908818 U88871 at a m79463_s_a M79463_s_	983]			0.317977	0.17929956 U		EIF2B Eukaryotic translation initiation factor 2B epsilon
1S_A 0.1992204 0.3812349 0.317812 0.17926472 t HG162 A 0.1992204 0.3812349 0.317721 0.17908818 U88871 at		S					S	
15_A 0.1992306 0.3812621 0.317814 0.17918429 HT3165_at 1s_A 0.1992204 0.3812349 0.317721 0.17908818 U88871 at	984				0.317842			PML Probable transcription factor PML {alternative products}
IS_A 0.1992204 0.3812349 0.317721 0.17908818 U88871 at	985	<u>S</u>			0.317814	Н 0.17918429 Н		Tyrosine Kinase, Receptor Axl, Alt. Splice 2
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	986	<u>s</u>	0.1992204	0.3812349	0.317721	0.17908818		Peroxisome targeting signal 2 receptor (Pex7) mRNA

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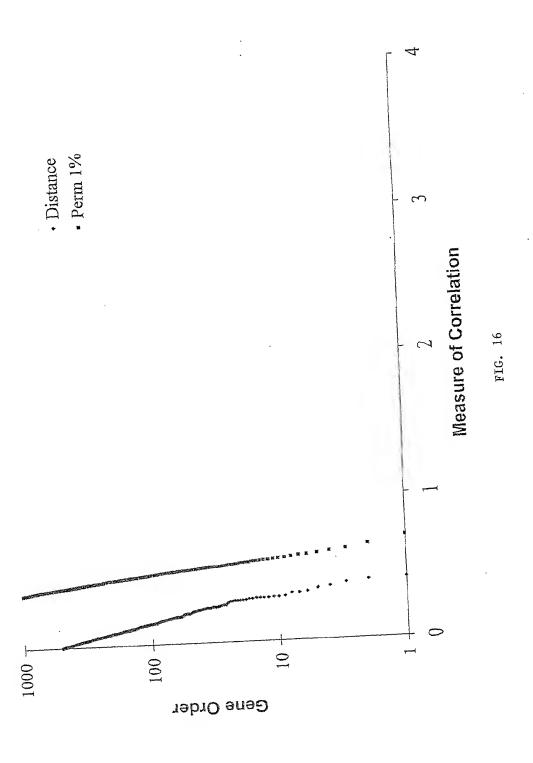
	no sapiens	()				•					T	it	cke le: ent	G	en	eti	c N	Лa	5.2 rke Rai	ers	fo	r T	วาร	nors
	RC_AA1560 EST: zo45d03.s1 Stratagene endothelial cell 937223 Homo sapiens	cDNA clone 589829 3', mRNA sequence. (from Genbank)	JTV-1 (JTV-1) mRNA		Ribosomal protein S24		FKBP1 FK506-binding protein 1 (12kD)		Niemann-Pick C disease protein (NPC1) mRNA	Lymphoma proprotein convertase (LPC) mRNA	Not56-like protein		60S RIBOSOMAL PROTEIN L23		Hs-cul-3 mRNA, partial cds		CRAT Camitine acetyltransferase		GP36b glycoprotein mRNA		Bet1p homolog (hbet1) mRNA		MitF mRNA	KIAA0n64 gene
strike delta delta delta	3C_AA1560				M31520_at		M34539_at	AF002020_a			Y09022 at		D21260 at		U58089_at		X78706_at		U10362_at	AF007551_a	•		Z29678_at	D31764 at
	<u> </u>	0.17902529 97_s_at	0.17900302 U24169_at		0.17890997 M31520_at		0.17886396 M34539_at		0.178793 t	0.17864256 U33849_at	0.1785778 Y09022 at		0.17849502 D21260 at		0.17842768 U58089_at		0.17835084 X78706_at		0.1782915 U10362_at		0.17820579 t		0.1781075 Z29678 at	0.17806113 D31764_at
		0.317703	0.317657		0.317656		0.317608		0.317467	0.317436	0.317378		0.317372		0.317316		0.317306		0.317271		0.317134		0.316759	0.316736
		0.3810806	0.3810107		0.380966		0.3809179		0.3806631	0.3806556	0.3803781		0.3802463		0.3800167		0.379923		0.3798698		0.3797584		0.3796913	0.1972284 0.3794312
		0.1990439	0.1988667 0.3810107		0.1987205		0.1986969 0.3809179		0.1985741	0.1983639	0.1982744		0.19822		0.1978276		0.1975586		0.1975501		0.1974711		0.1972353	0.1972284
	Uterus A	987 deno	Uterus_A 988 deno	Uterus A	989 deno	Uterus A	990 deno	Uterus_A	991 deno	Uterus_A 992 deno	Uterus A	I Harrise A		Uterus A	995 deno	Uterus A	996 deno	Uterus A	997 deno	Uterus A	998 deno	Uterus_A	999 deno	1000 deno
		286	988		686		066		991	992	993	2	994		995		966		997		366		666	1000

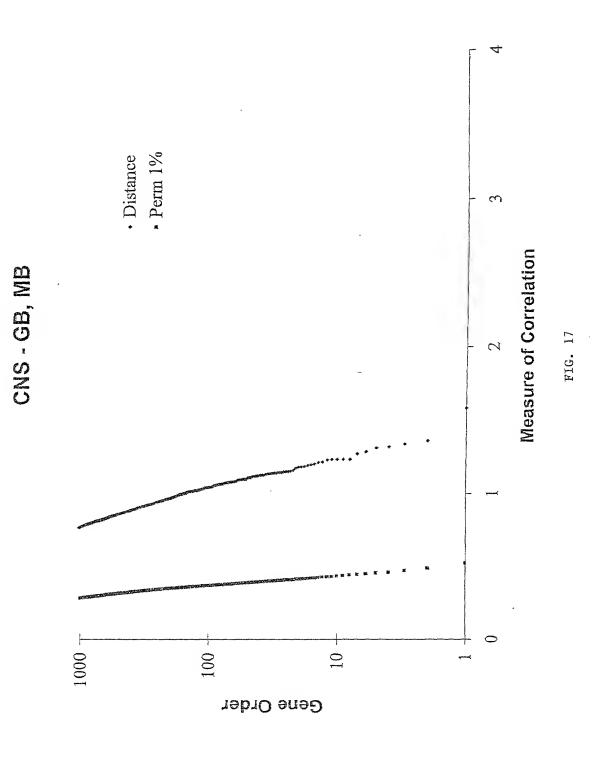
FIG. 14A



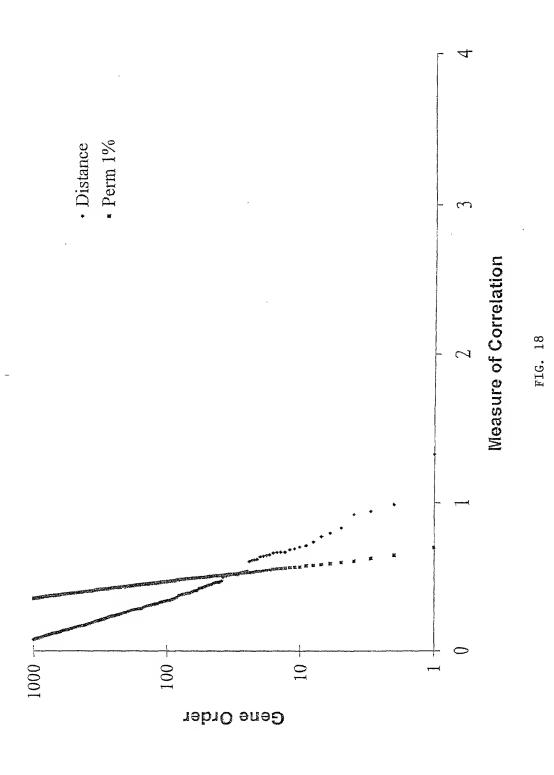
Breast Adenocarcinoma

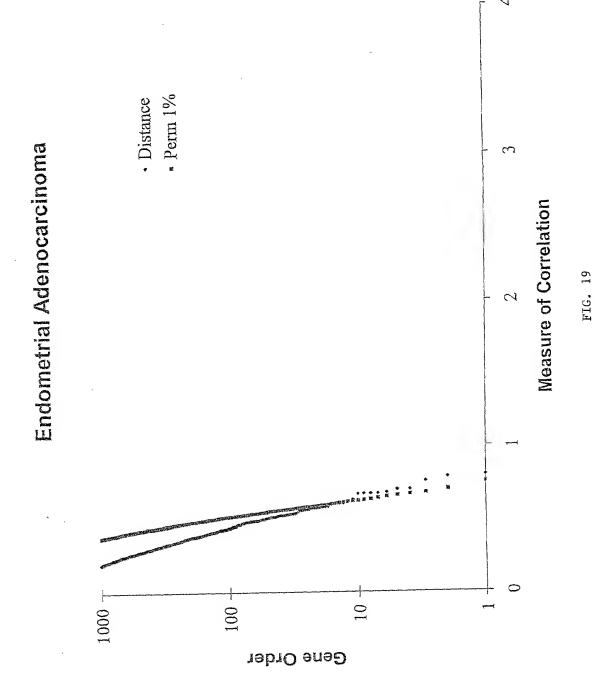
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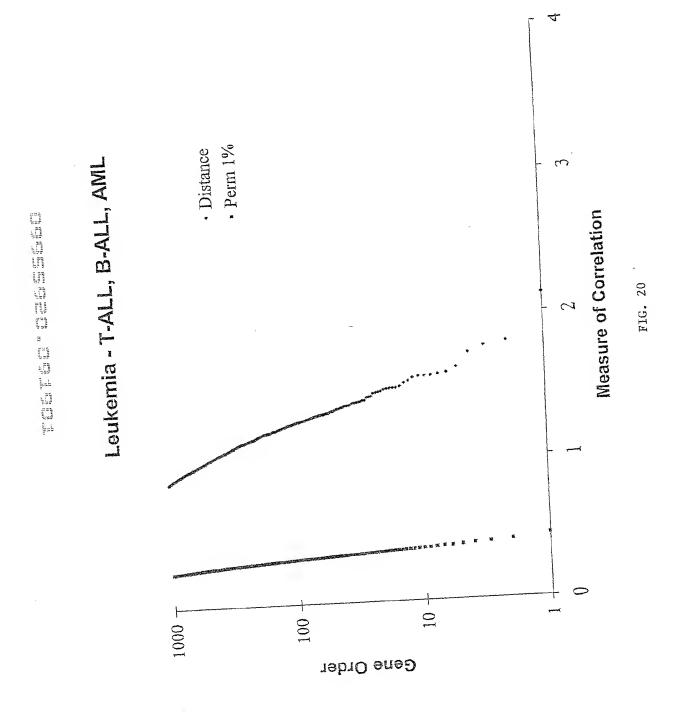


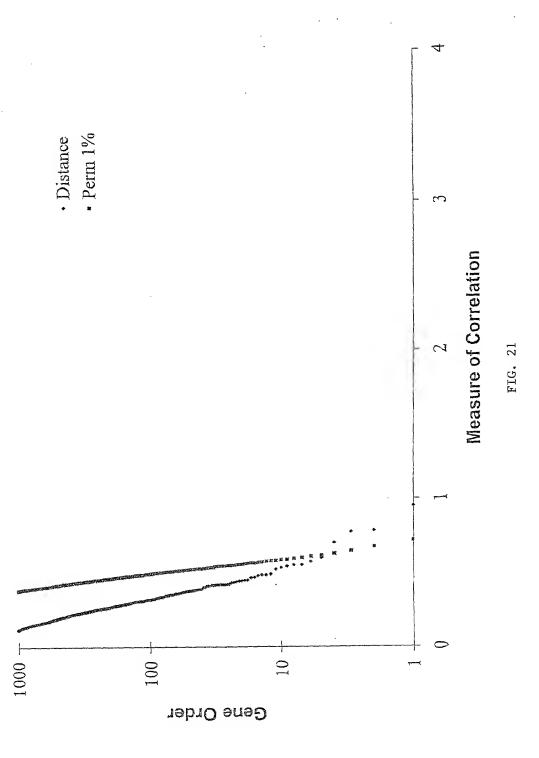


Colorectal Adenocarcinoma





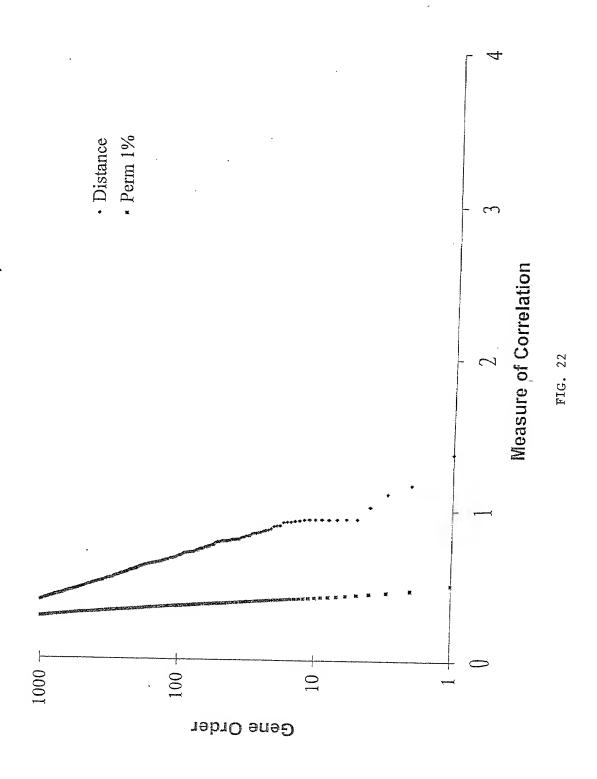


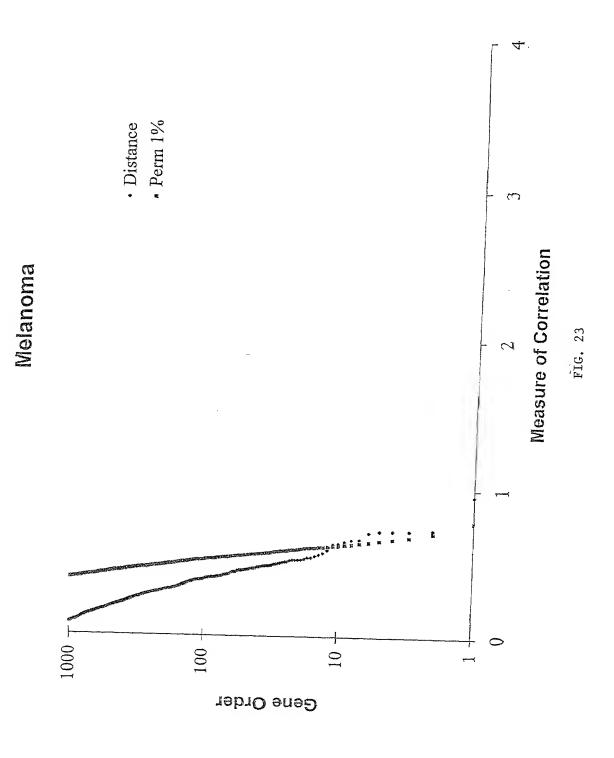


Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors

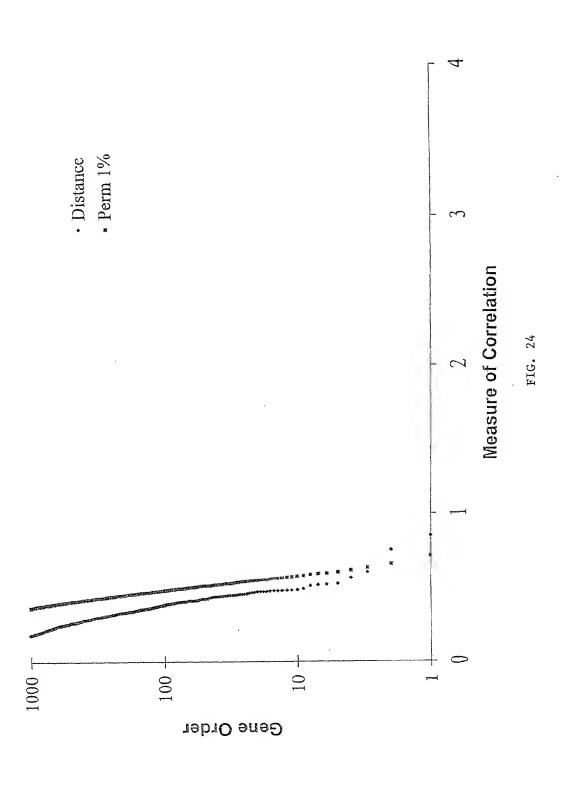
Inventors: Sridhar Ramaswamy, et al.







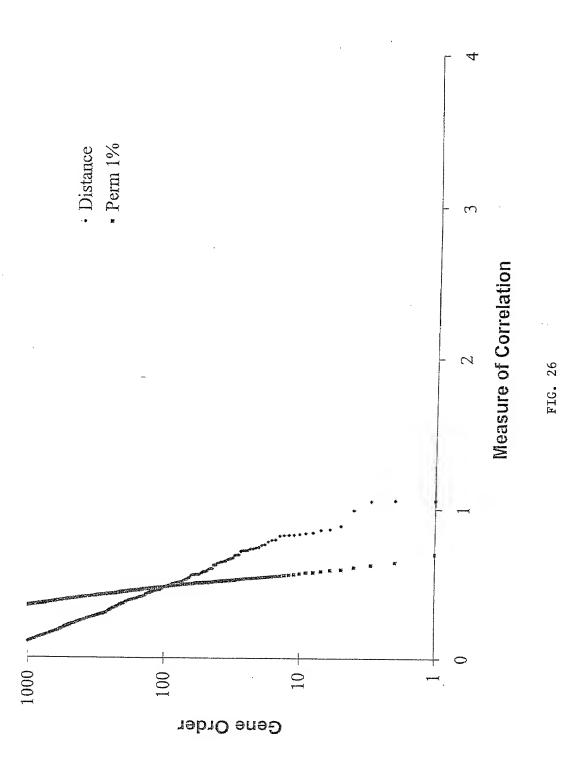
Ovarian Adenocarcinoma



* Perm 1% · Distance Pancreatic Adenocarcinoma Measure of Correlation FIG. 25 100 Gene Order

Pleural Mesothelioma

Docket No.: 2825.2020-002 Title: Genetic Markers for Tumors Inventors: Sridhar Ramaswamy, *et al.*



Prostatic Adenocarcinoma

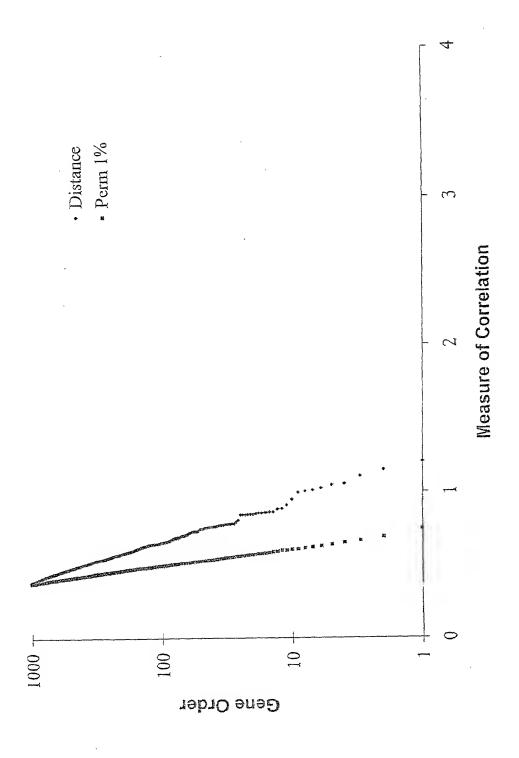


FIG. 27